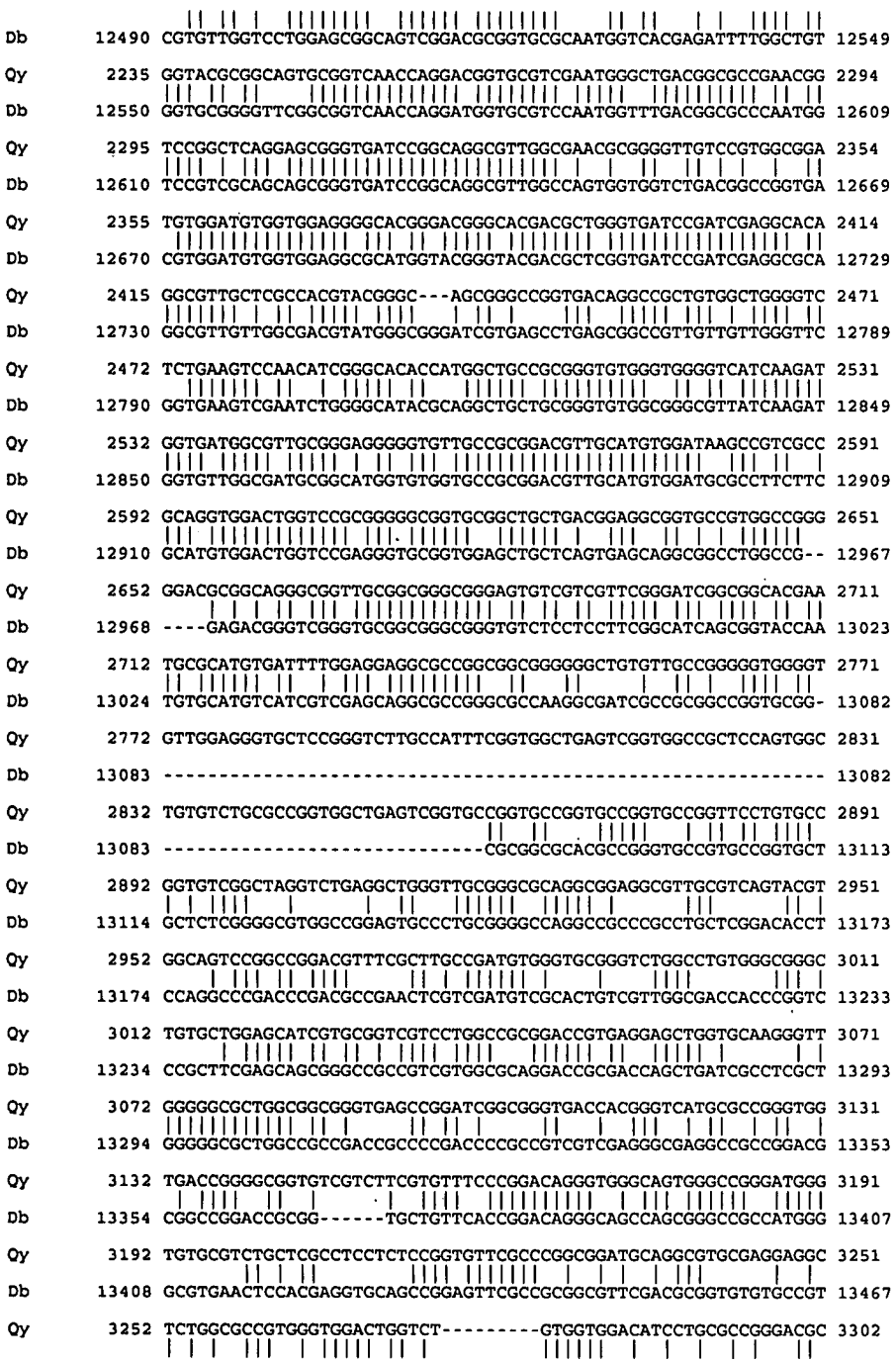

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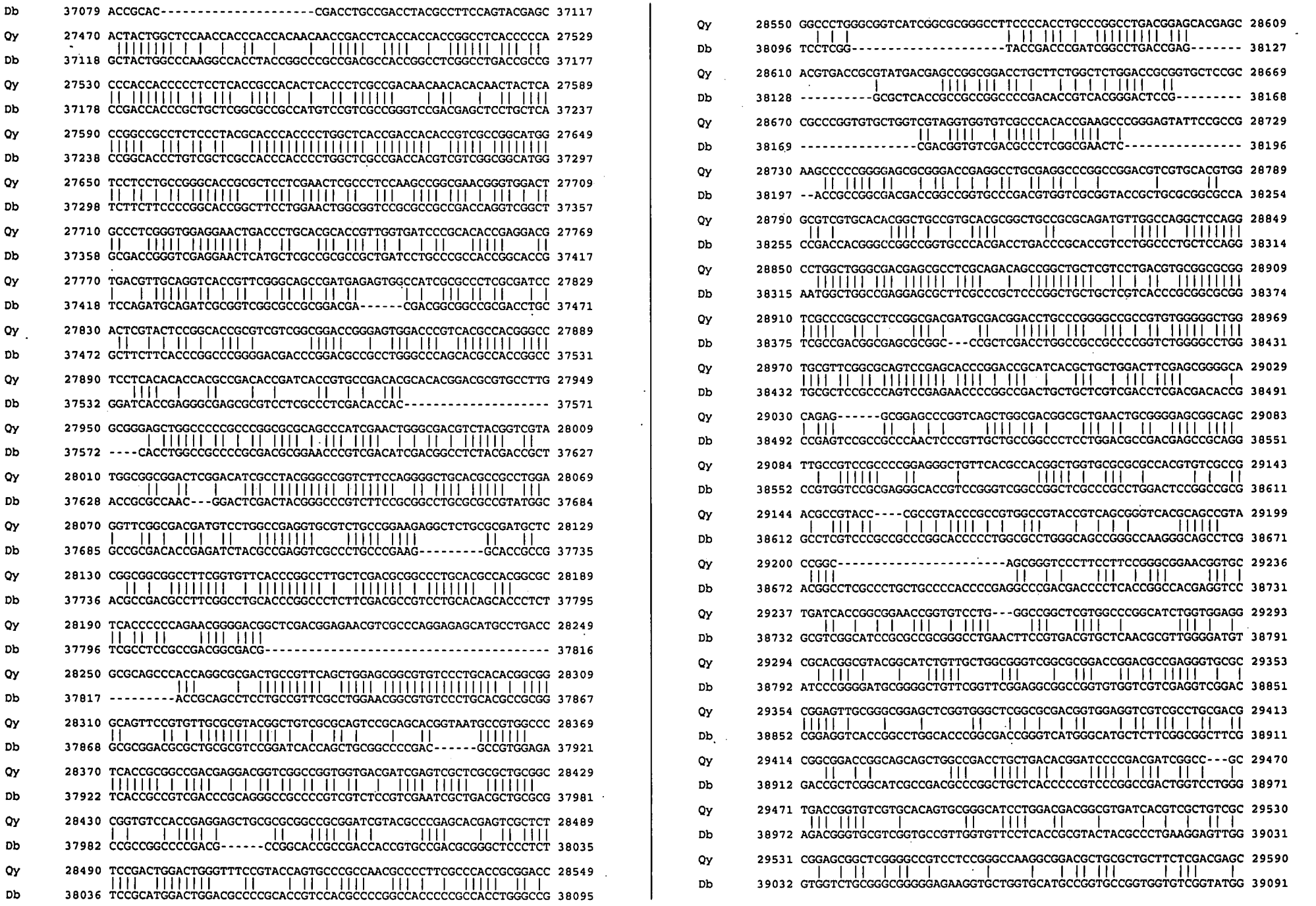
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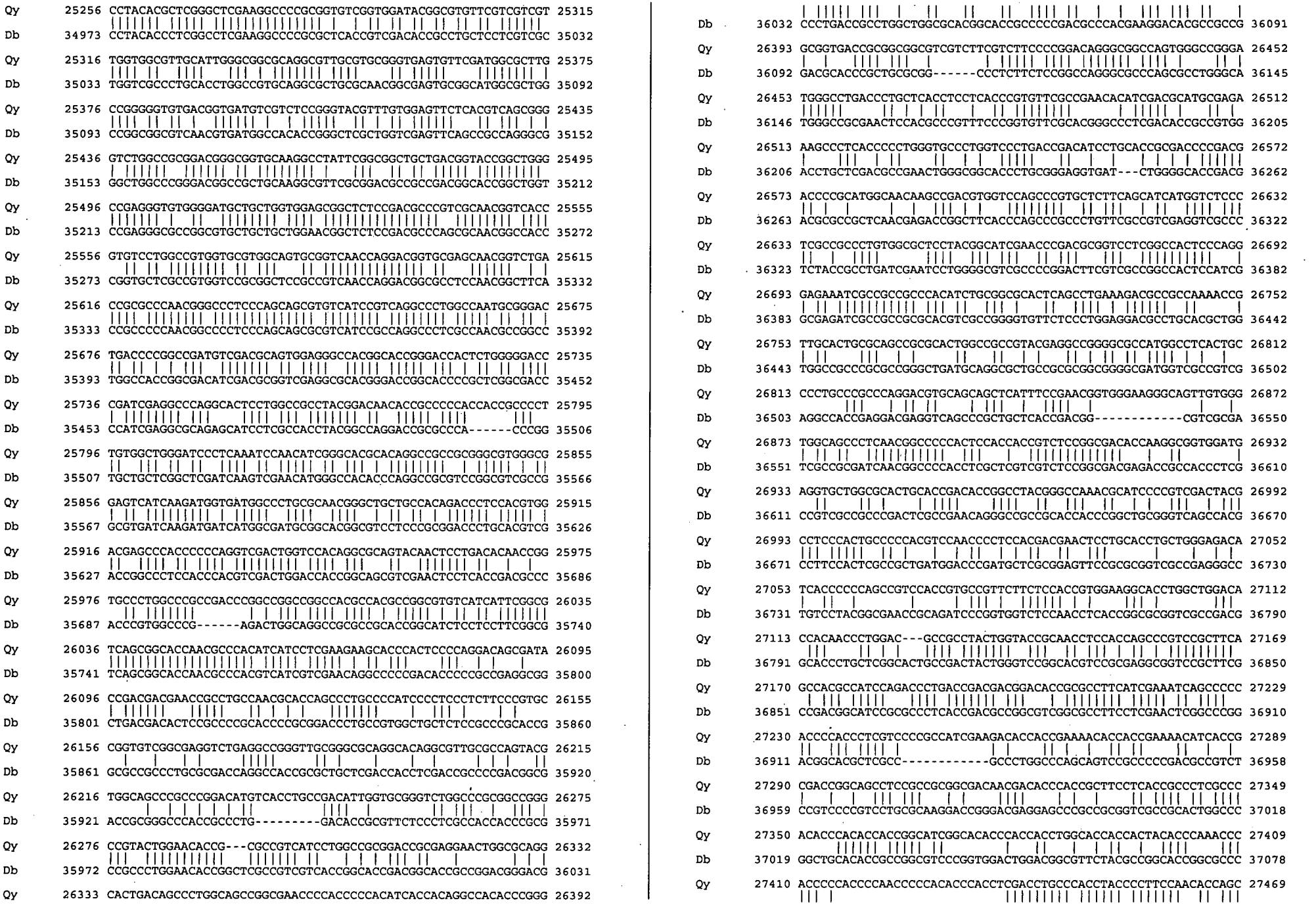
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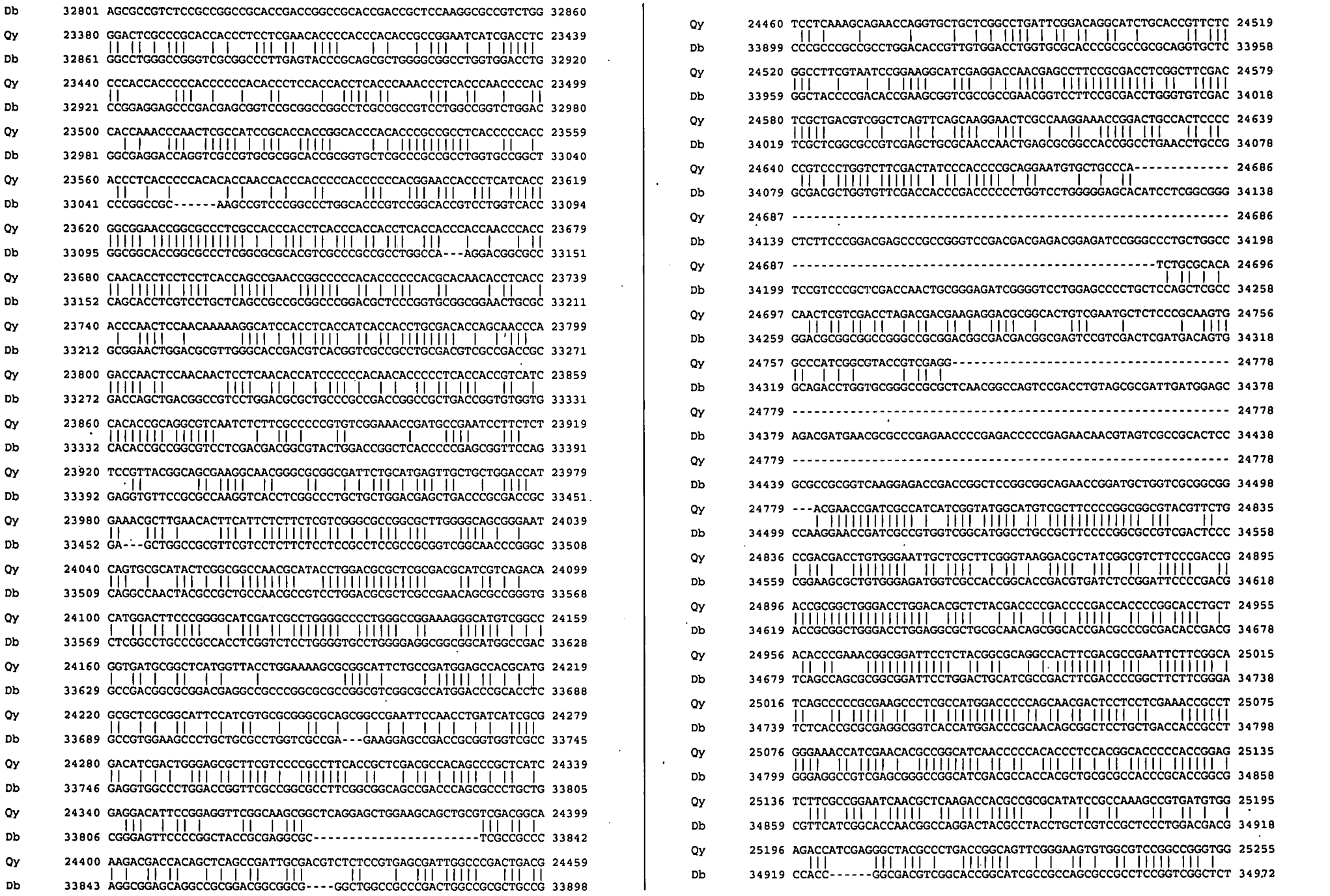
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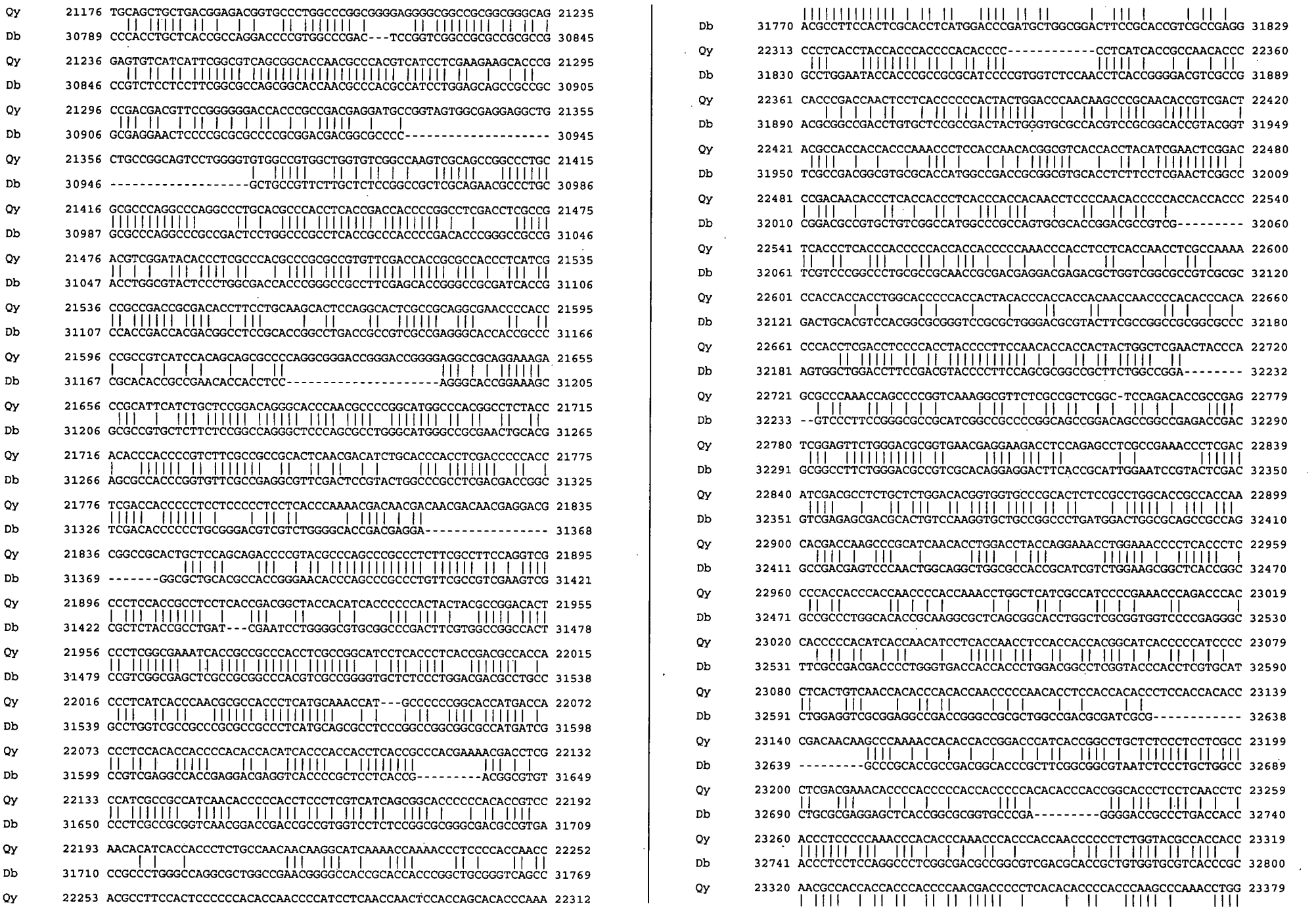
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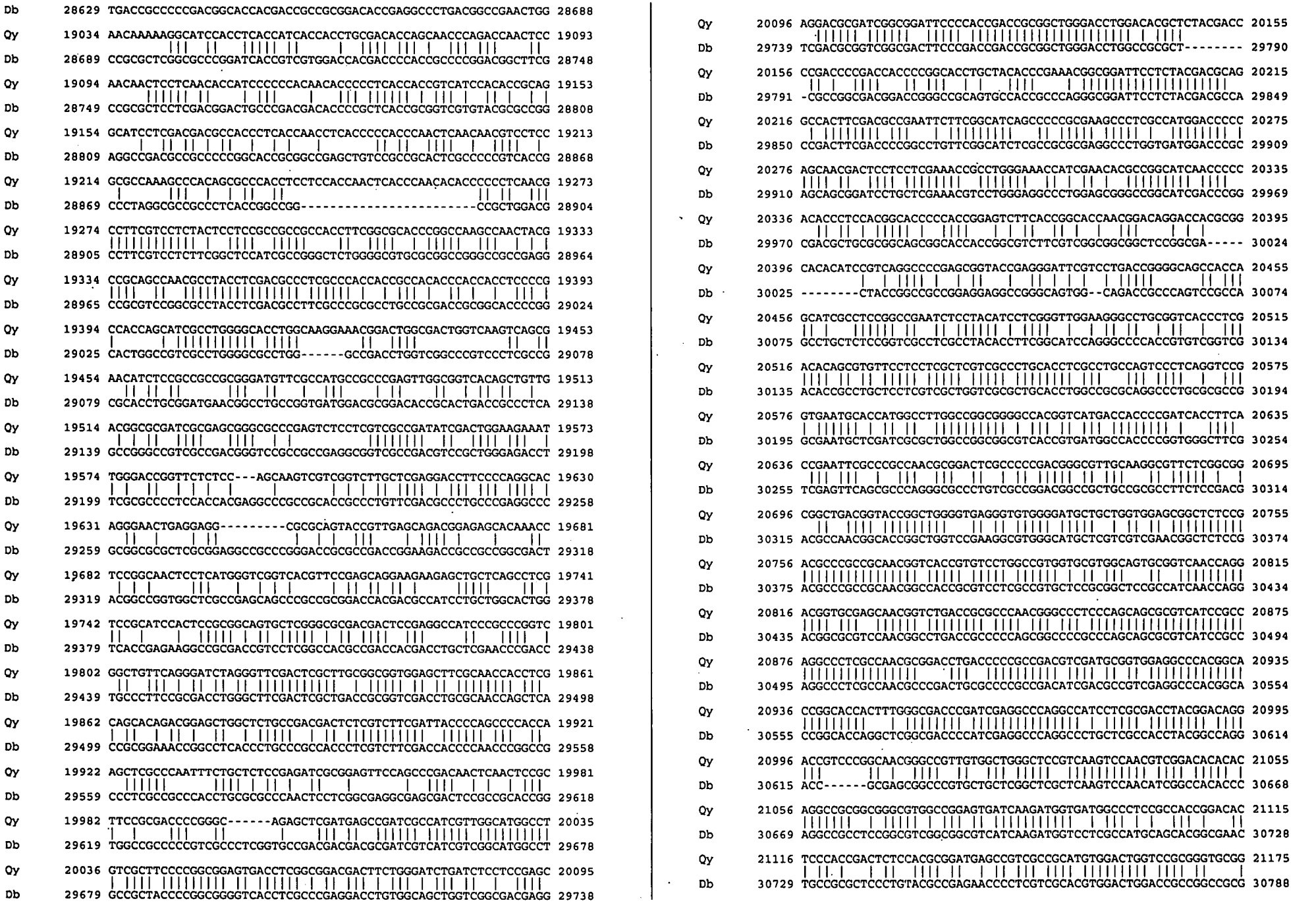
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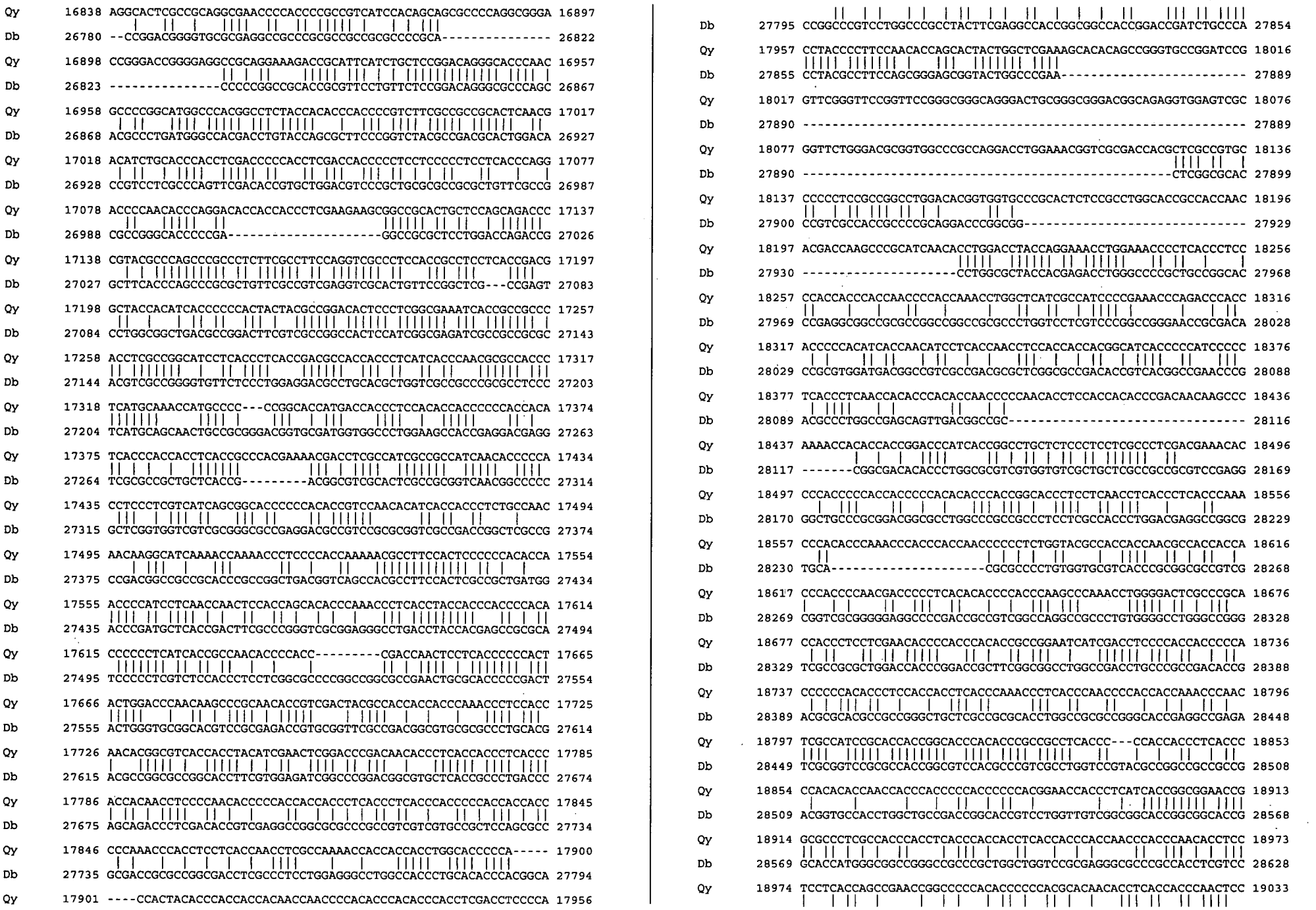


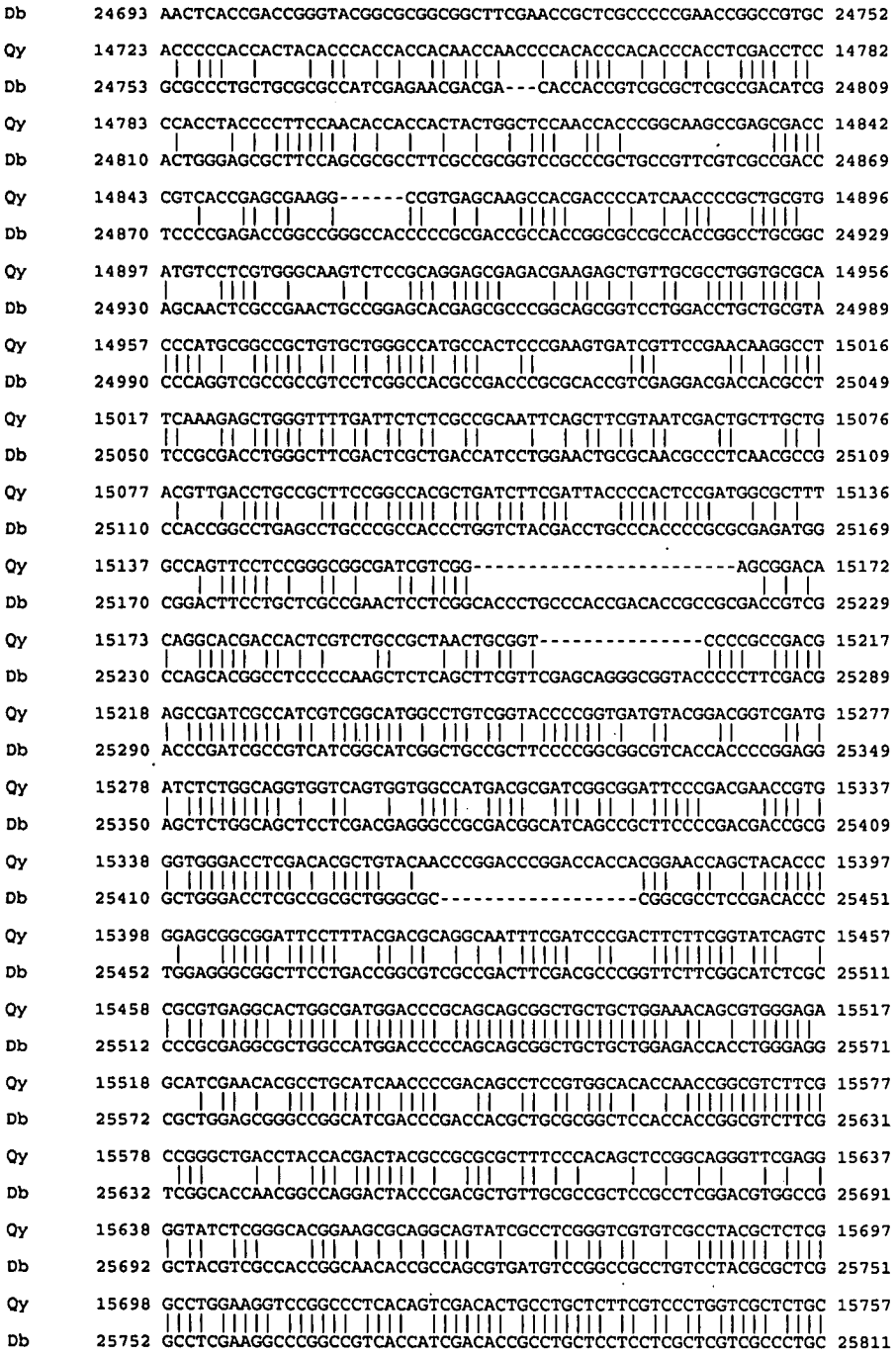


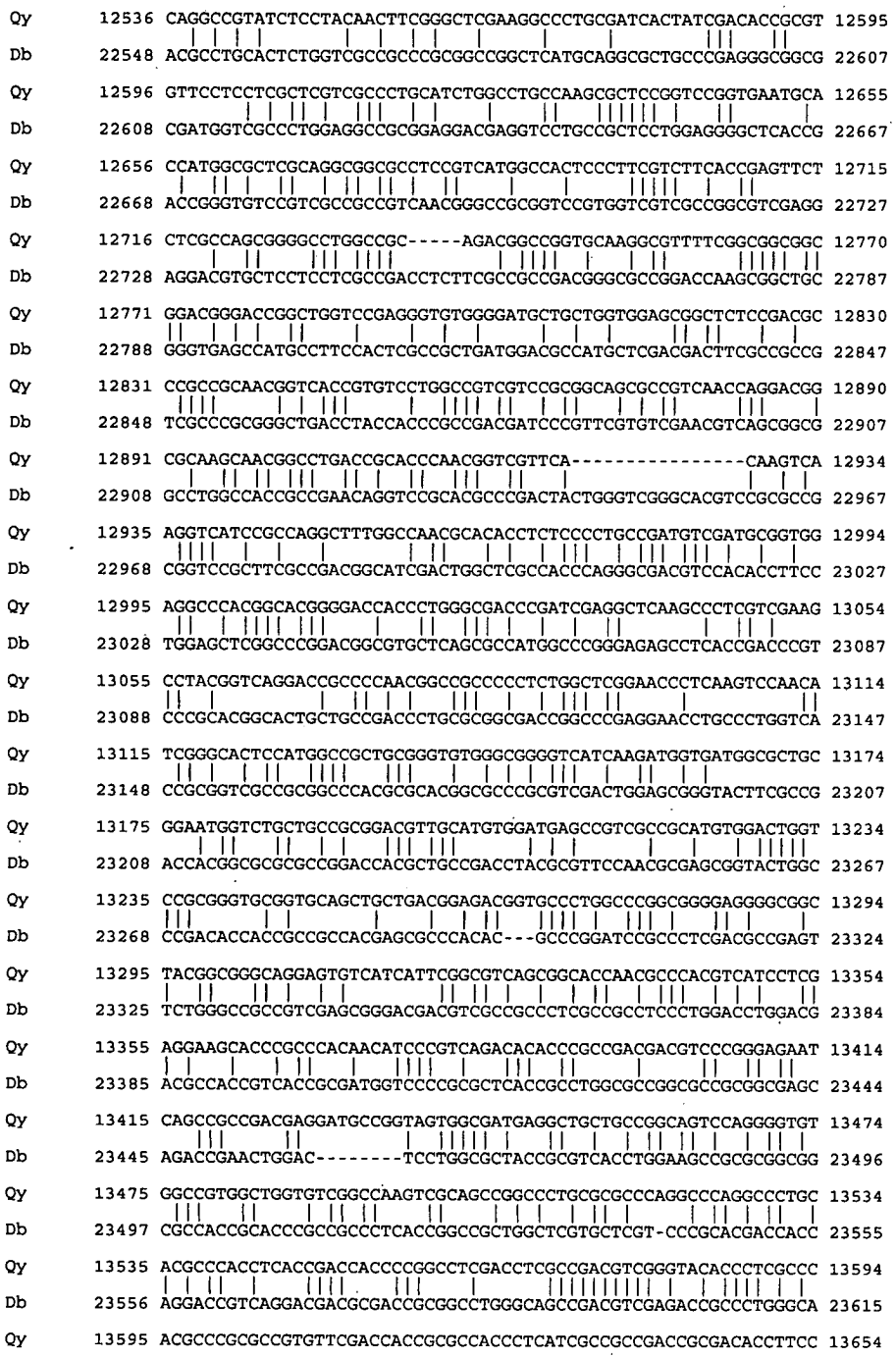


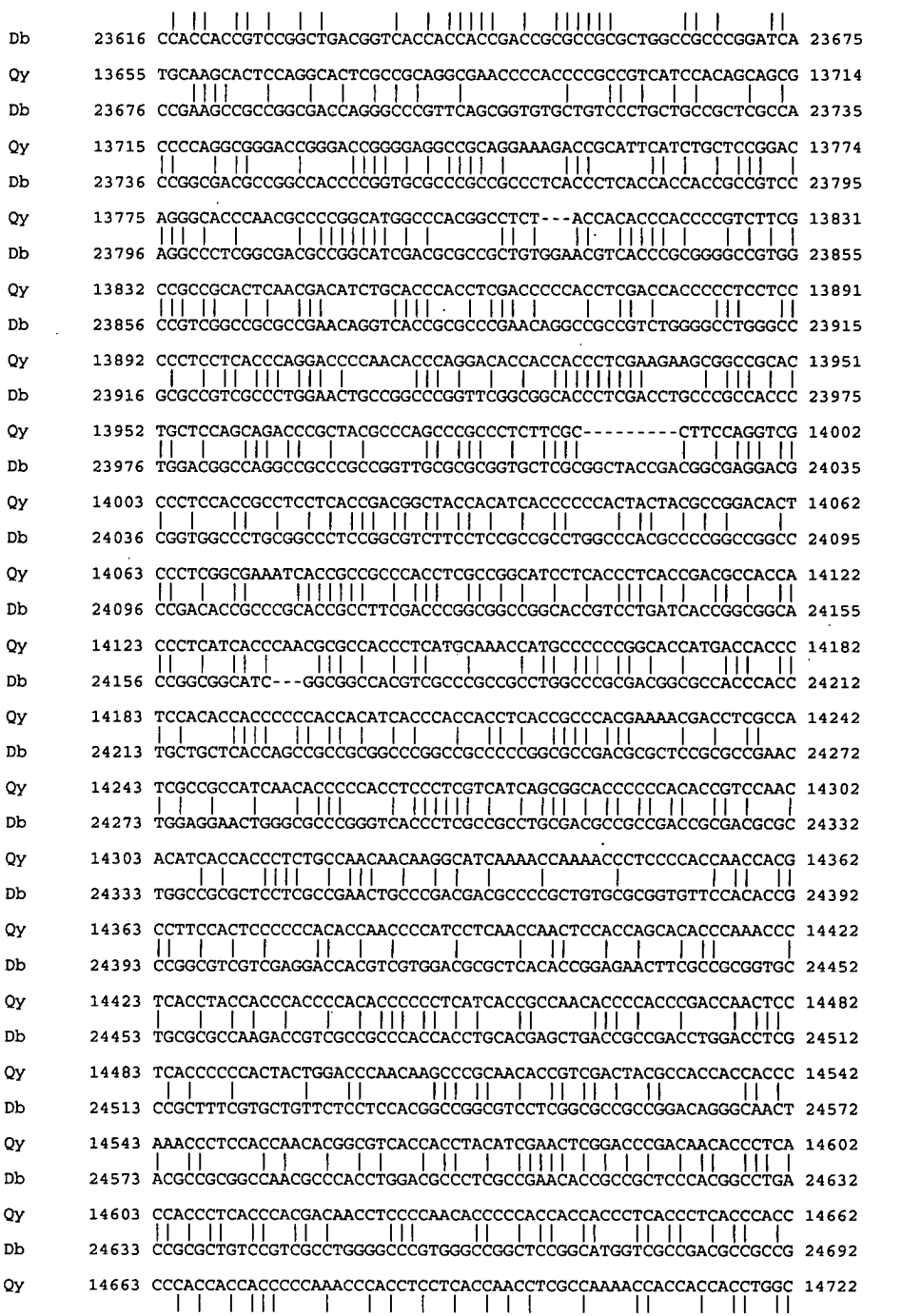


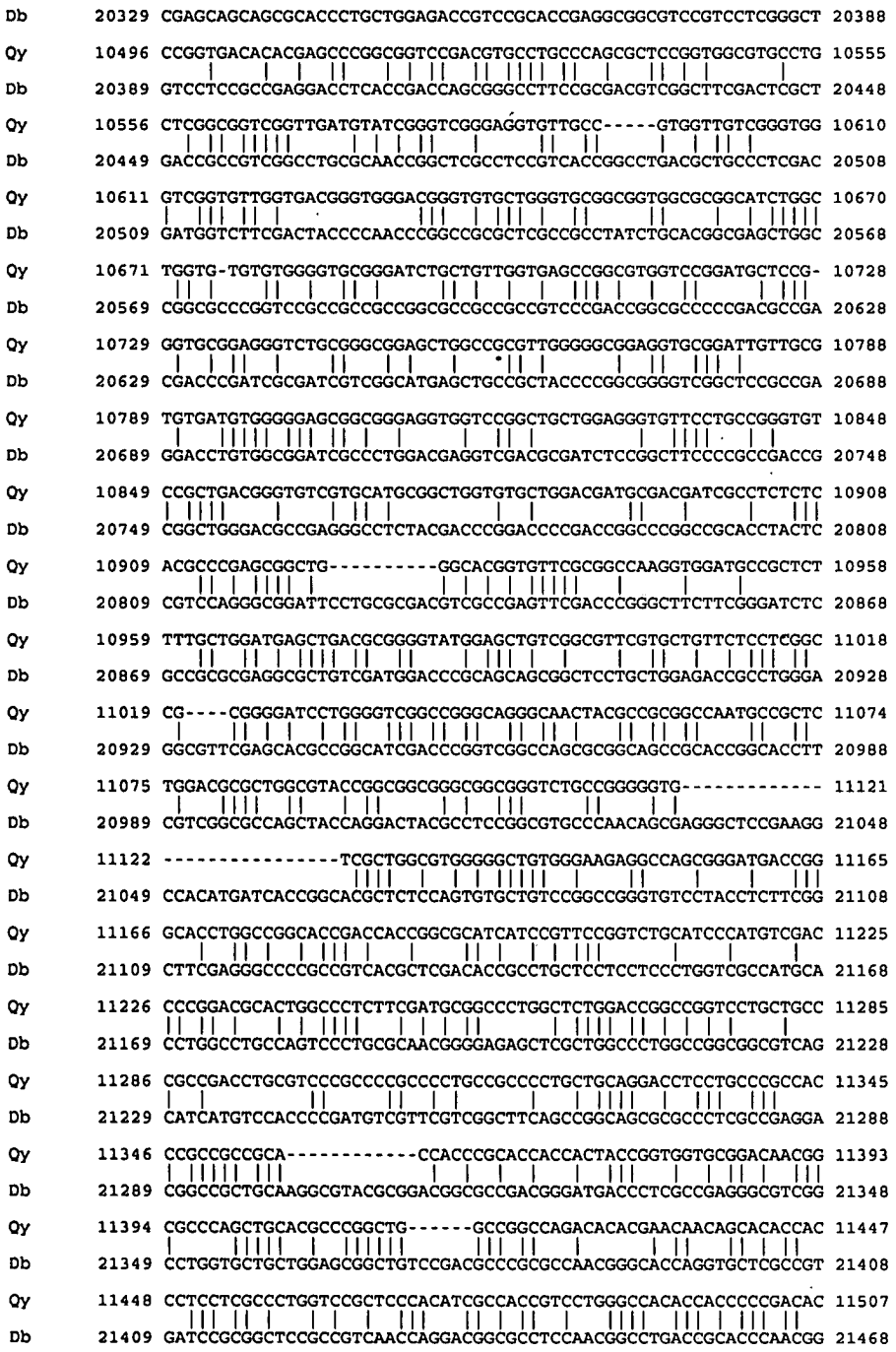


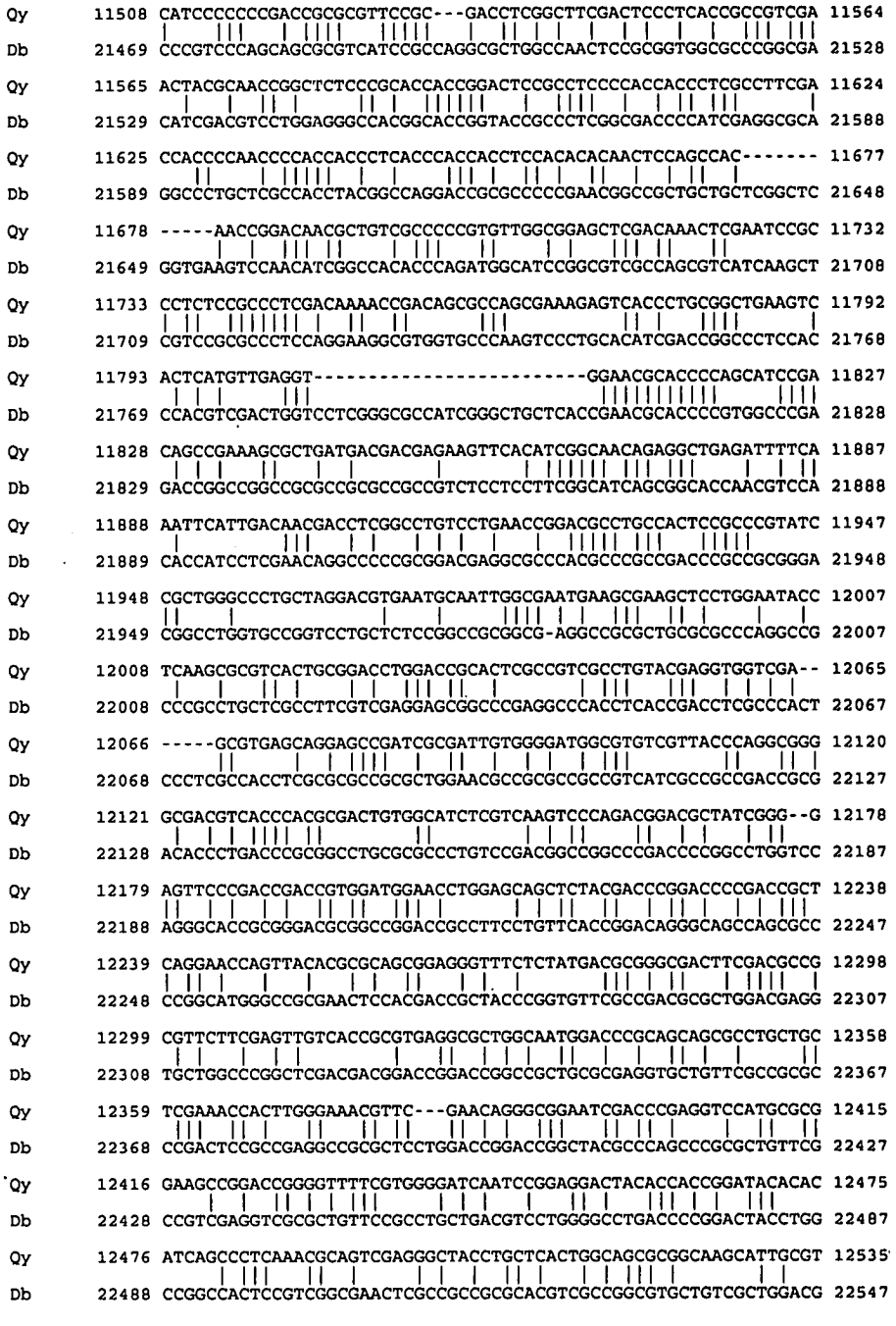


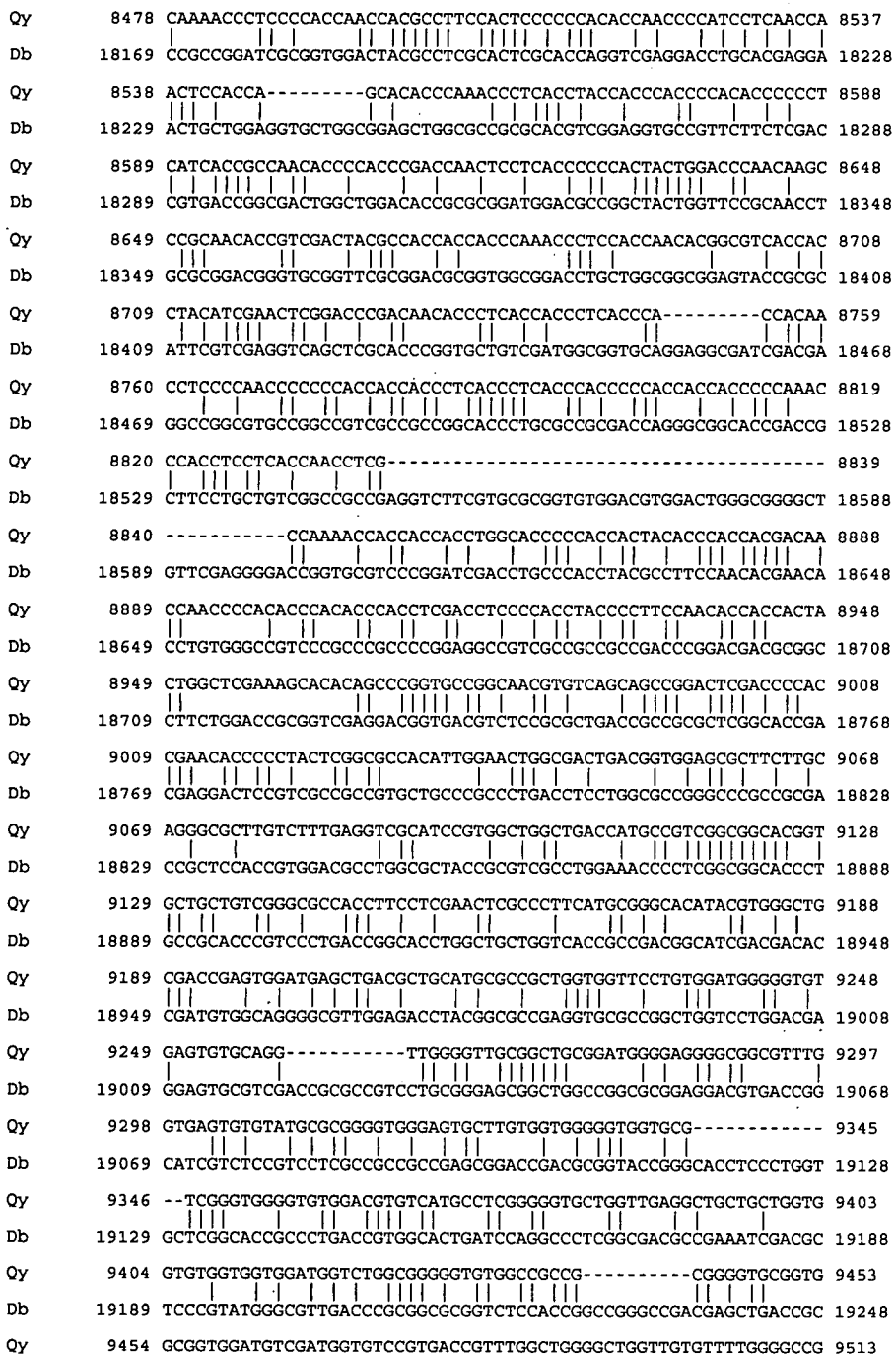

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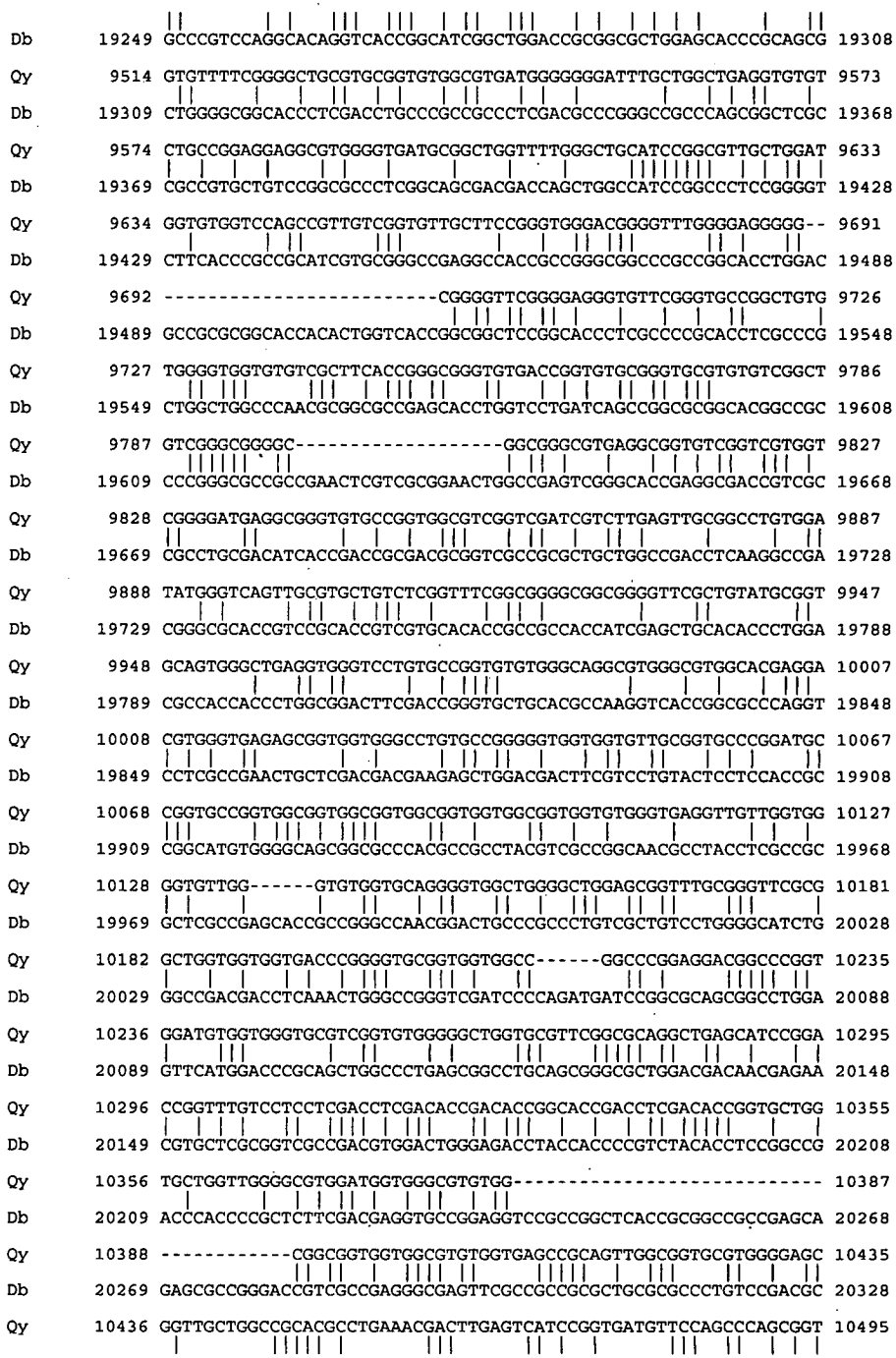

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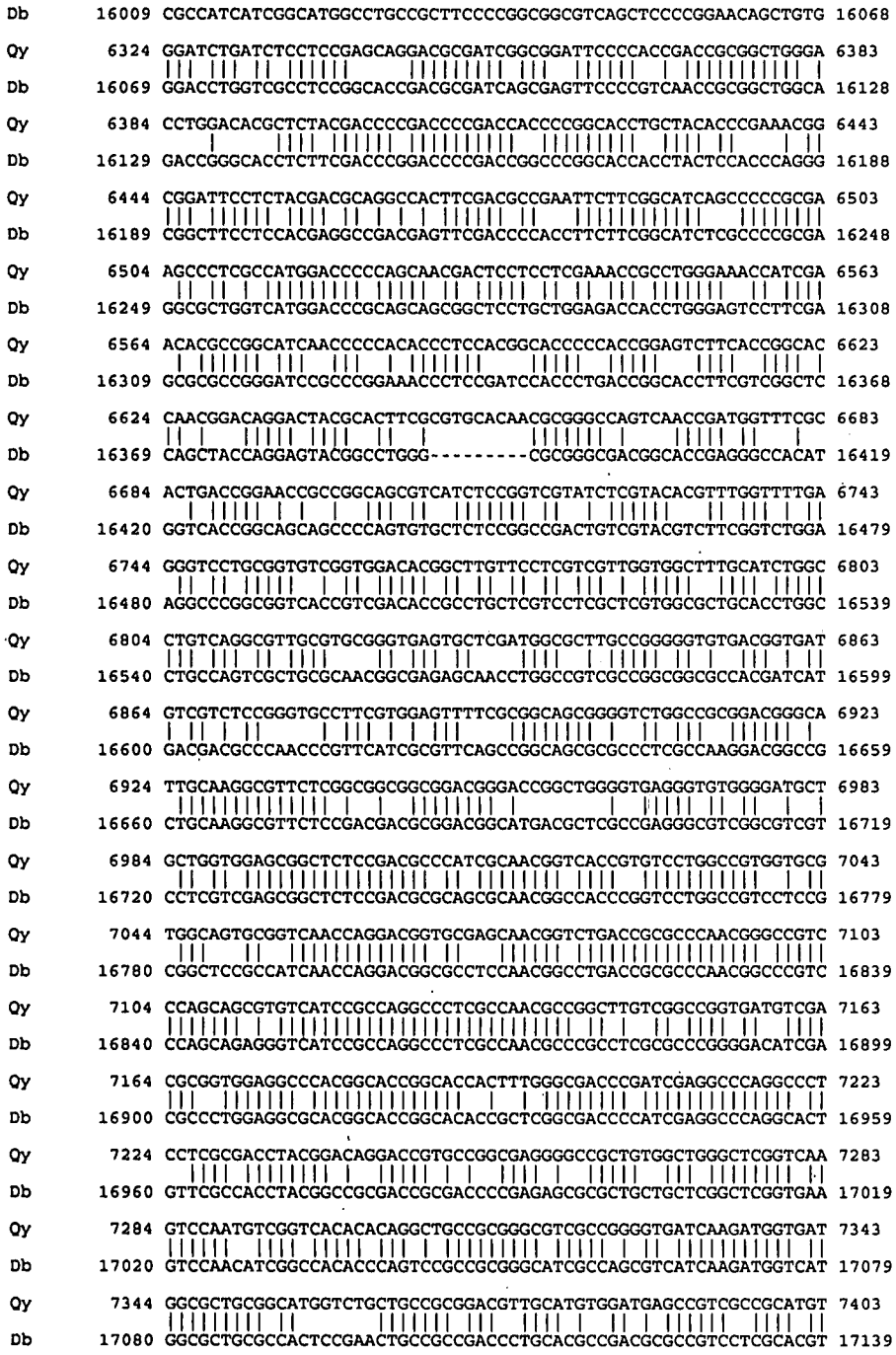

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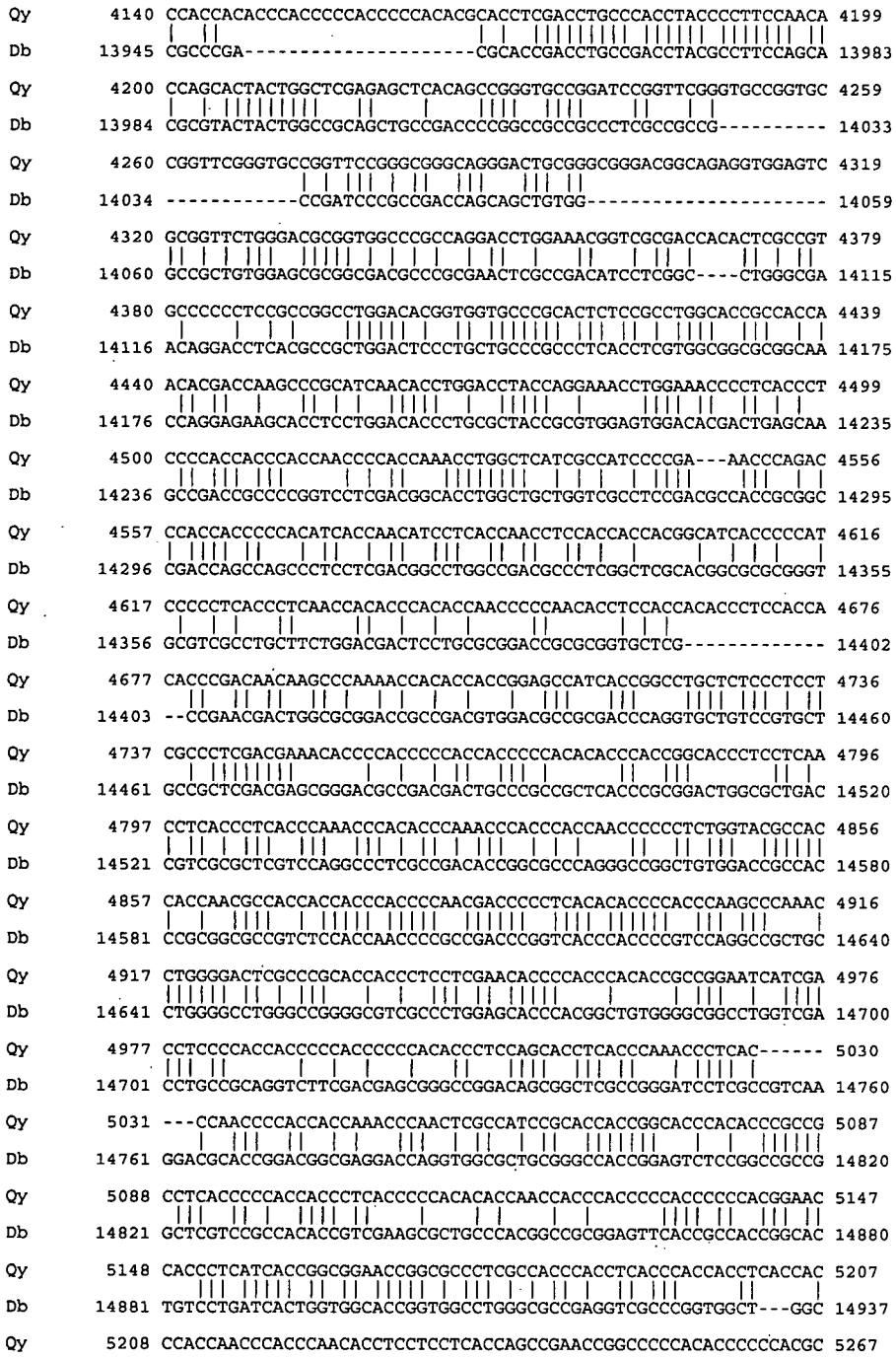

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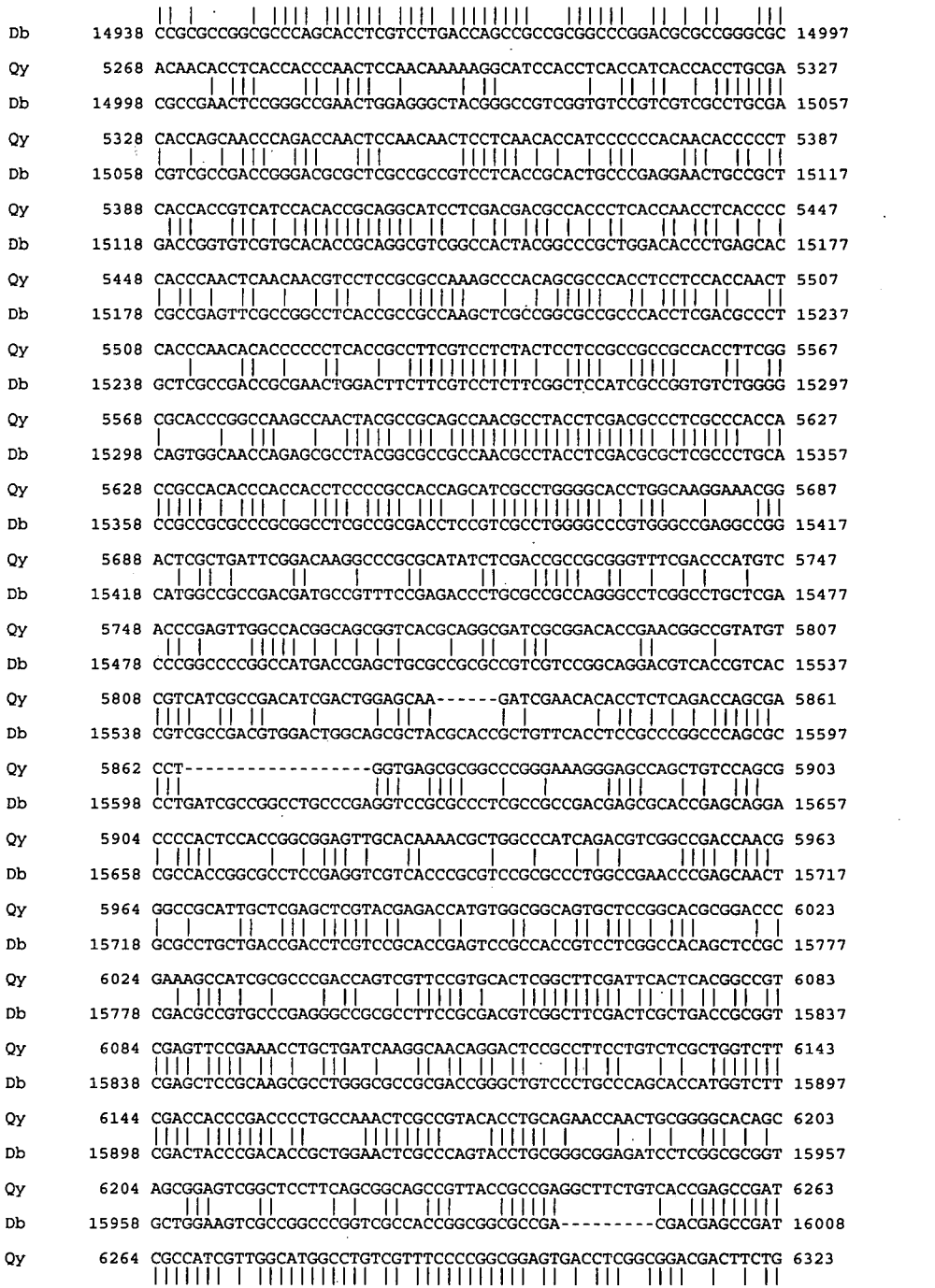

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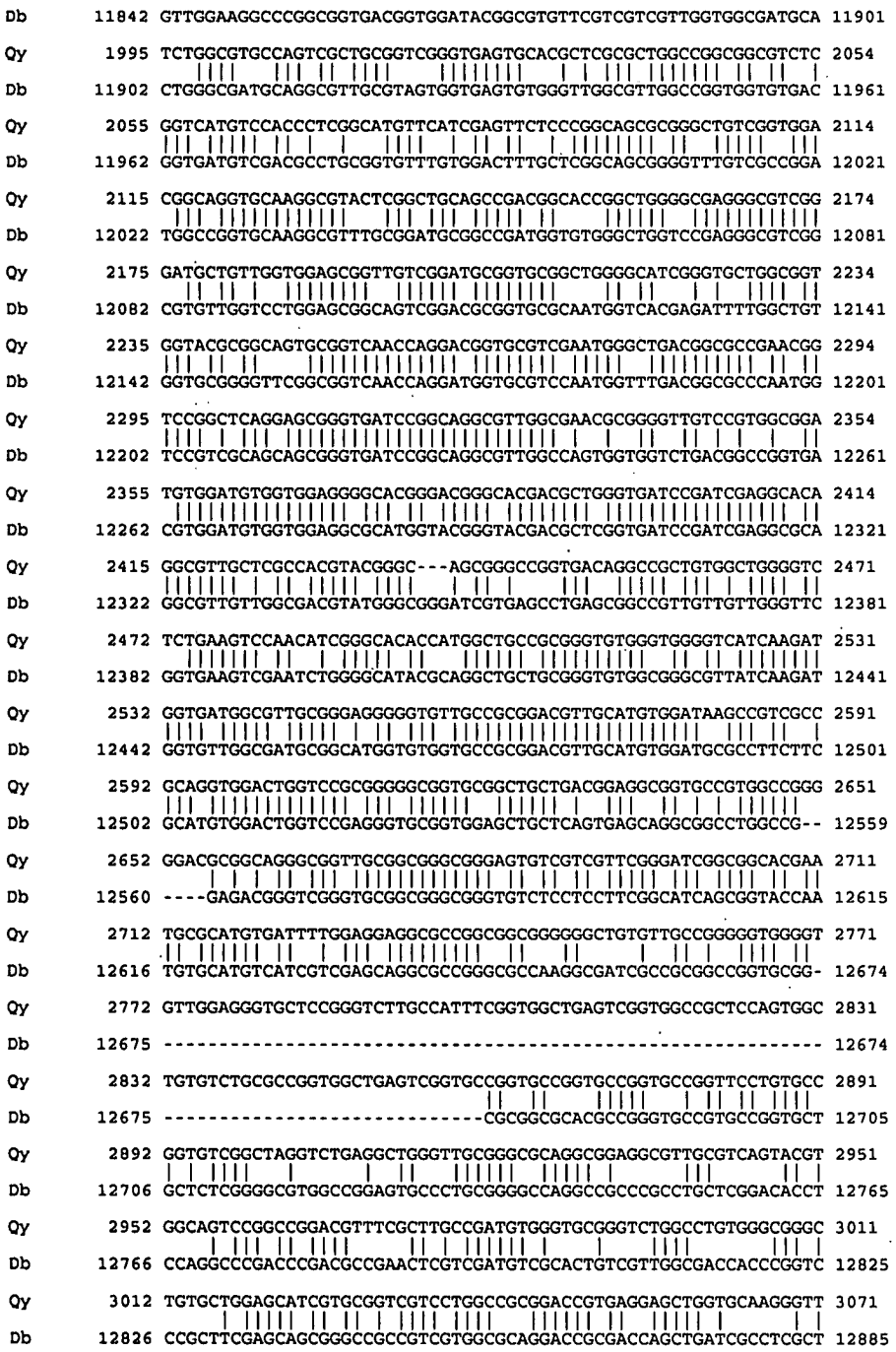





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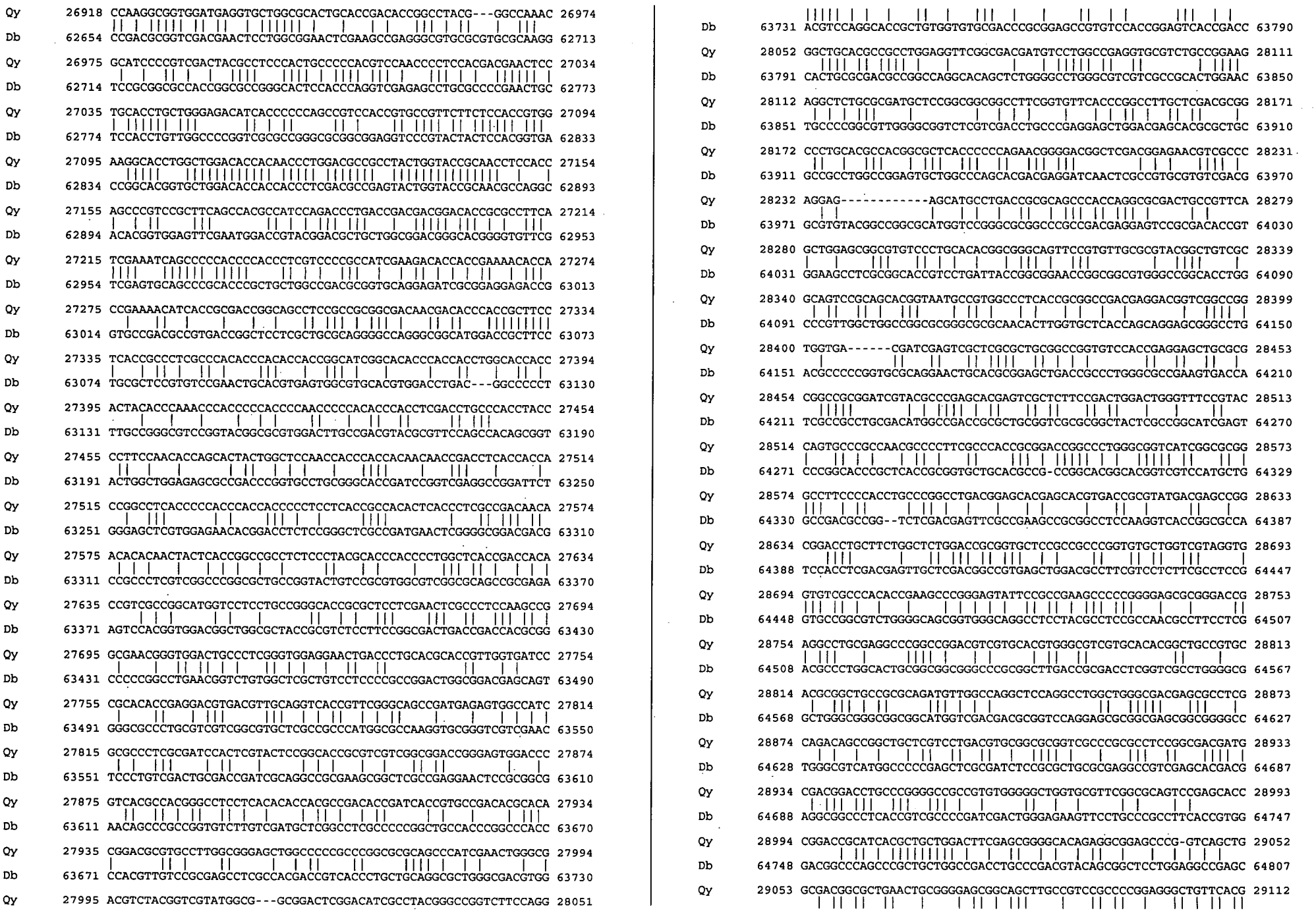
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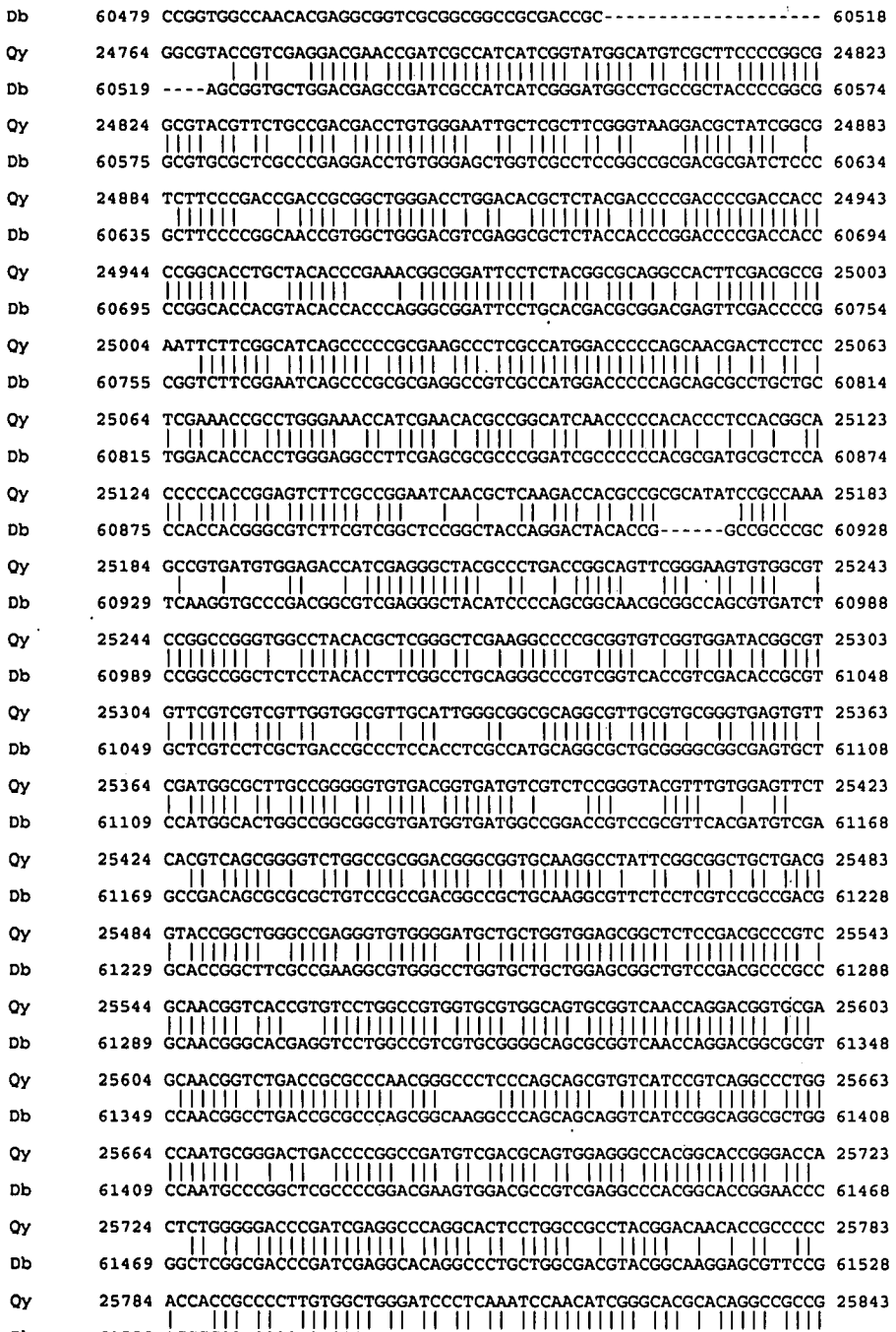
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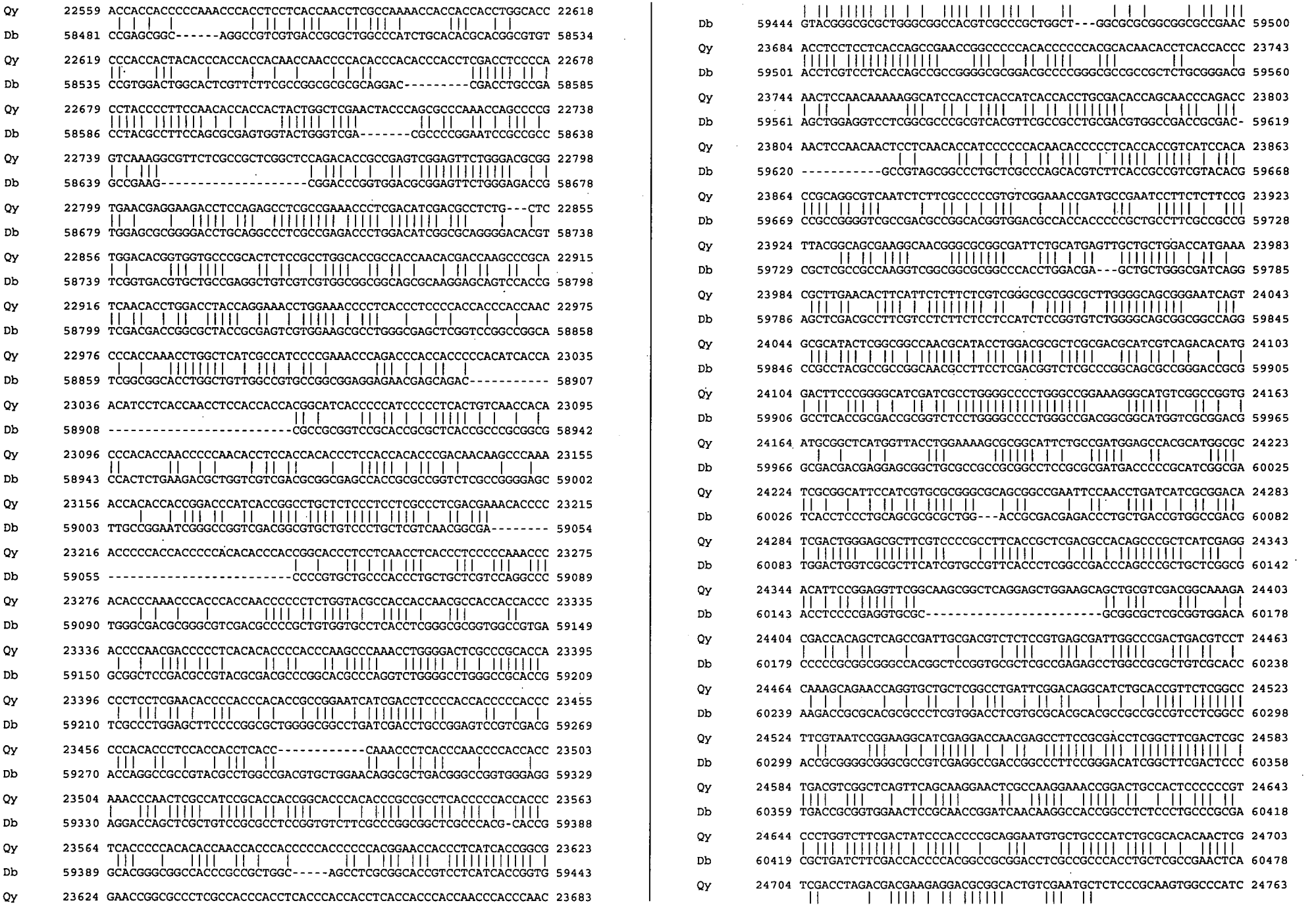
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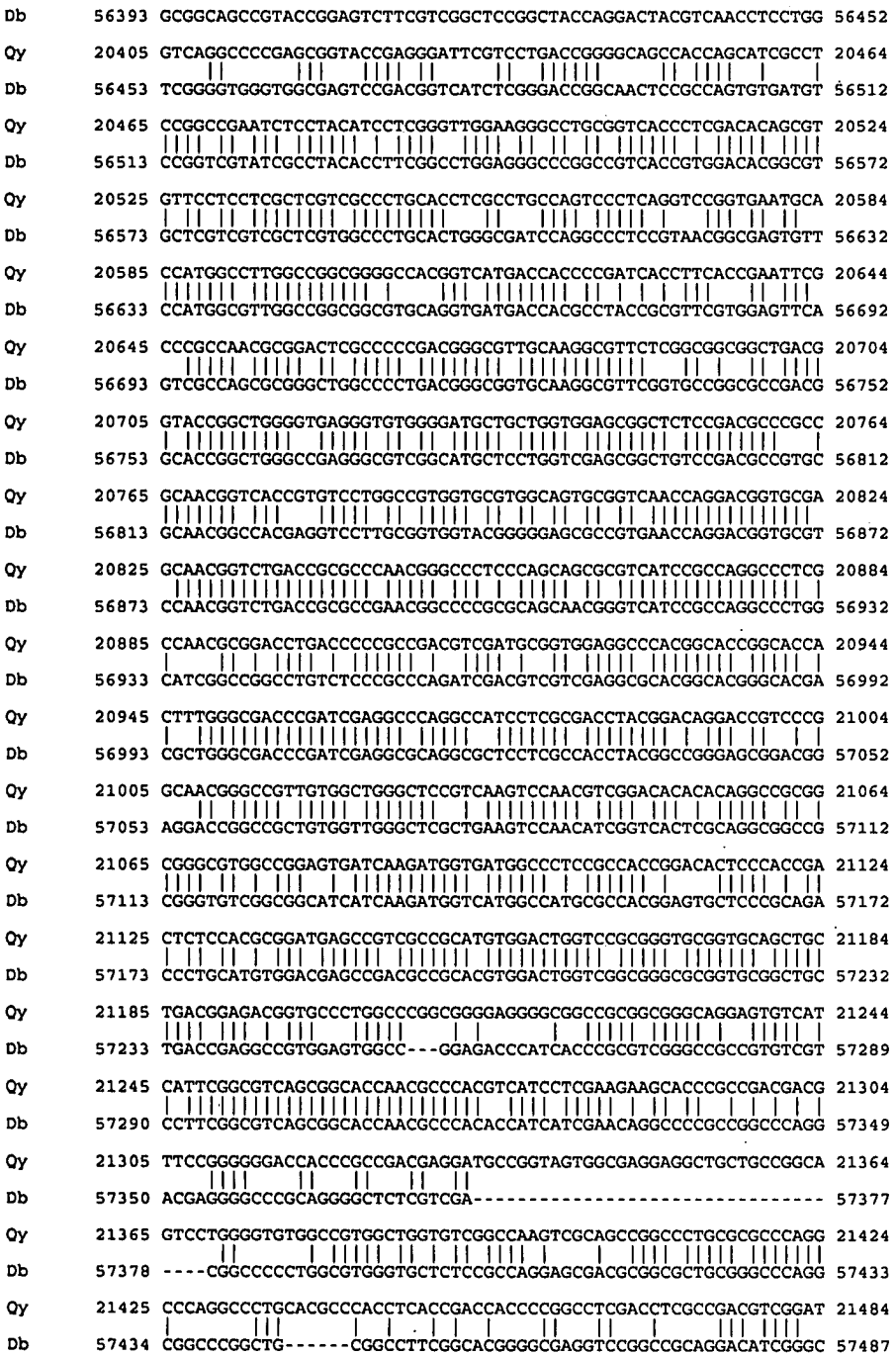
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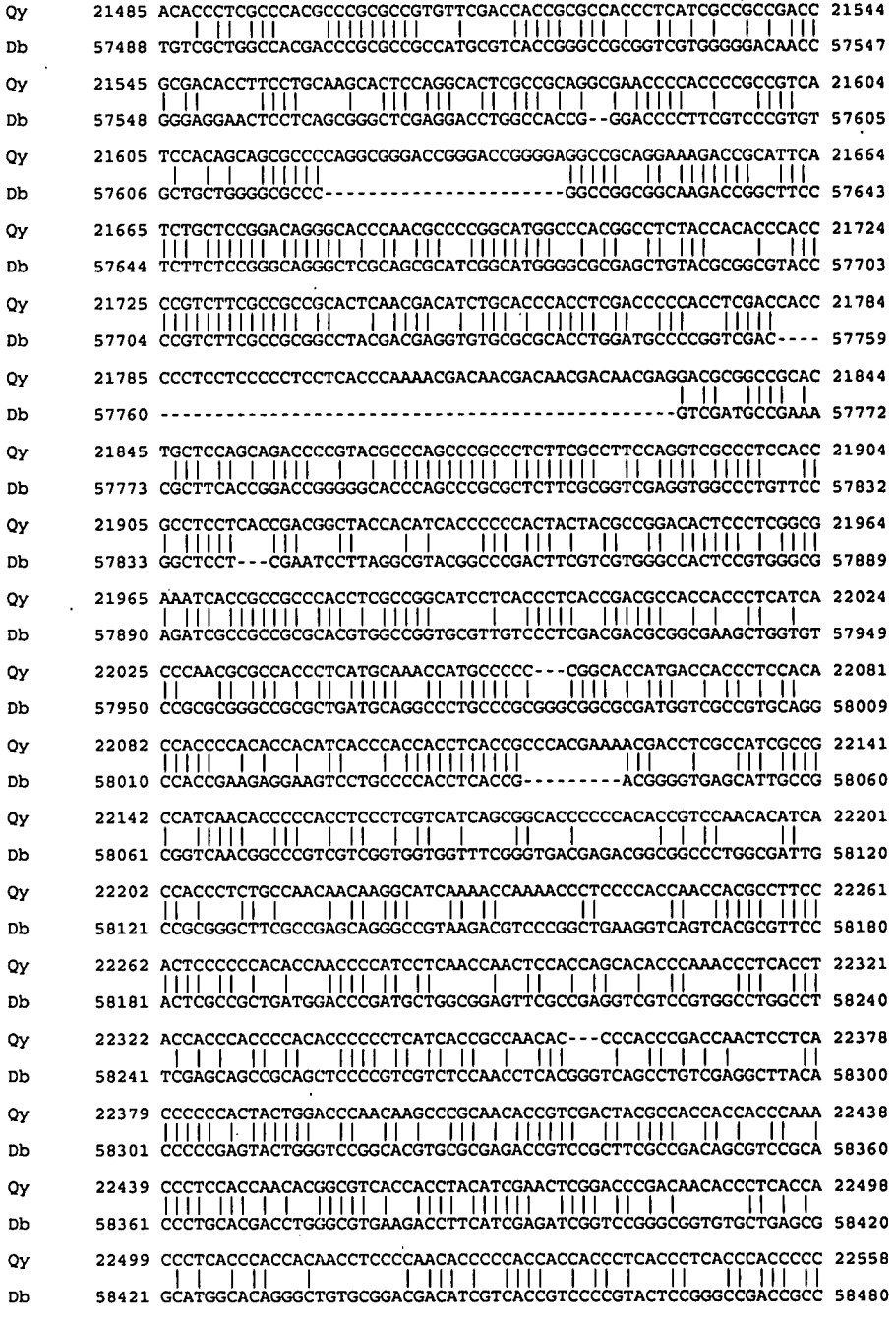

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DEFINITION  Streptomyces noursei ATCC 11455 nystatin biosynthetic gene cluster,
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VERSION     AF263912.1  GI:8050835
KEYWORDS    .
SOURCE      Streptomyces noursei.
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REFERENCE   1  (bases 1 to 123580)
  AUTHORS   Brautaset,T., Sekurova,O.N., Sletta,H., Ellingsen,T.E., StrLm,A.R.,
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  TITLE     Biosynthesis of the polyene antifungal antibiotic nystatin in
            Streptomyces noursei ATCC 11455: analysis of the gene cluster and
            deduction of the biosynthetic pathway
  JOURNAL   Chem. Biol. 7 (6), 395-403 (2000)
  MEDLINE   20334850
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  AUTHORS   Brautaset,T., Sekurova,O.N., Sletta,H., Ellingsen,T.E., Strom,A.R.,
            Valla,S. and Zotchev,S.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAY-2000) Unigen, NTNU, O. Kyrres gt. 3, Trondheim
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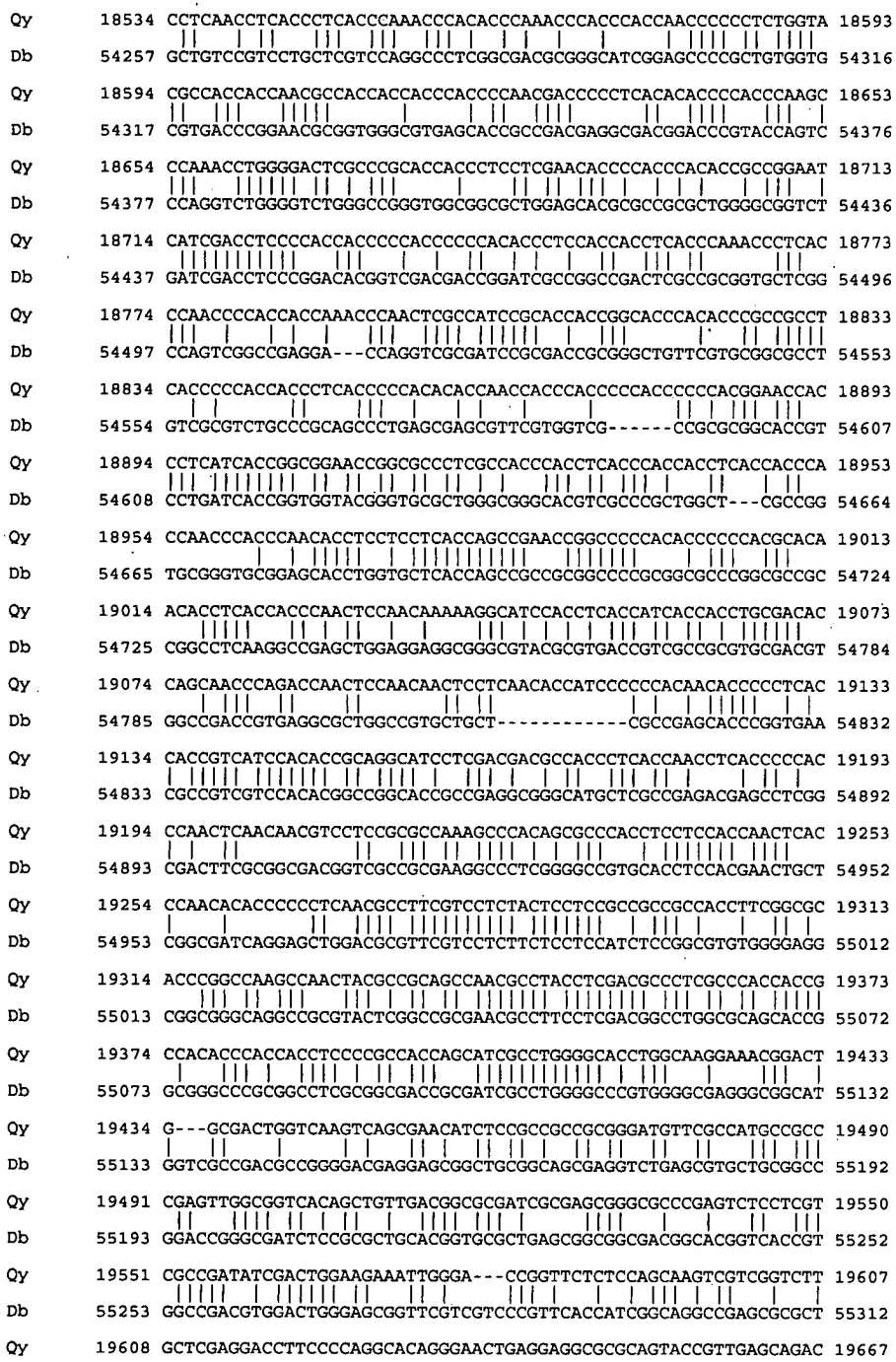


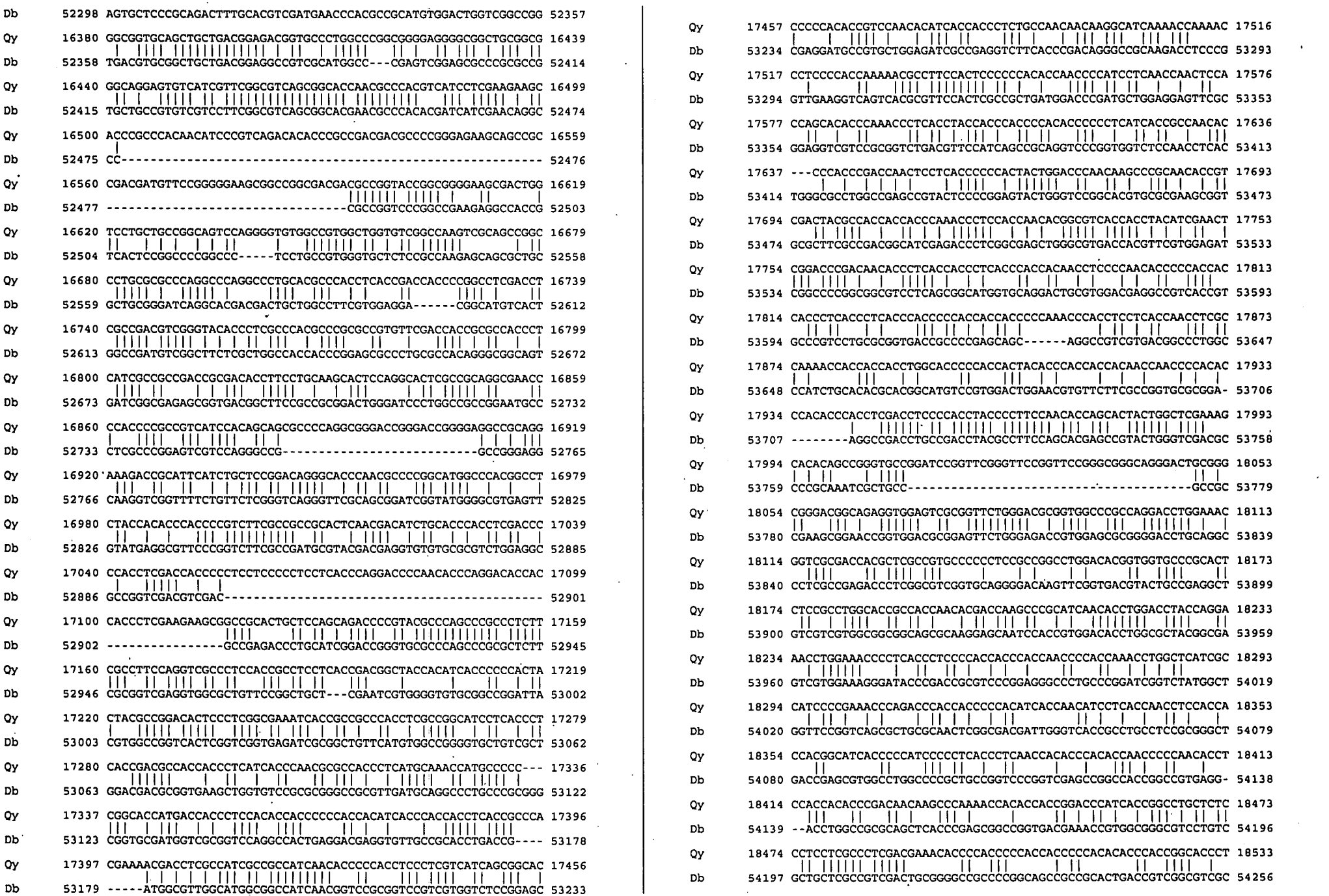

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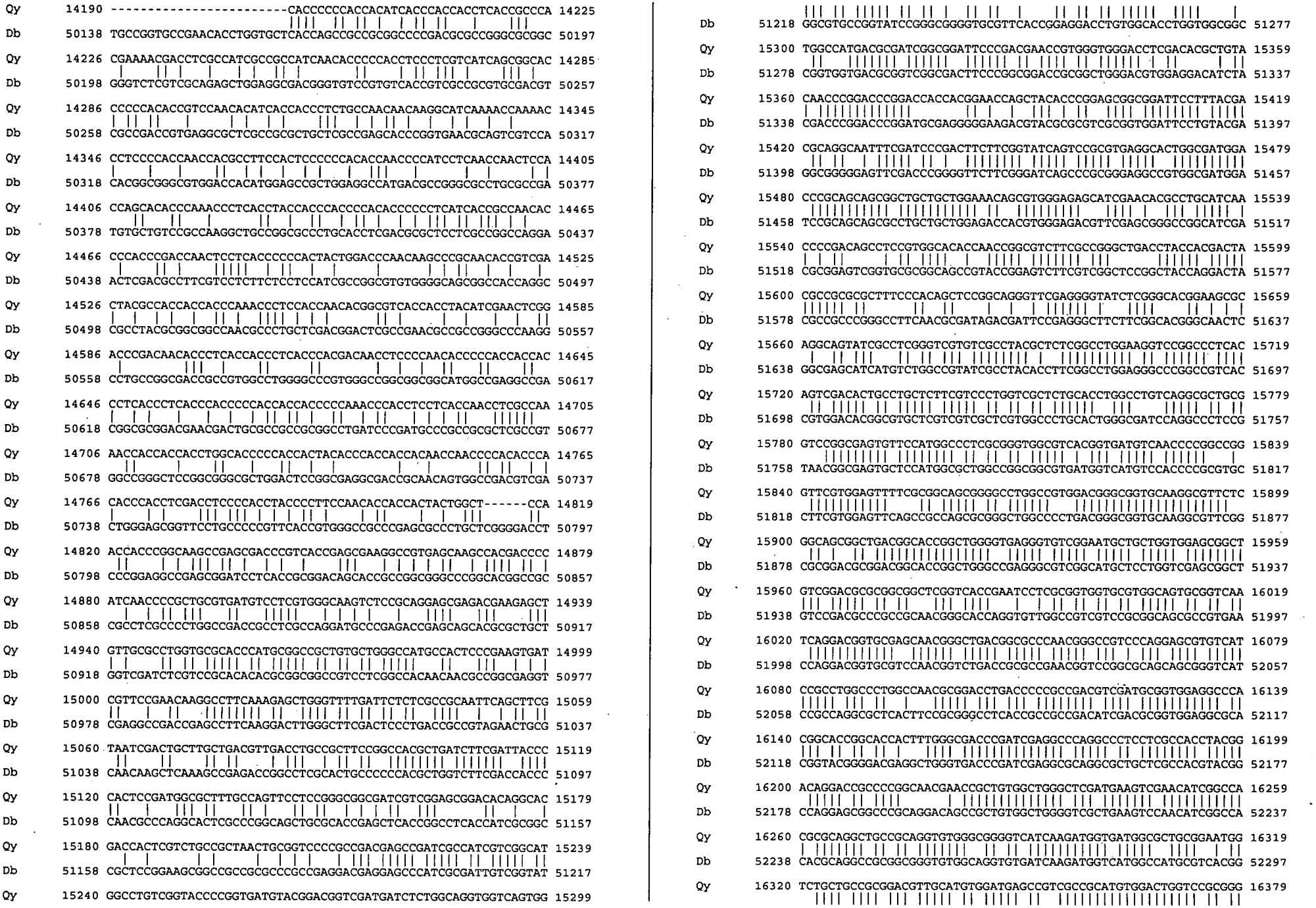


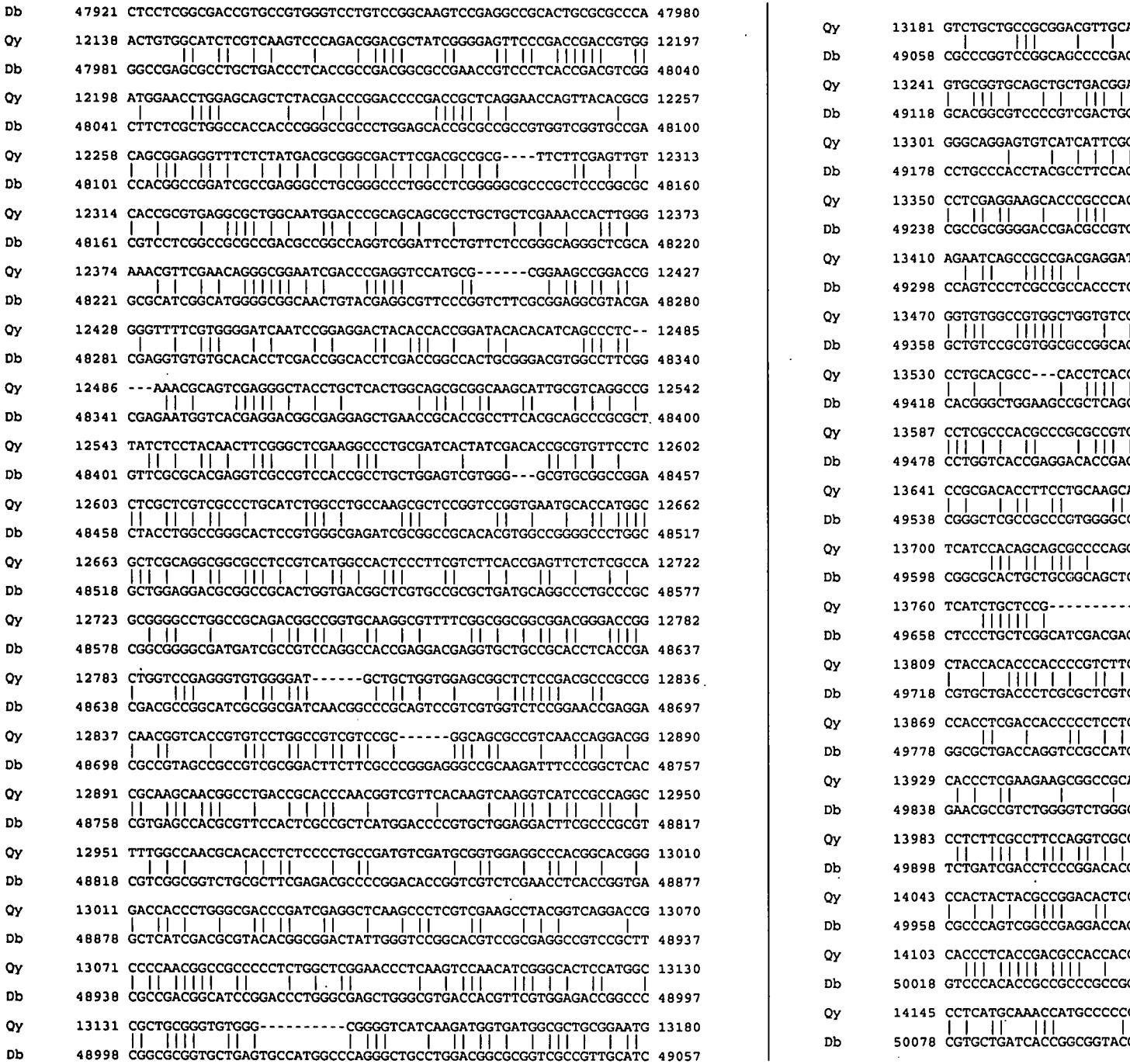


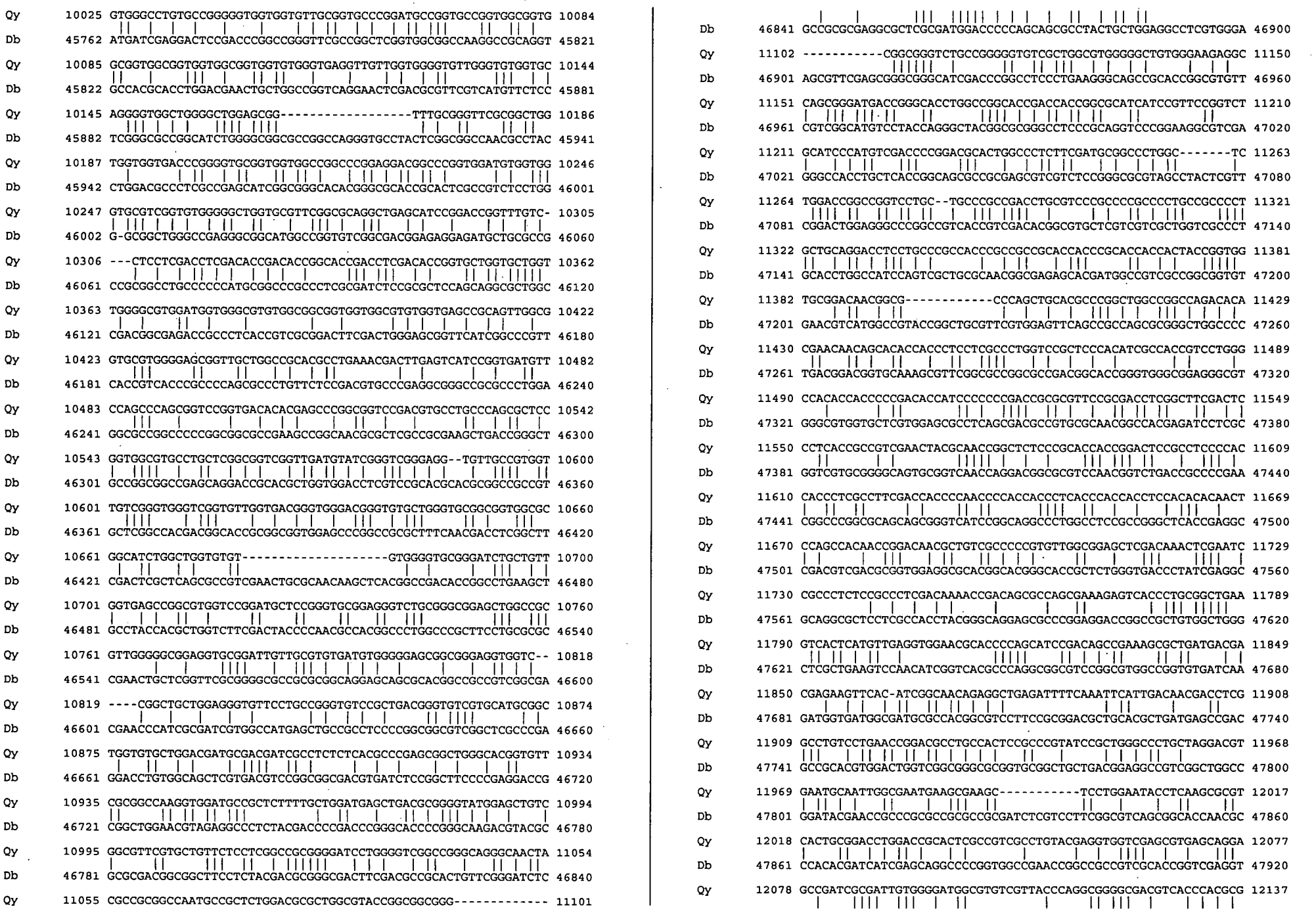


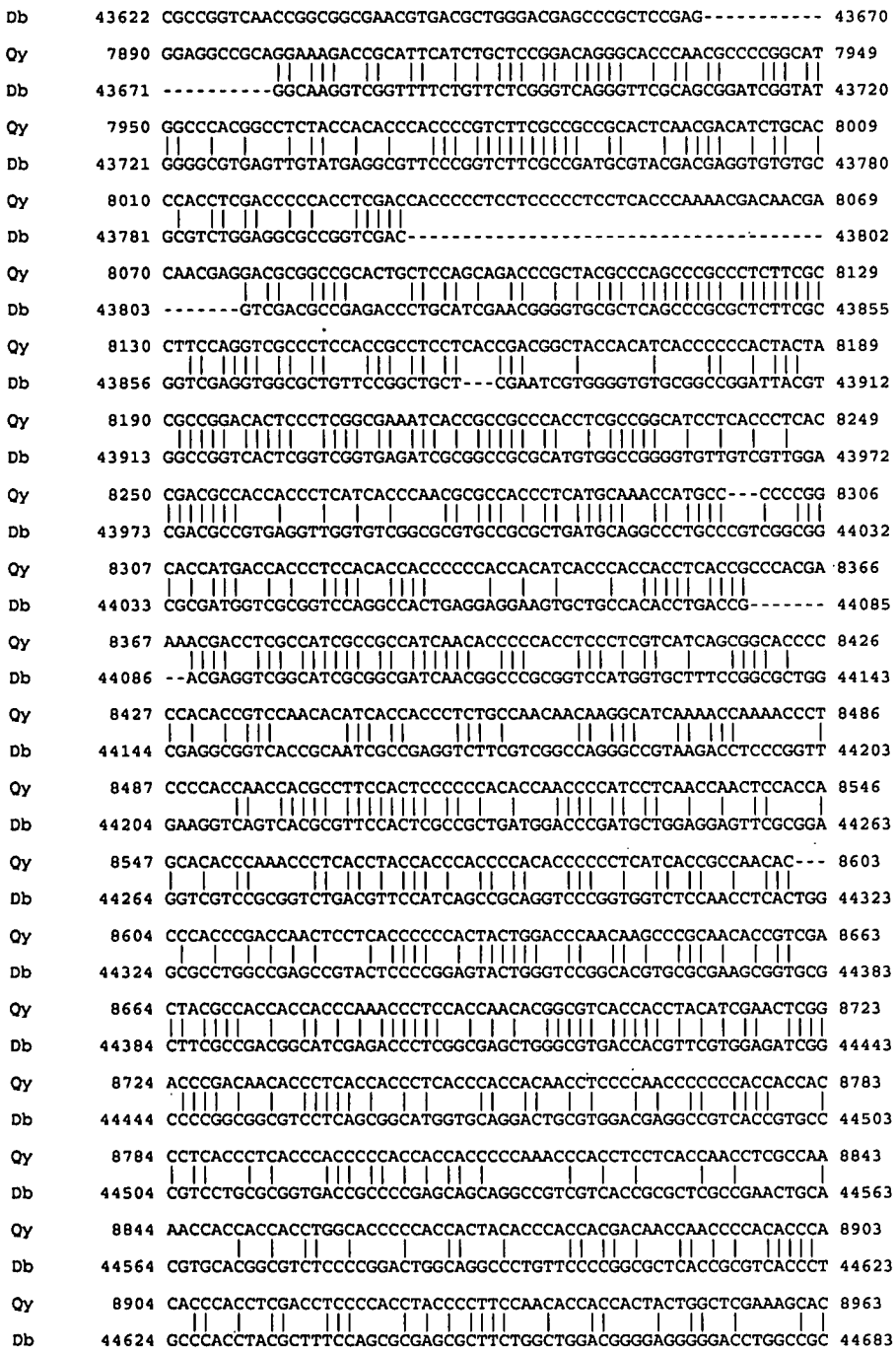

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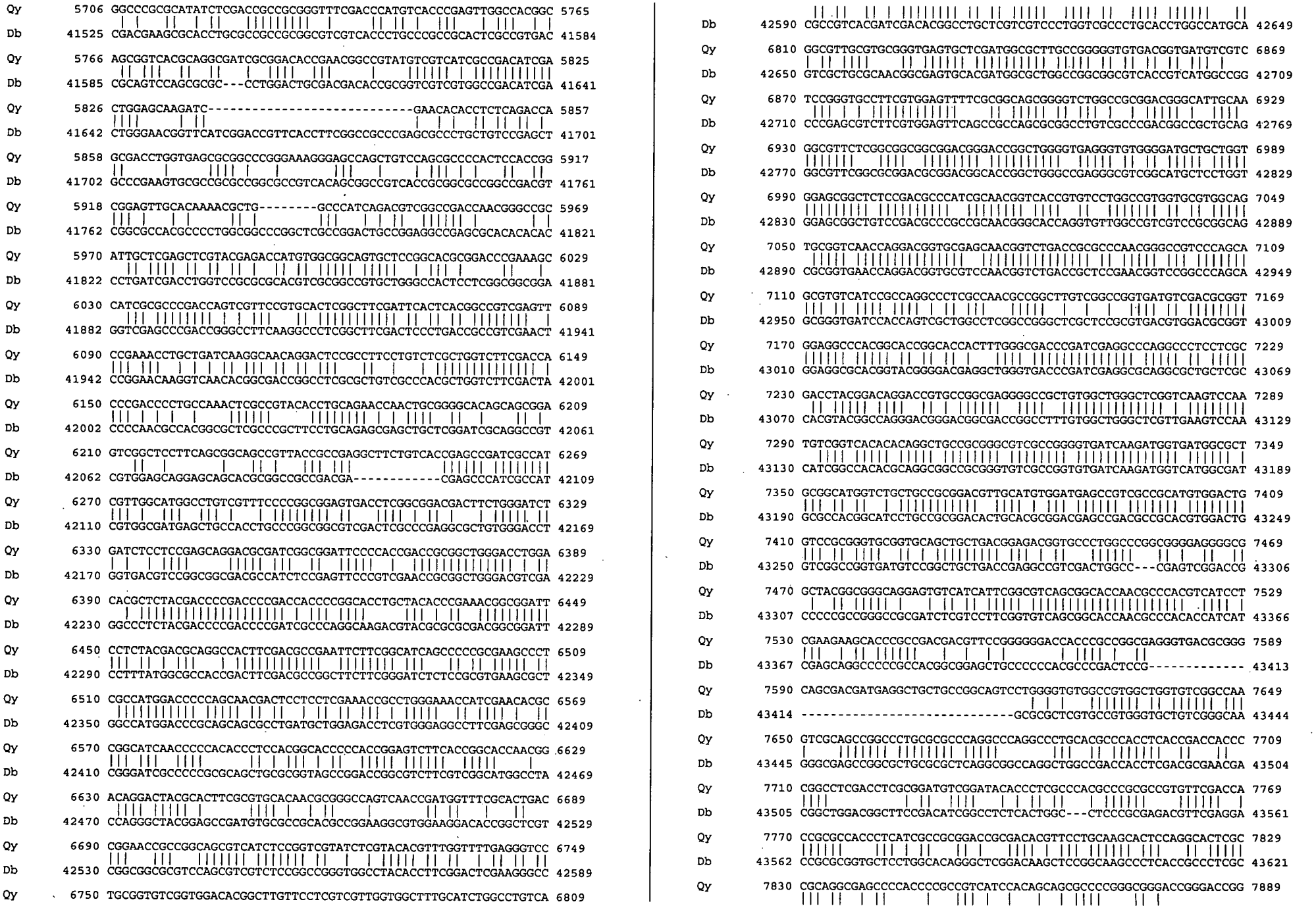


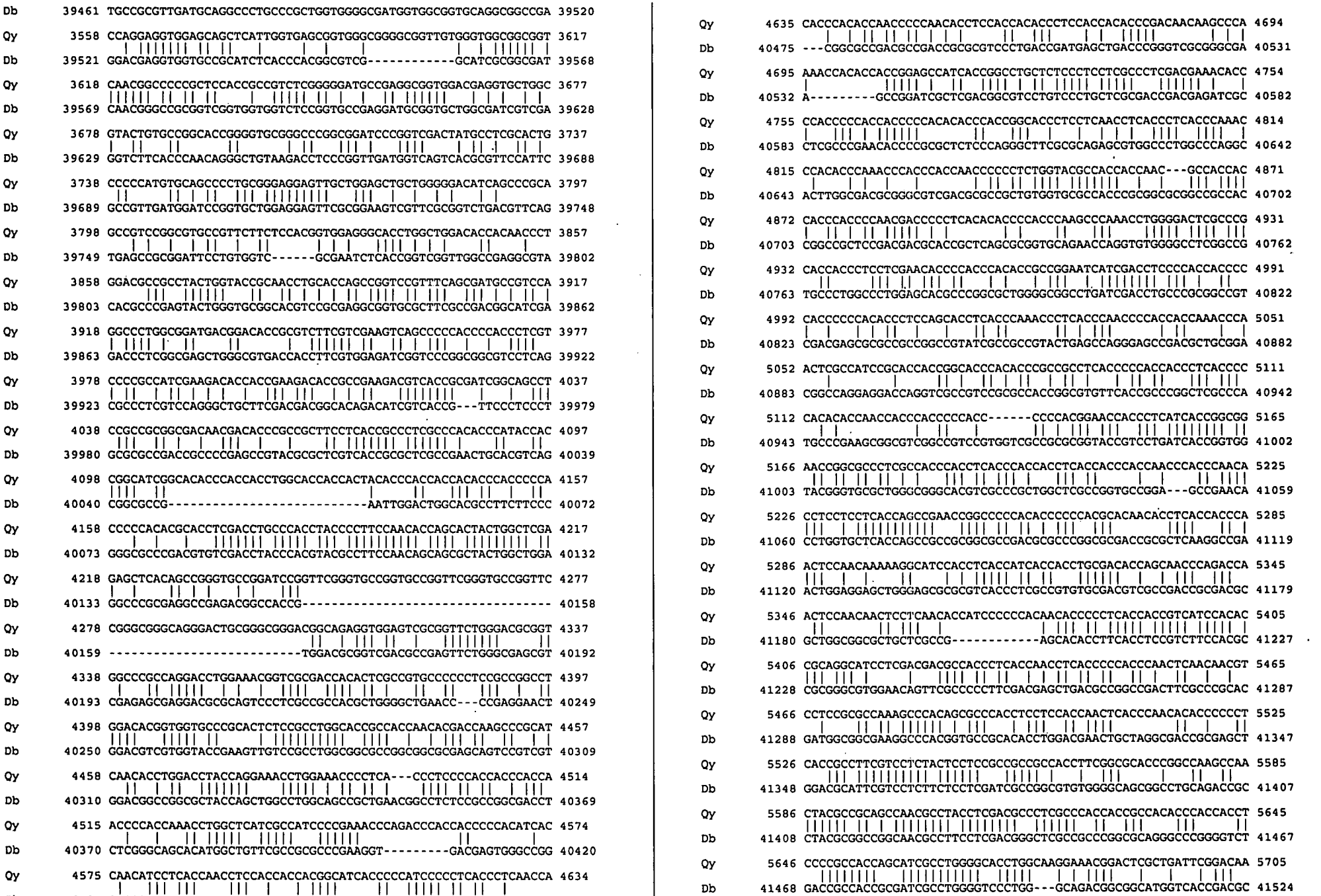


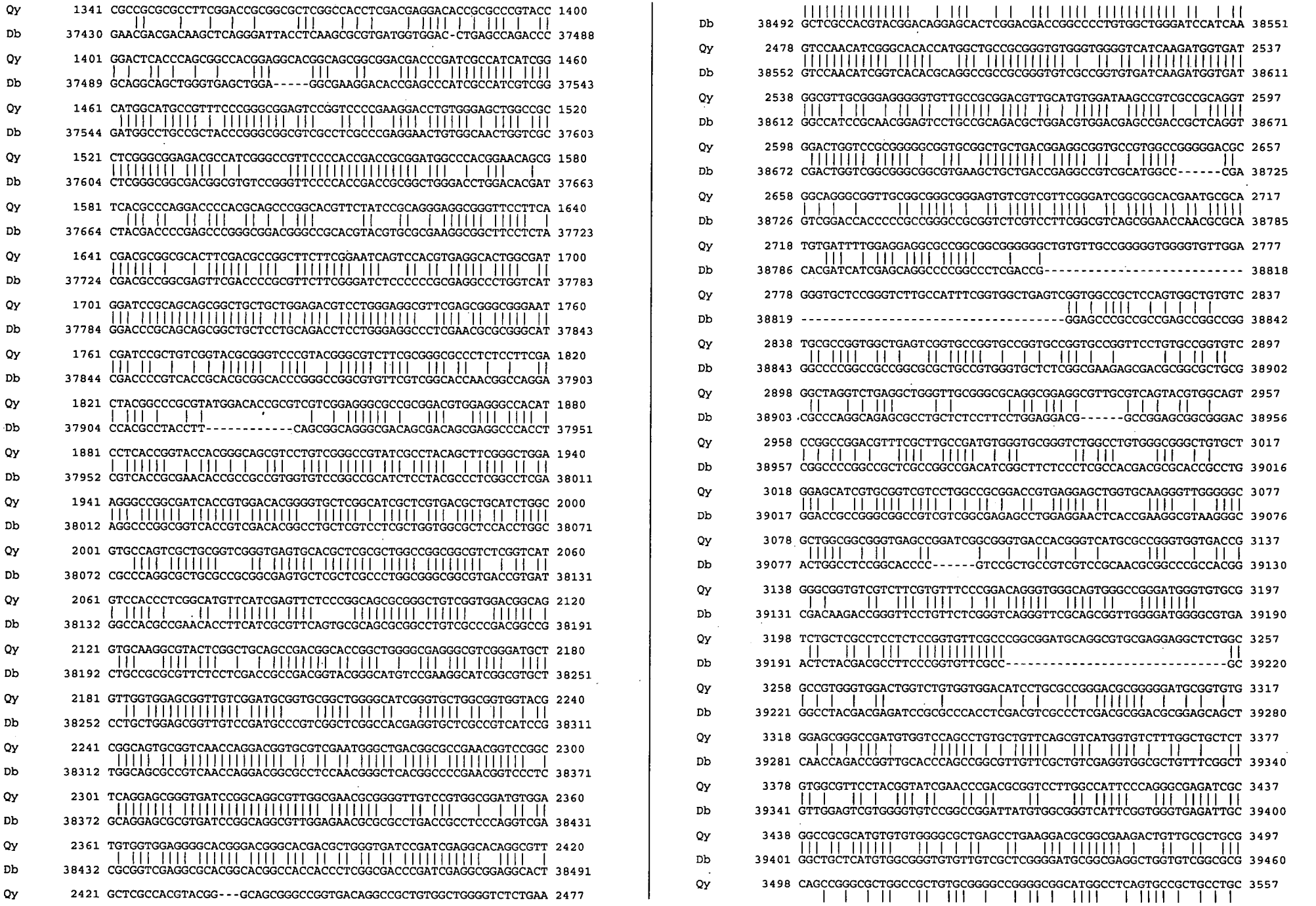





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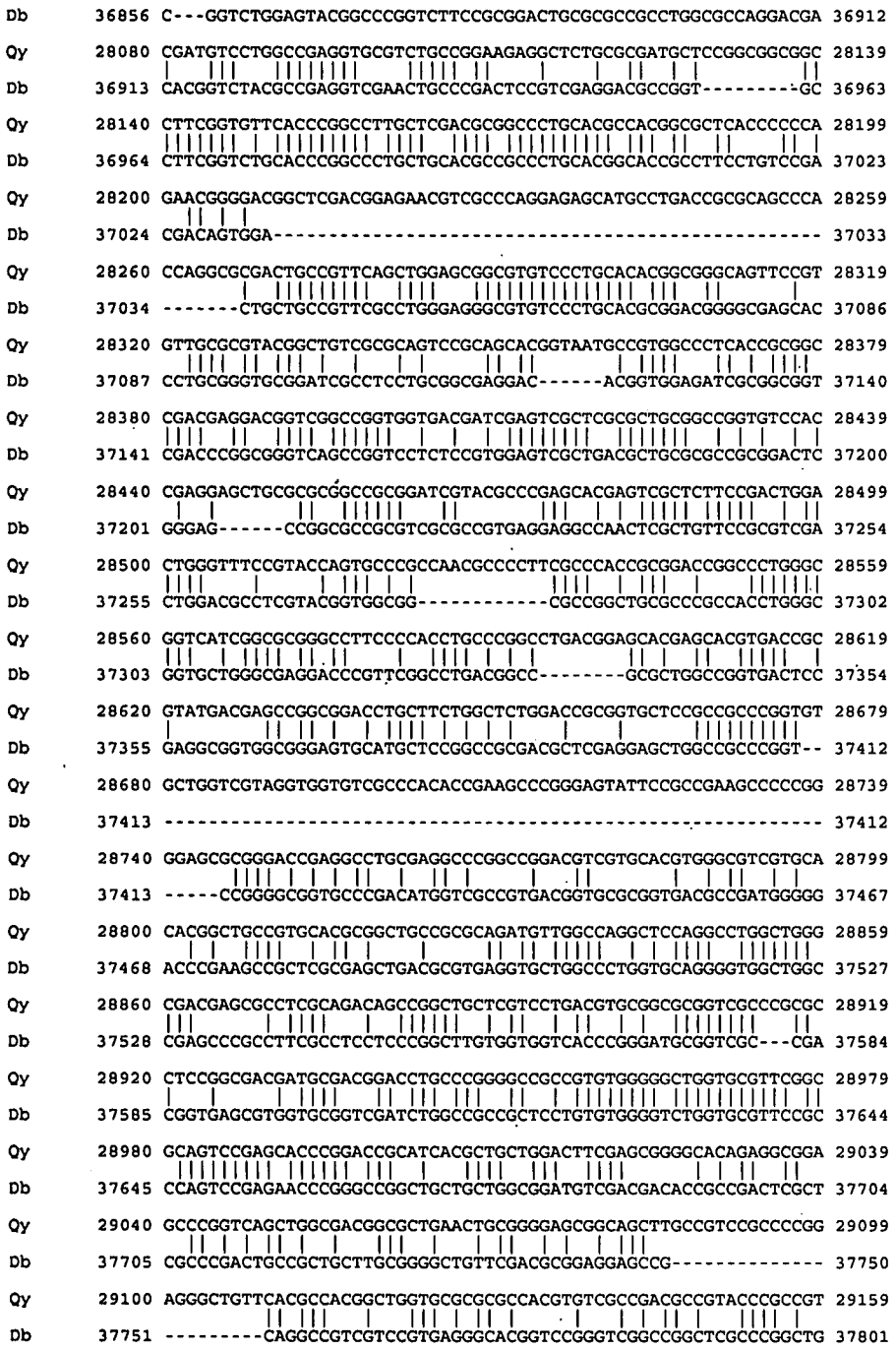
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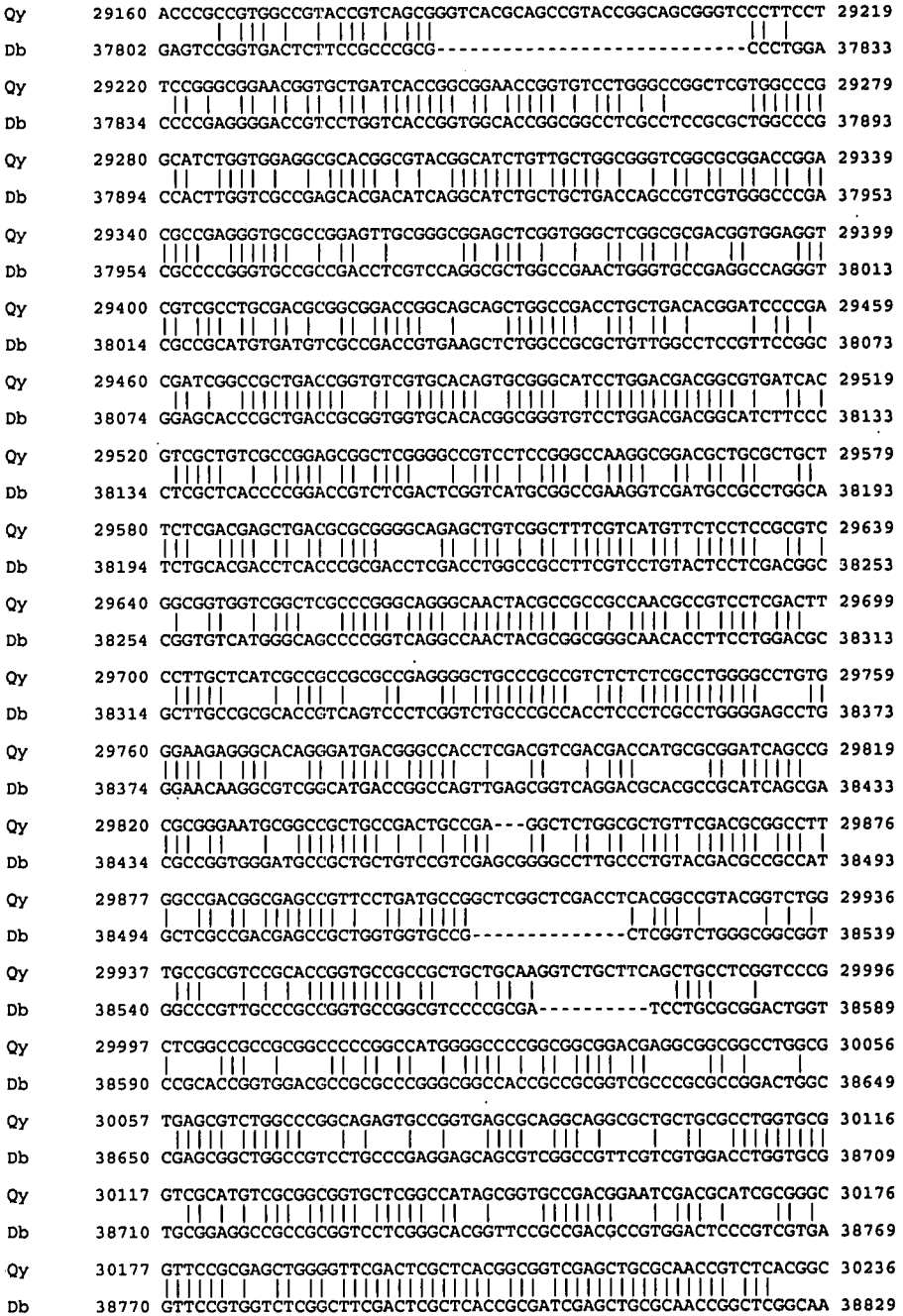
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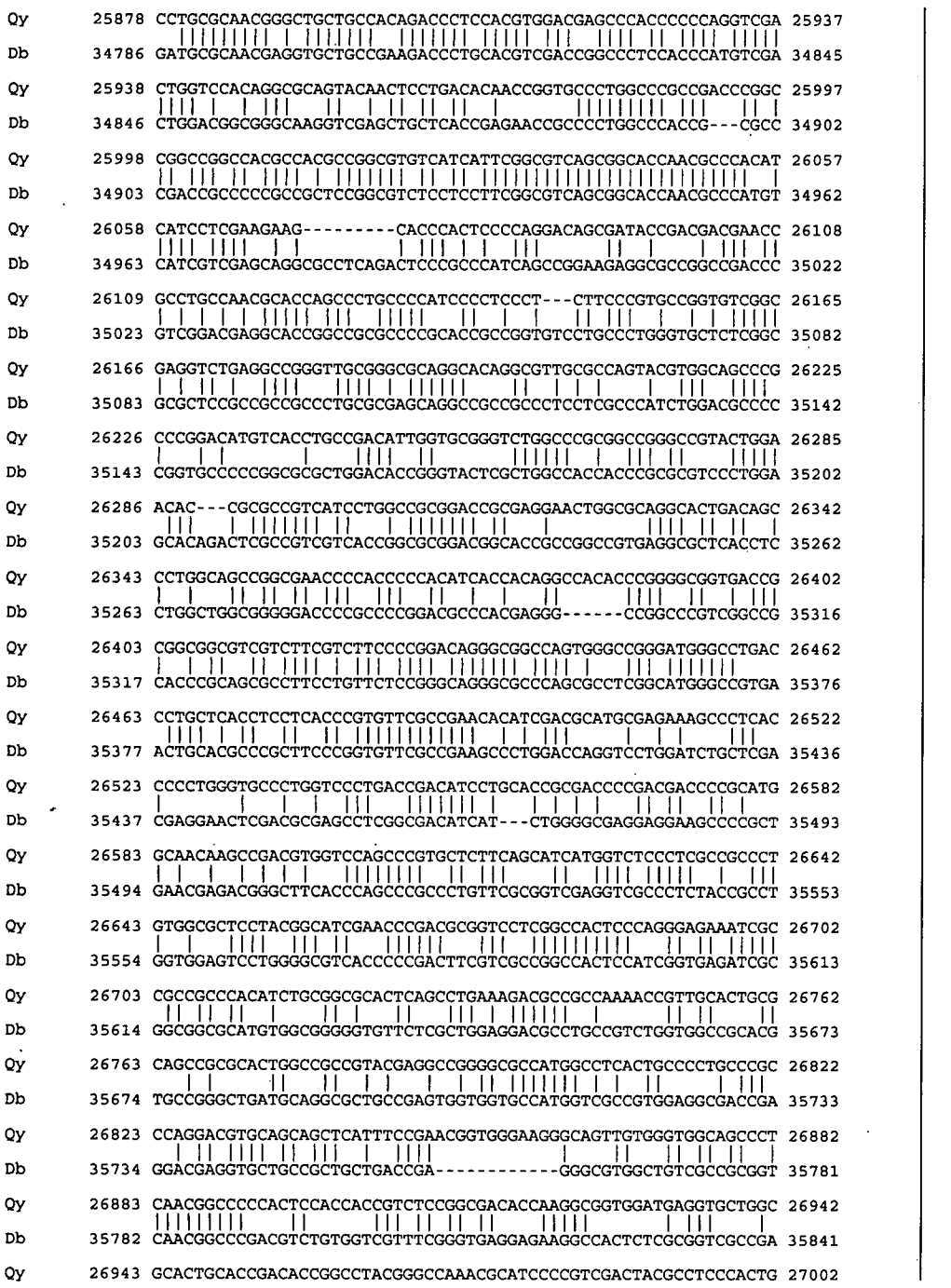
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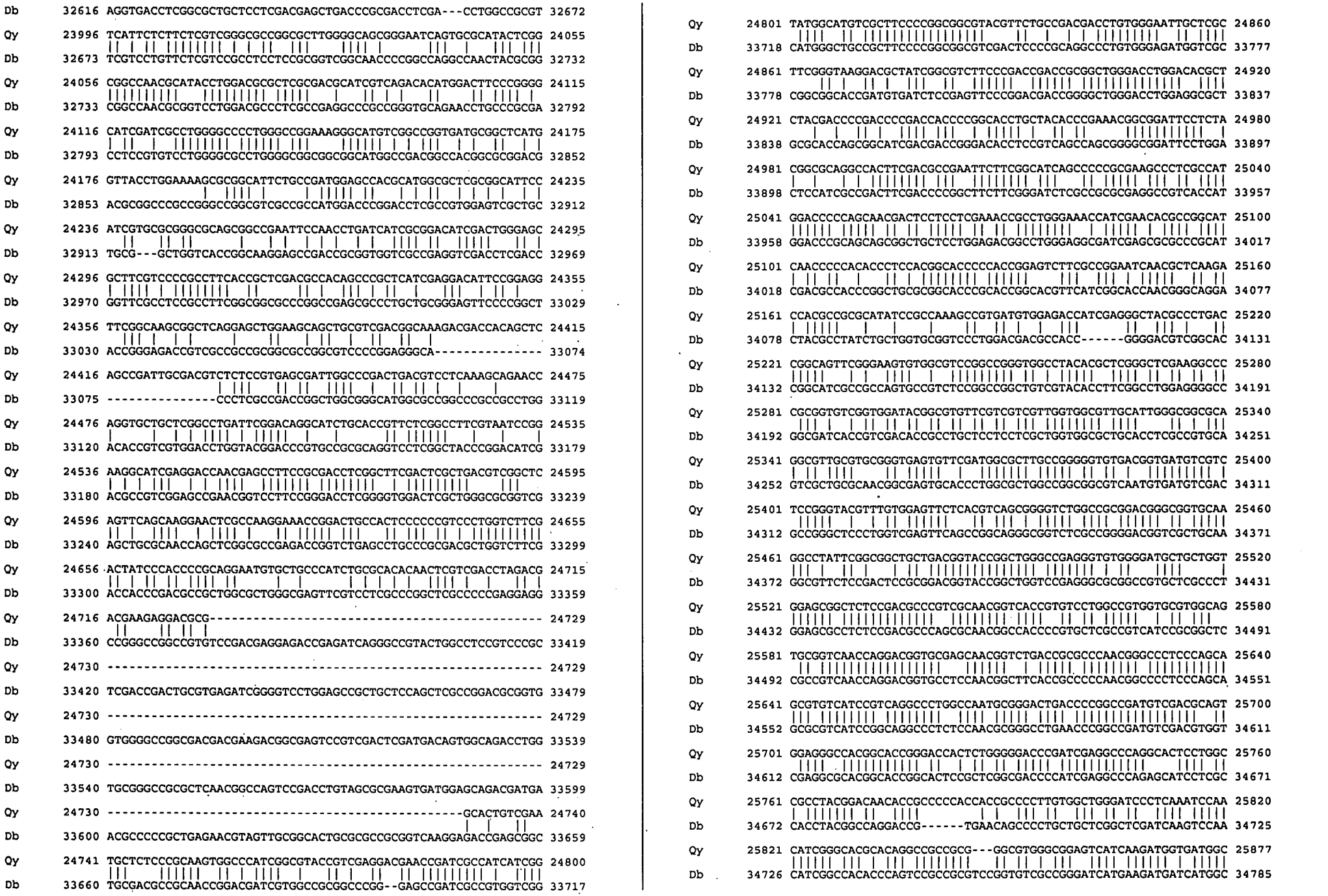
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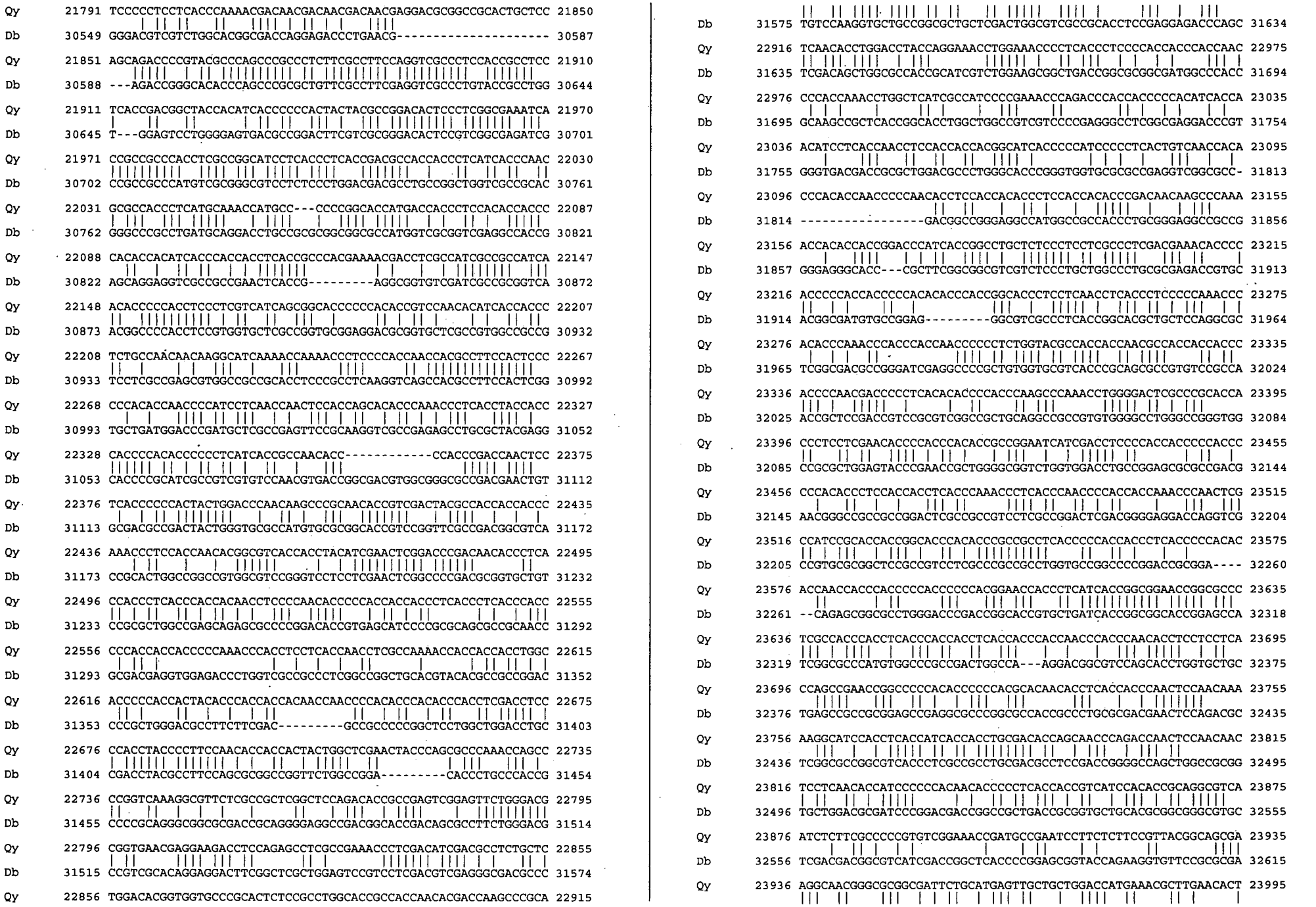
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ORGANISM Streptomyces avermitilis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE 1
AUTHORS Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C., Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osonoe,T., Kikuchi,H., Shiba,T., Sakaki,Y. and Hattori,M.
TITLE Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
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AUTHORS Ikeda,H.
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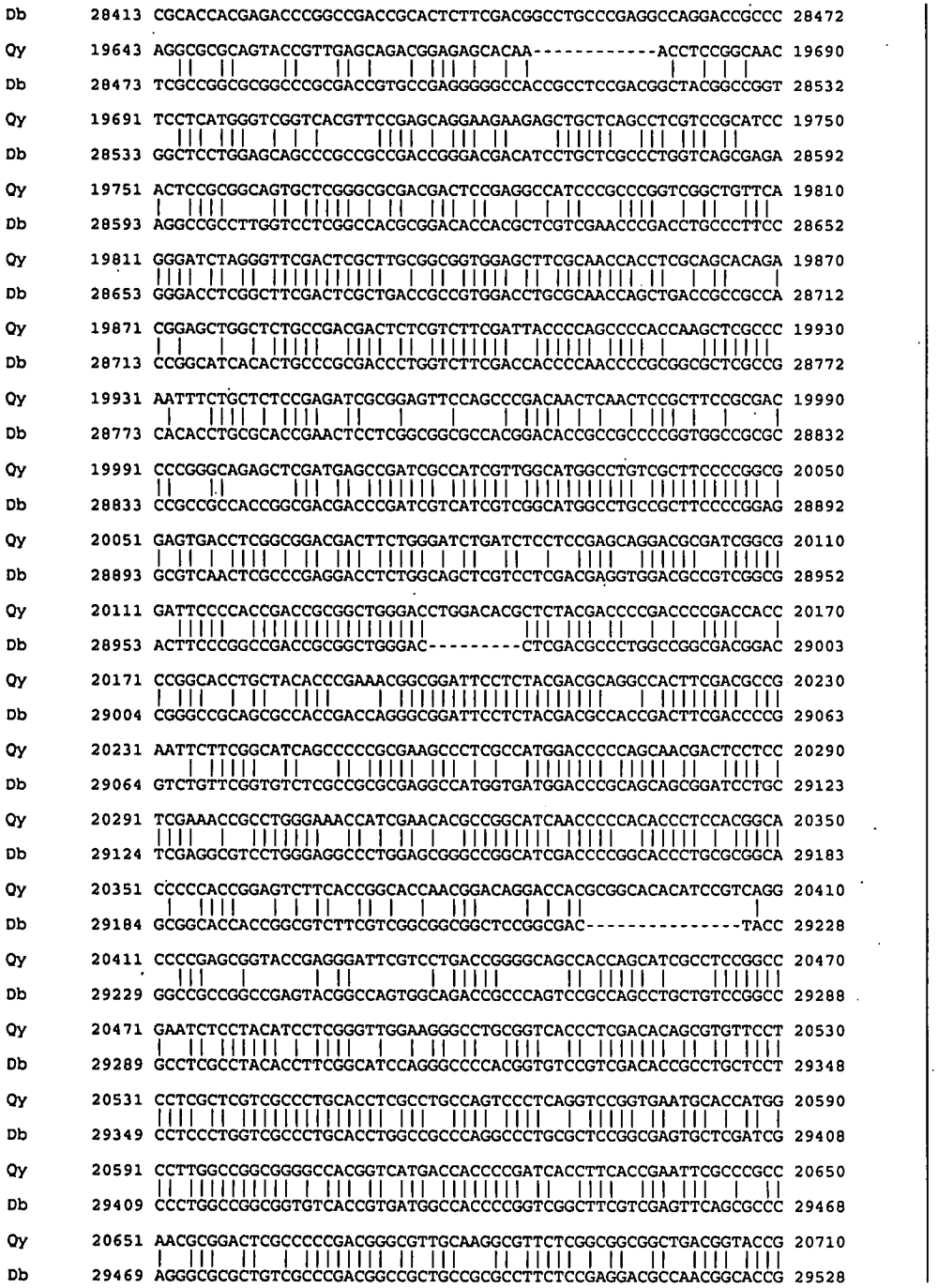


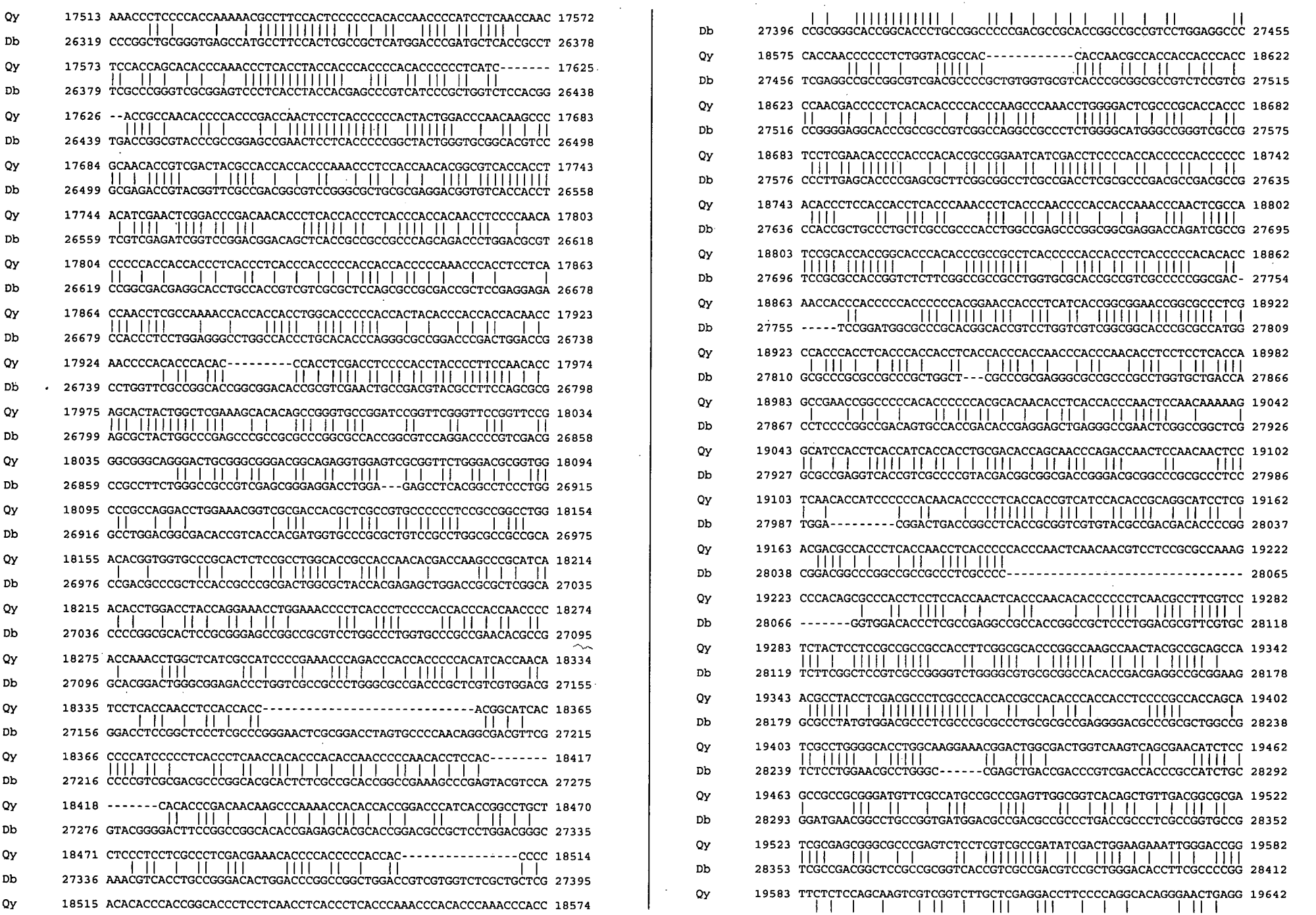


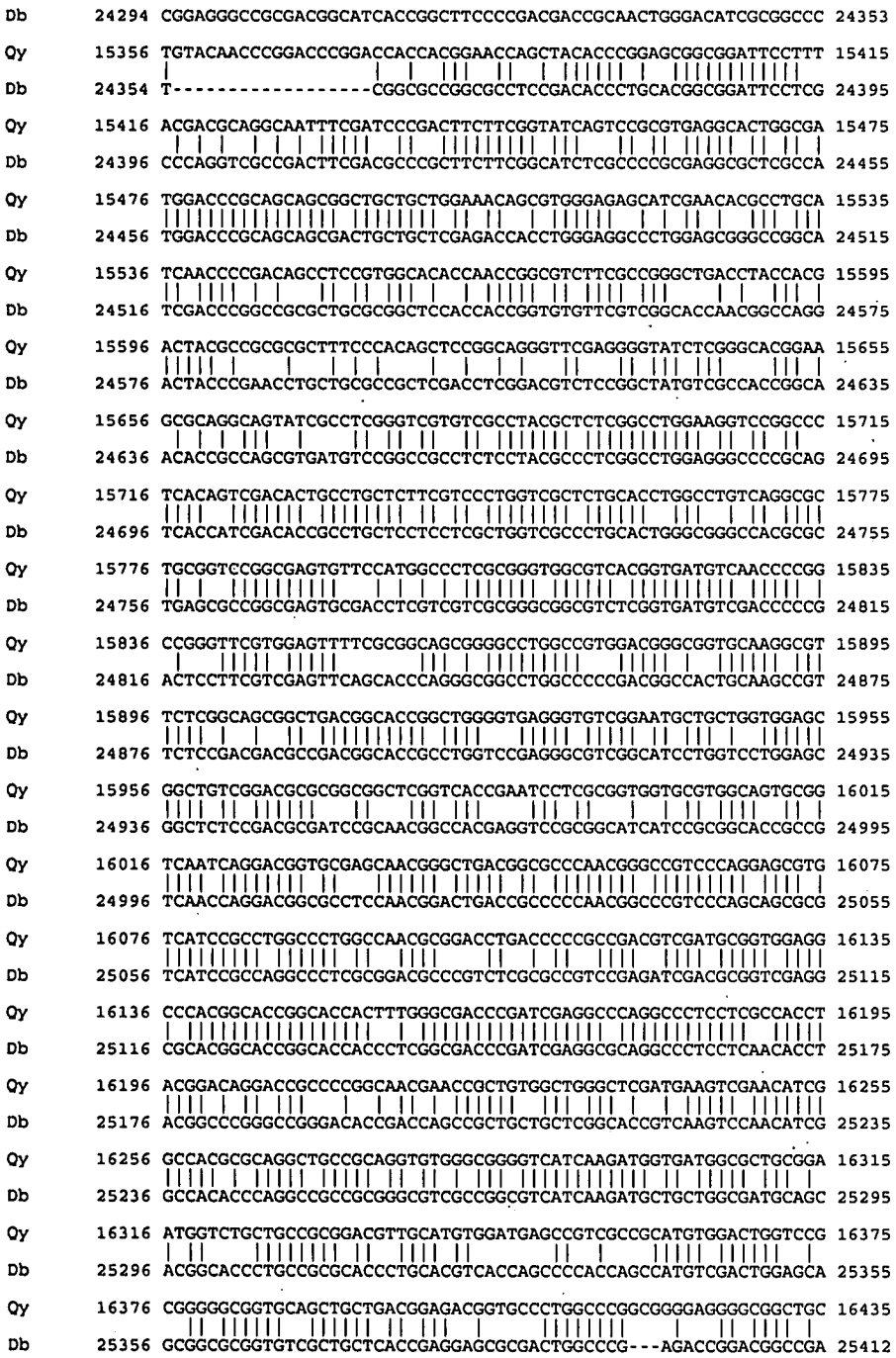


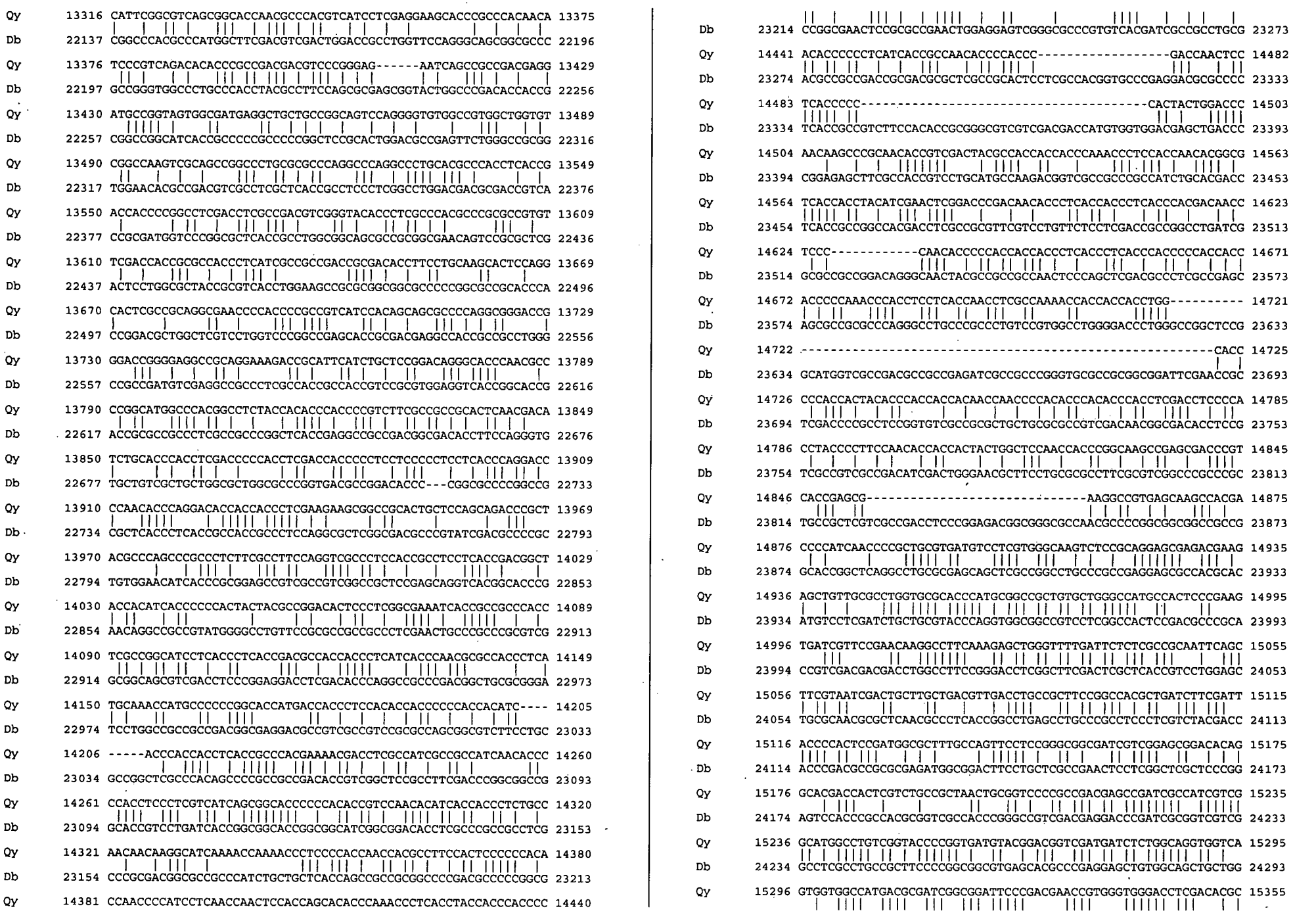


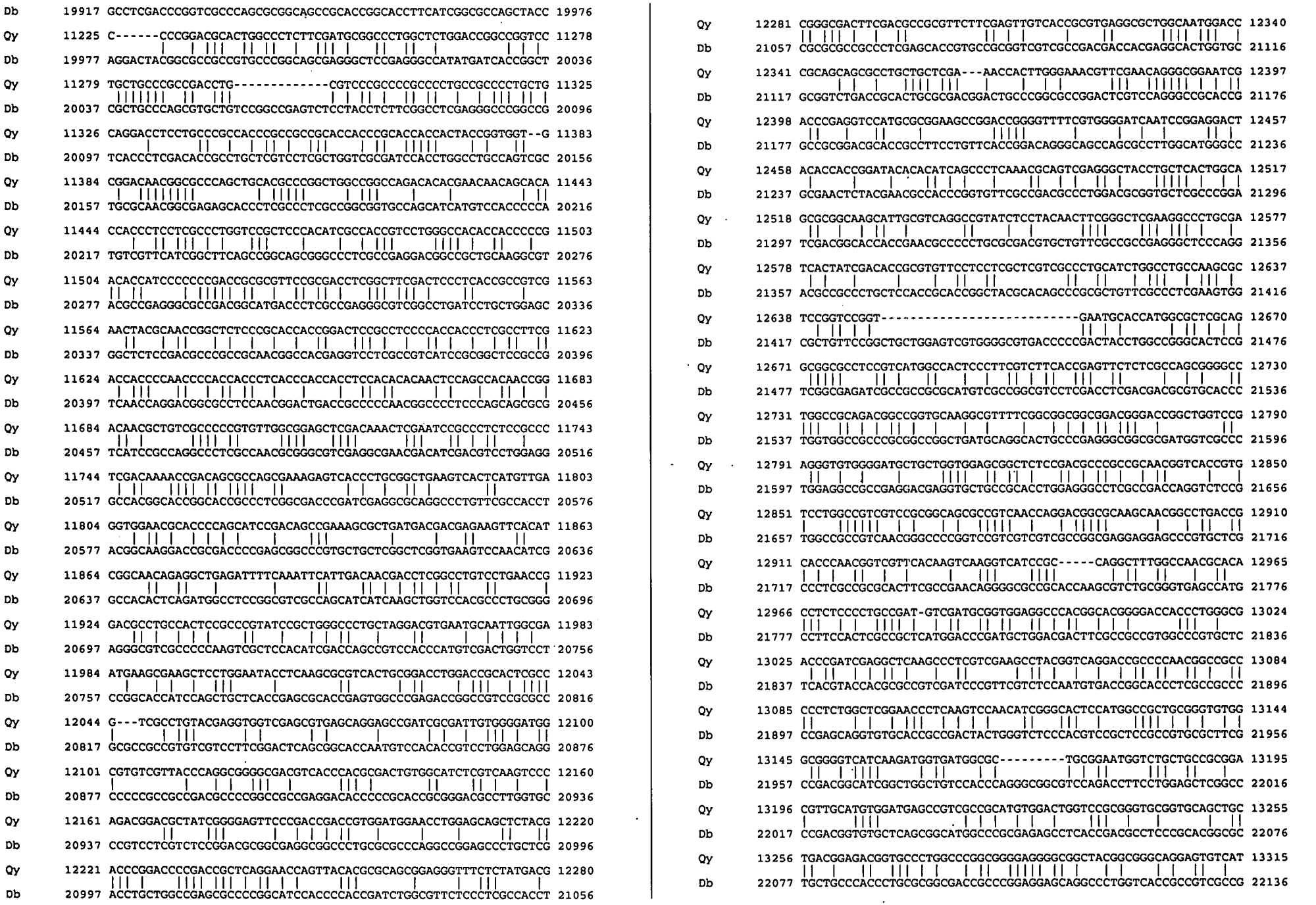


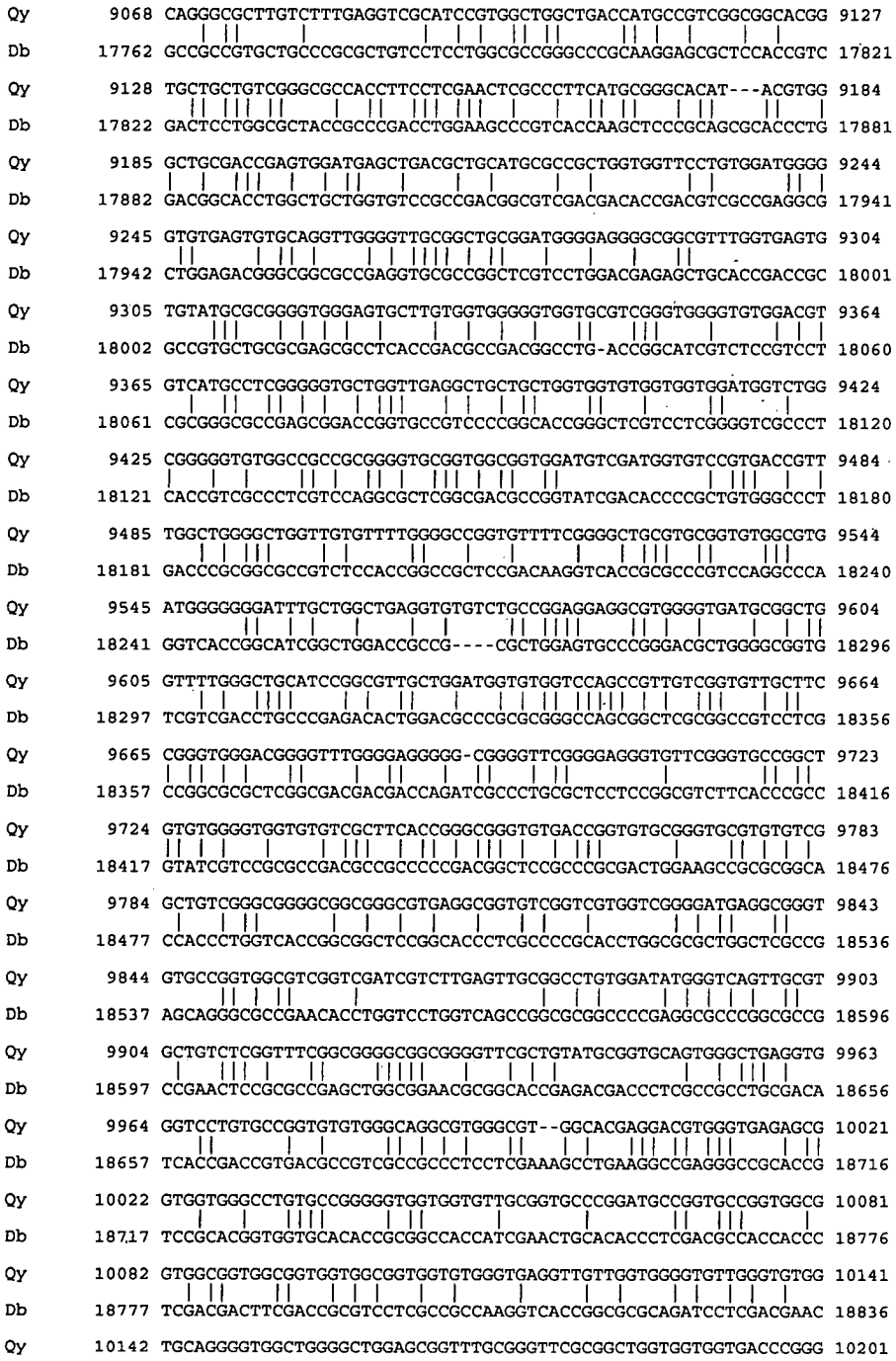

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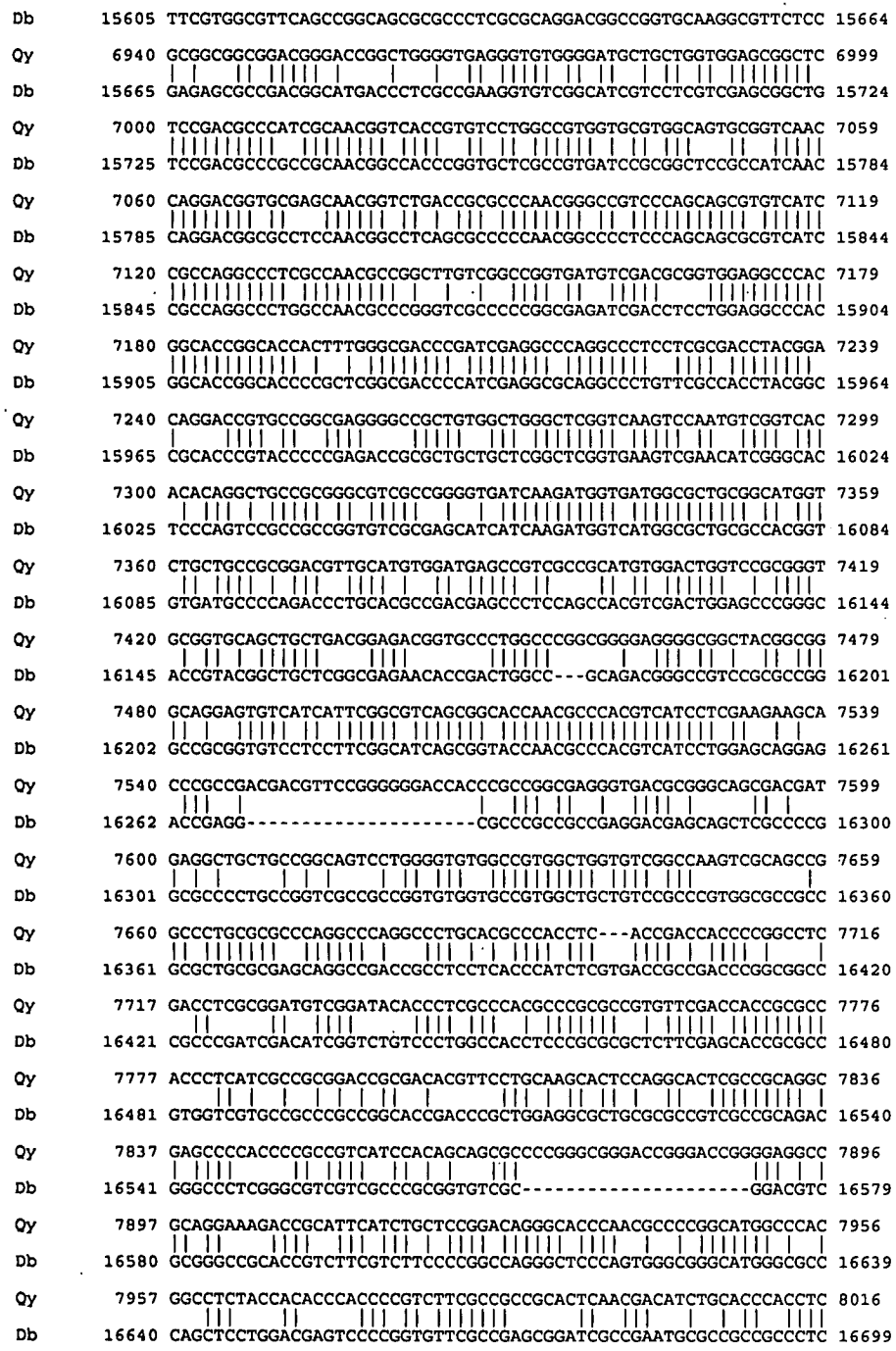


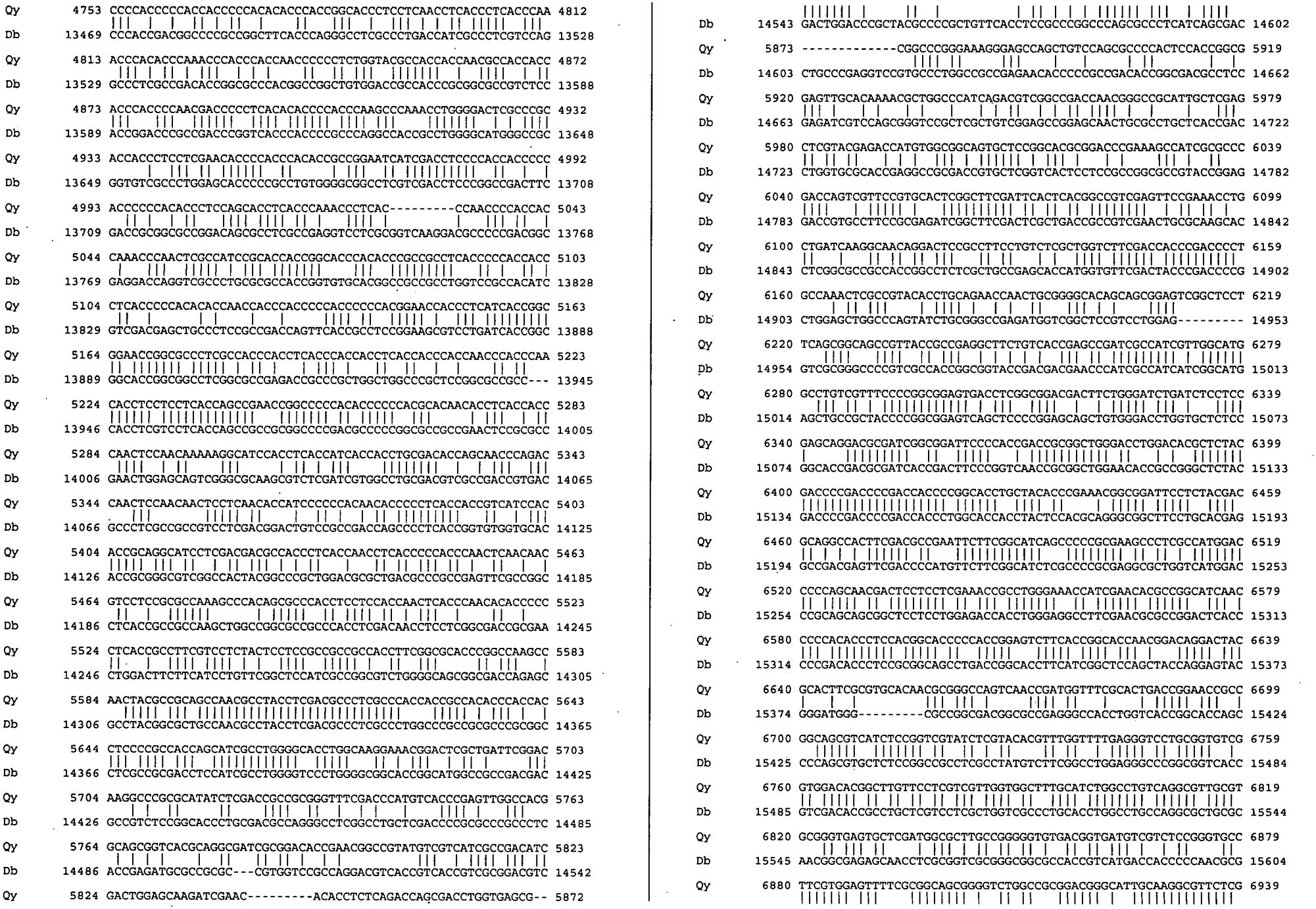

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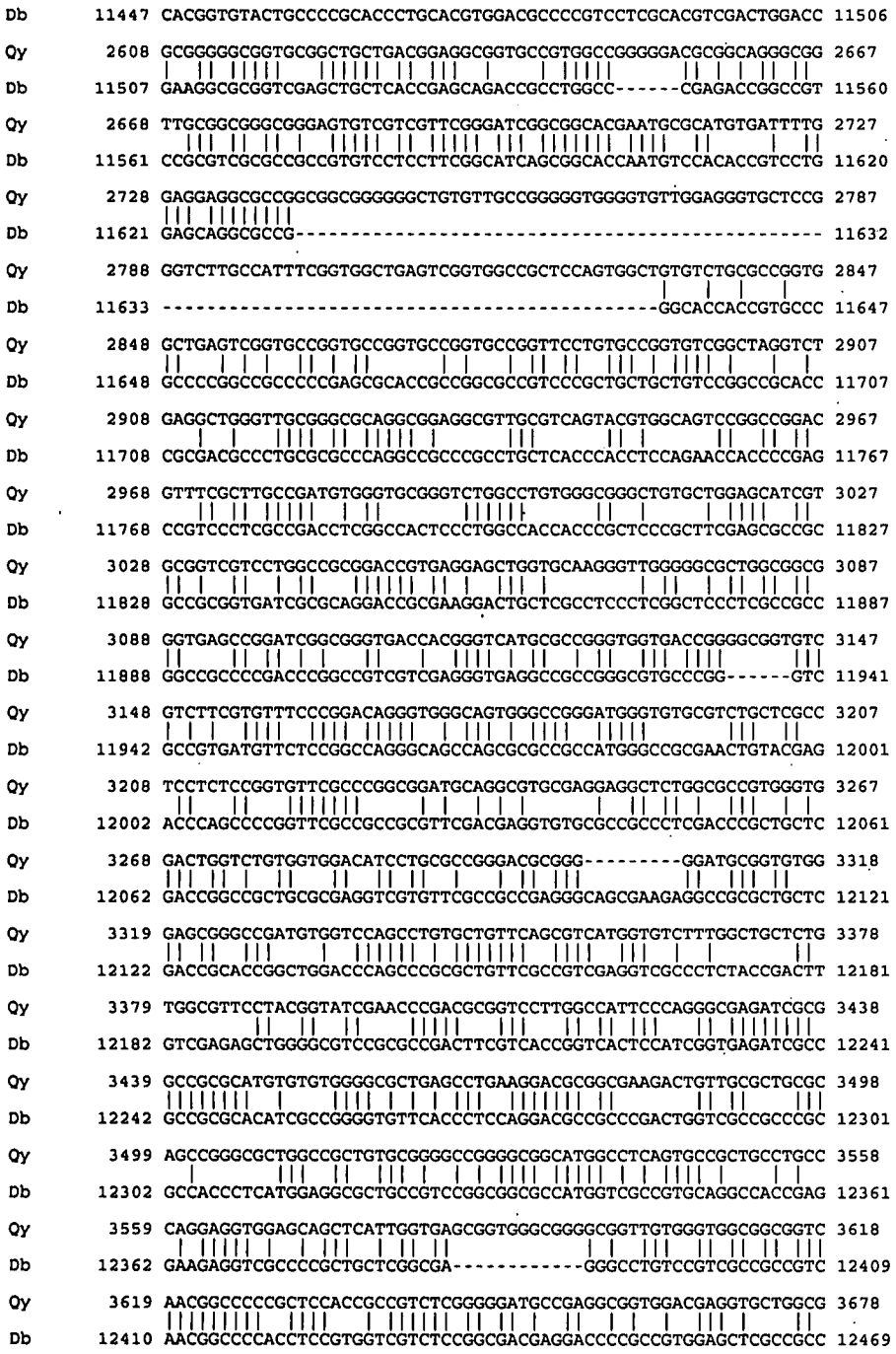


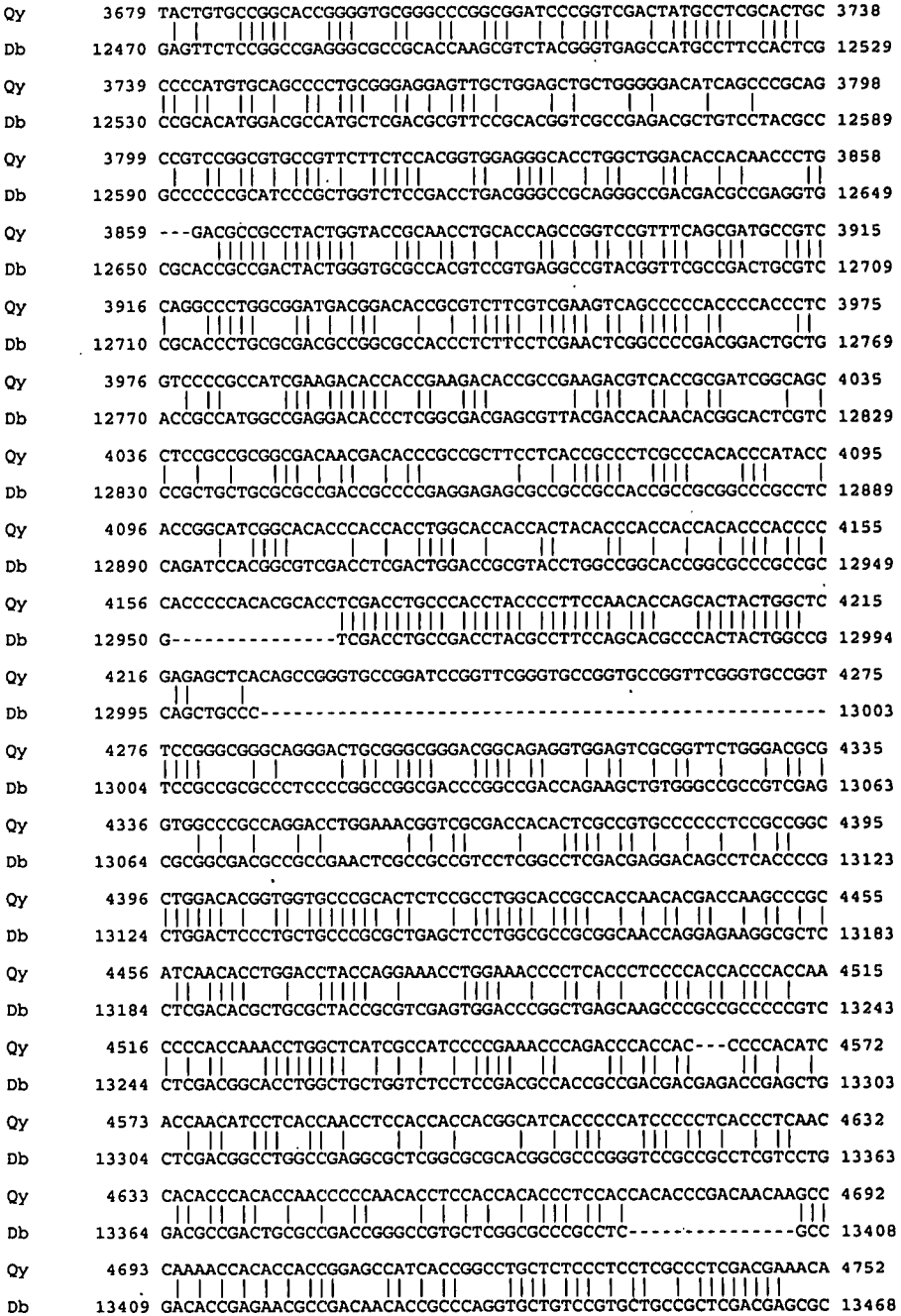



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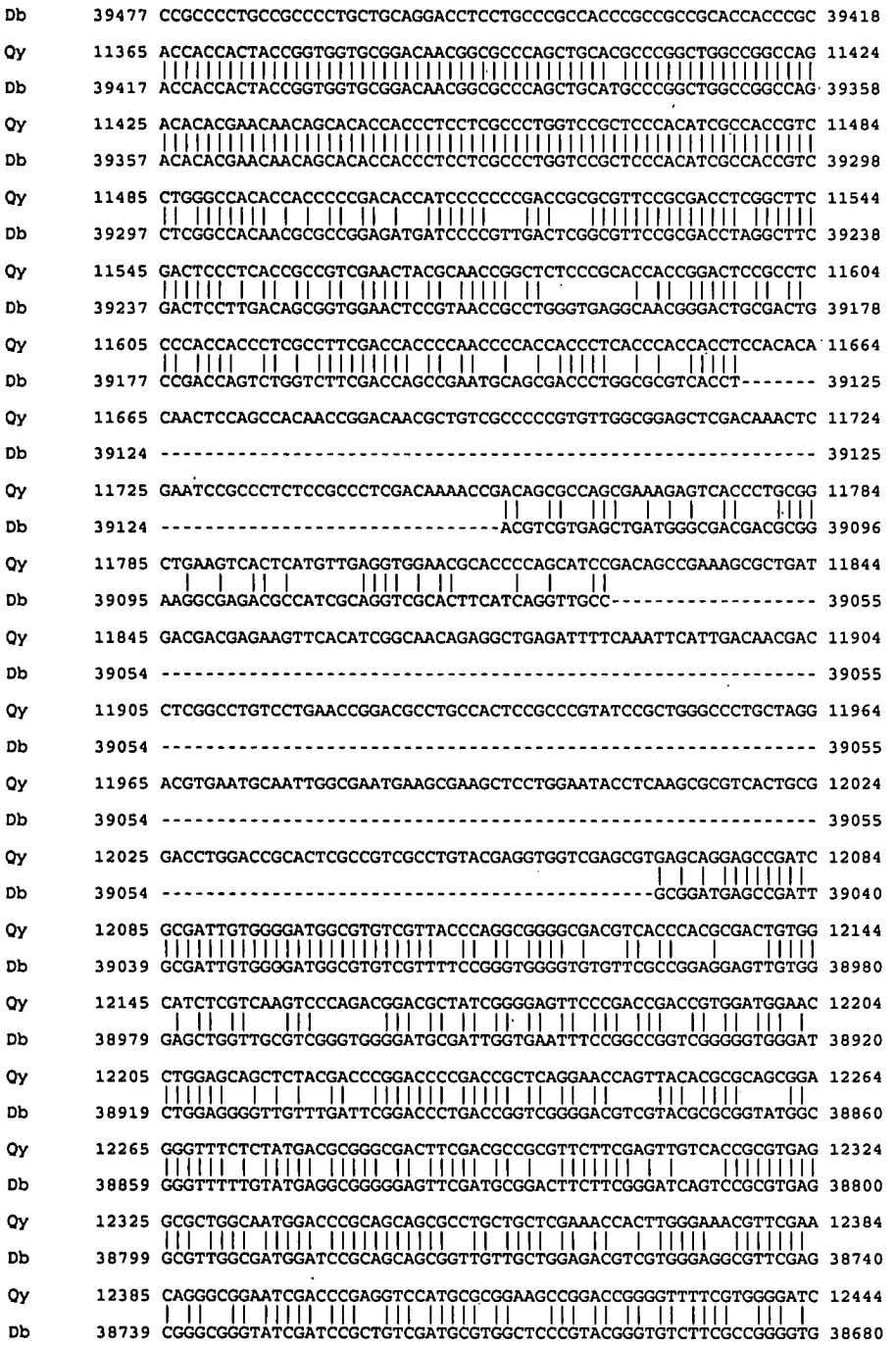
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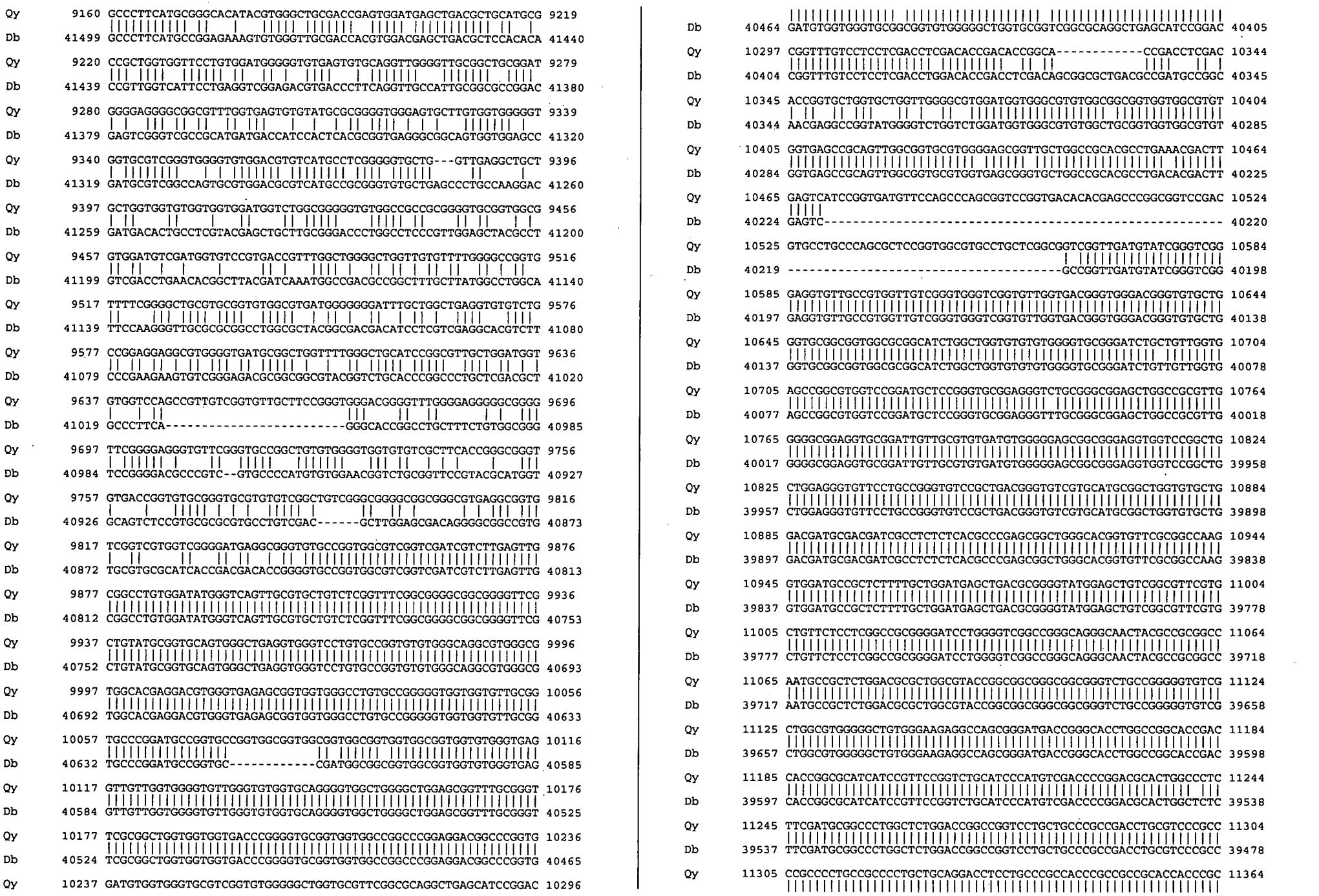
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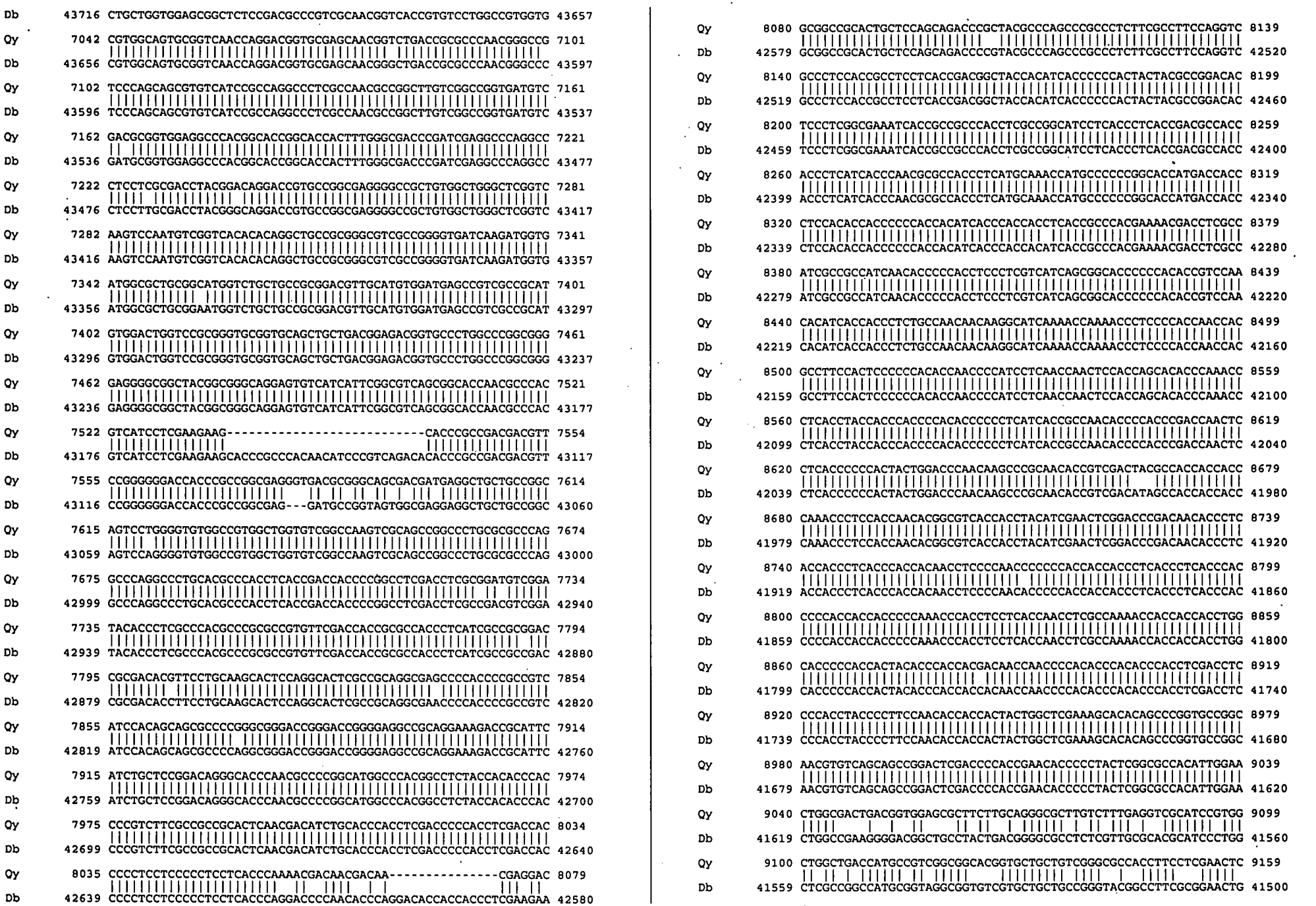
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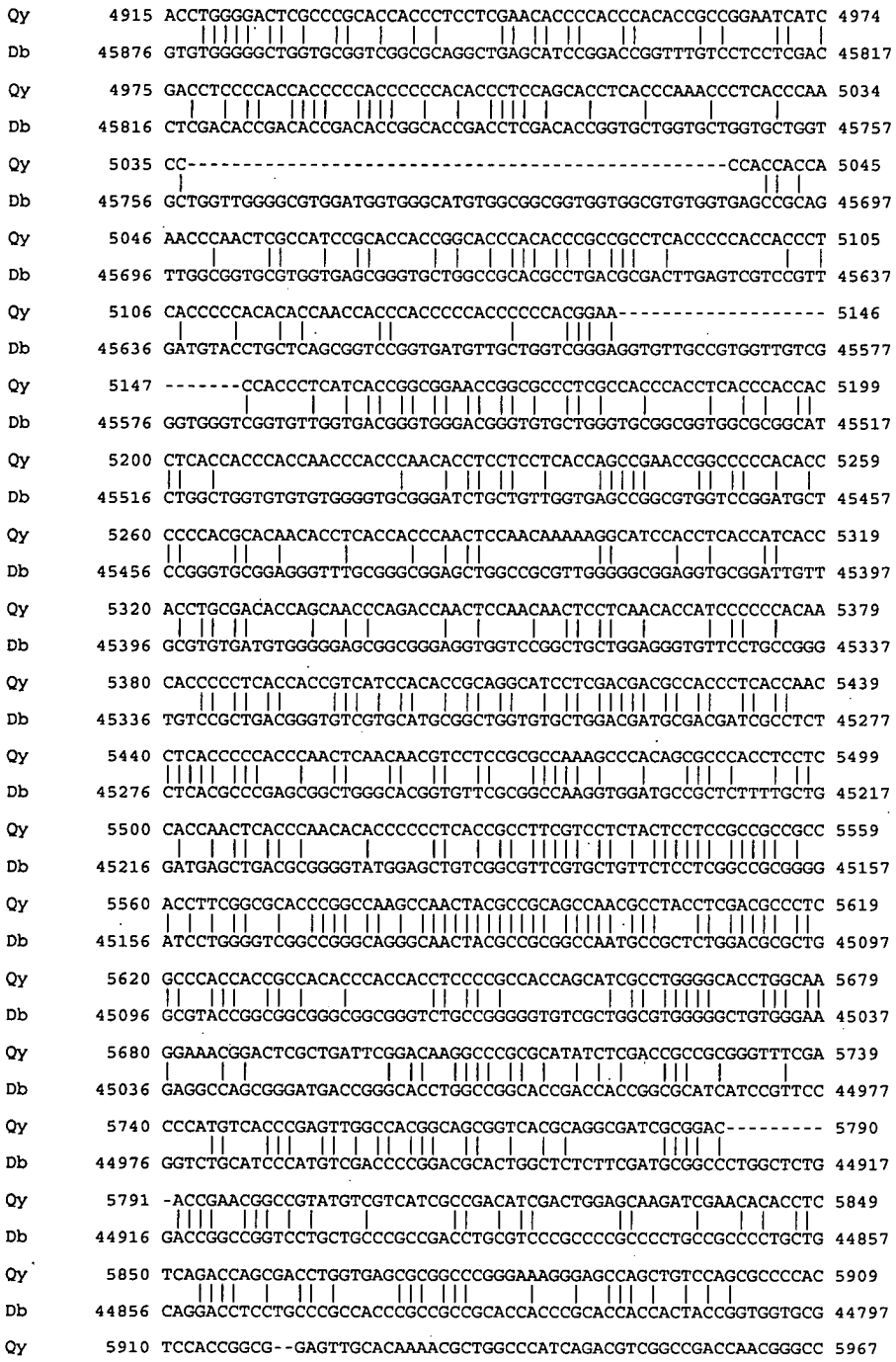
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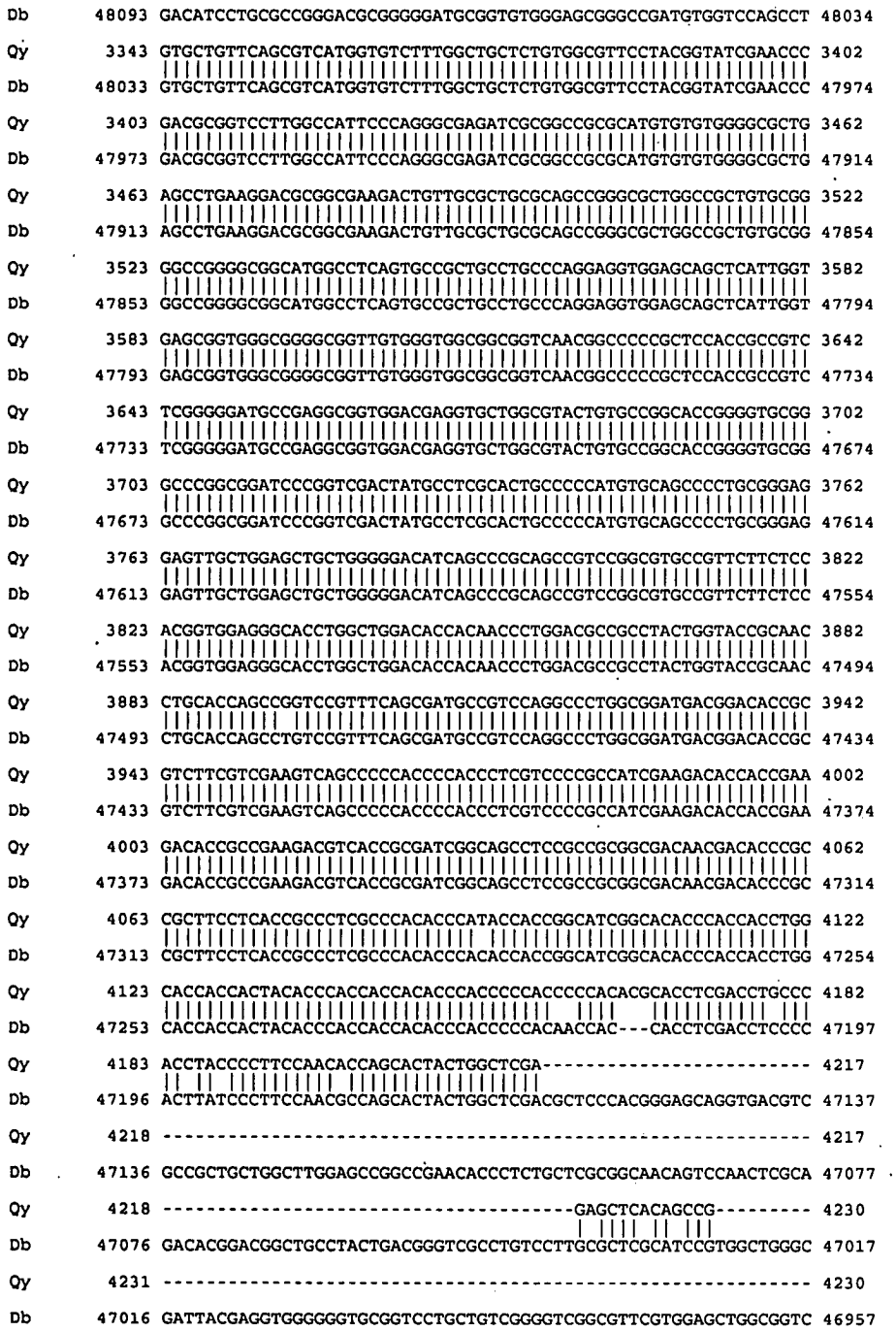
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  AUTHORS   Caffrey,P., Lynch,S.V., Flood,E.M., Finnan,S.M. and Oliynyk,M.
  TITLE     The amphotericin biosynthetic gene cluster from Streptomyces
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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 113193)
  AUTHORS   Caffrey,P., Lynch,S.V., Flood,E.M., Finnan,S.M. and Oliynyk,M.
  TITLE     Direct Submission
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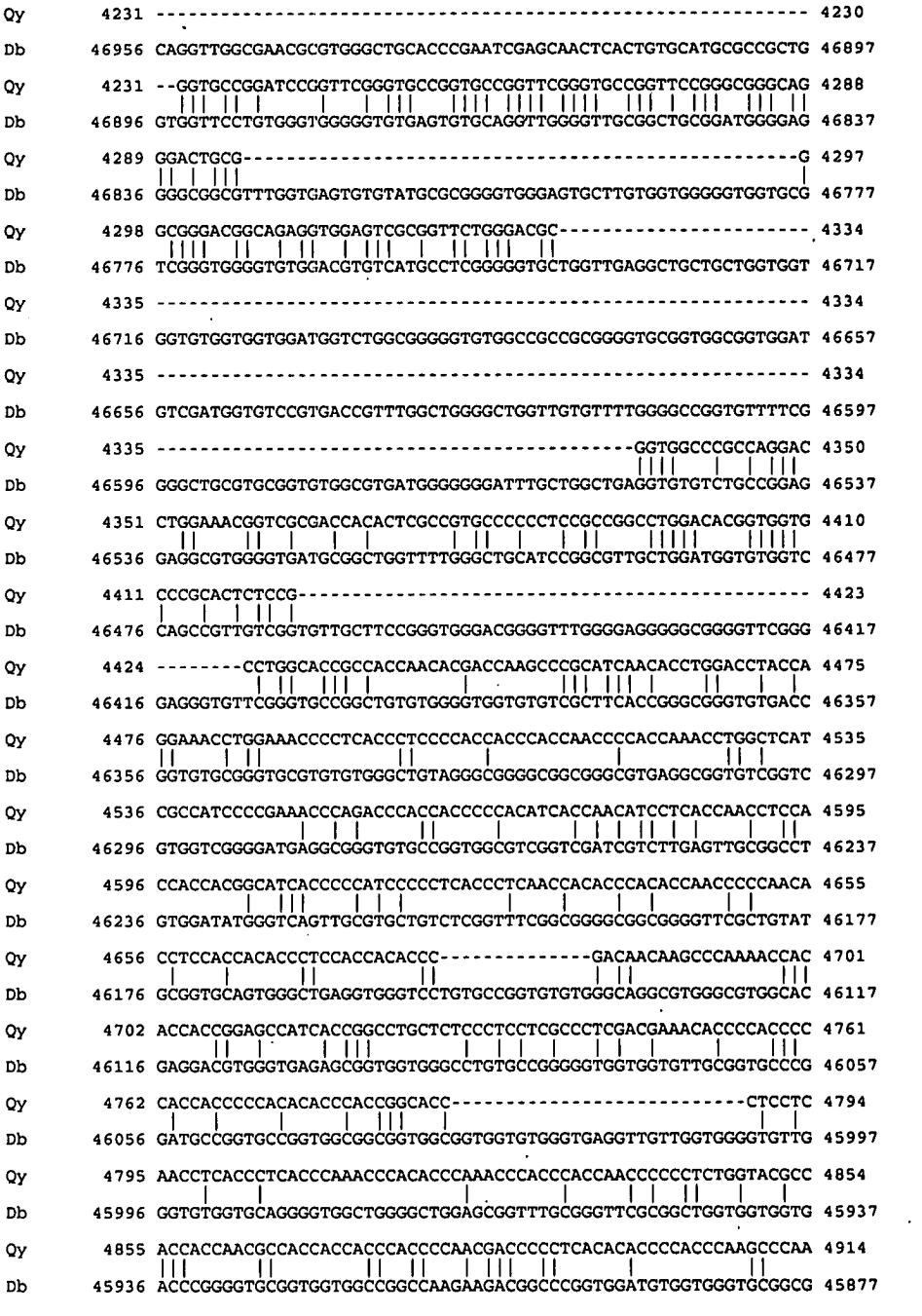

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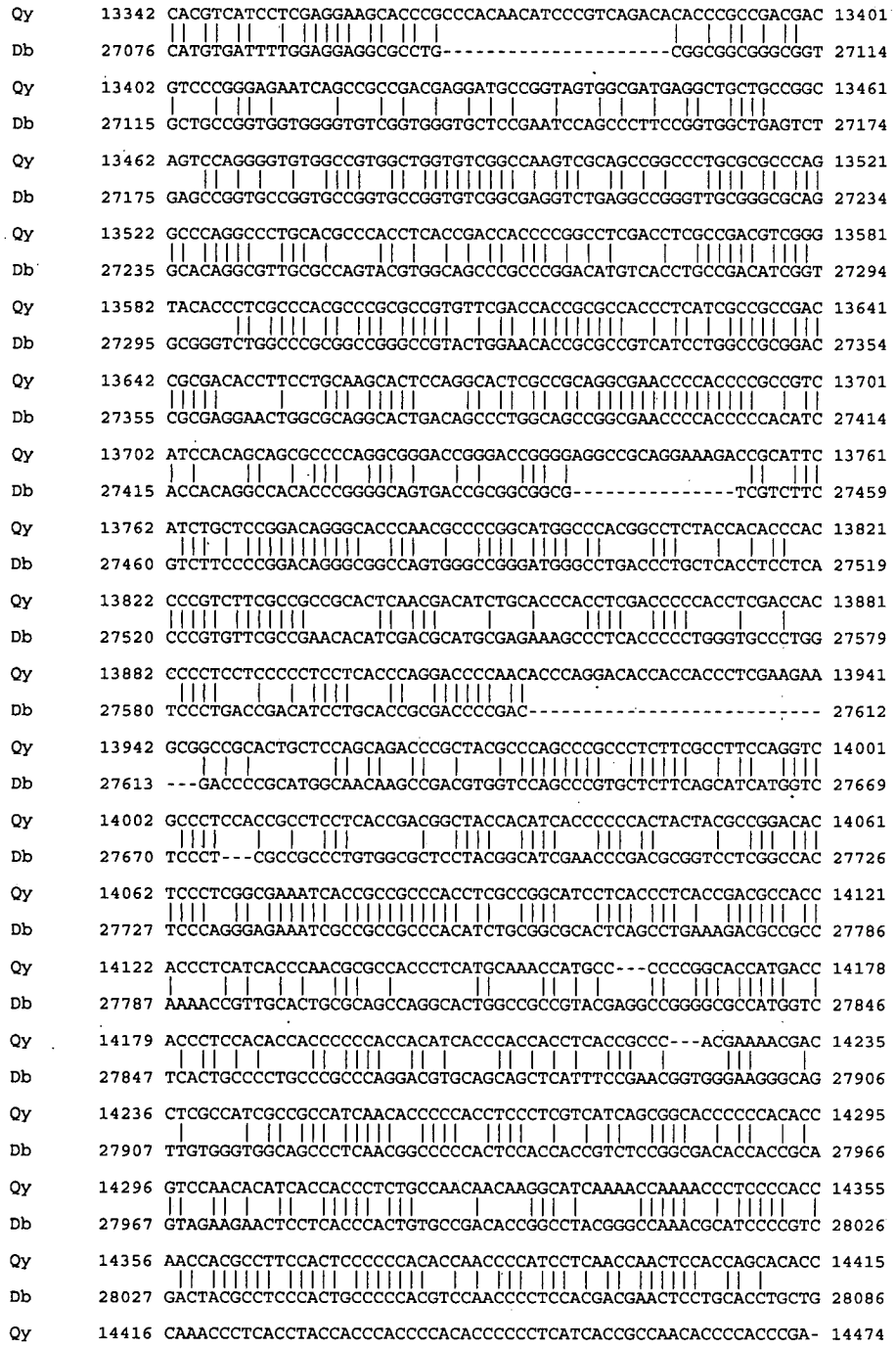
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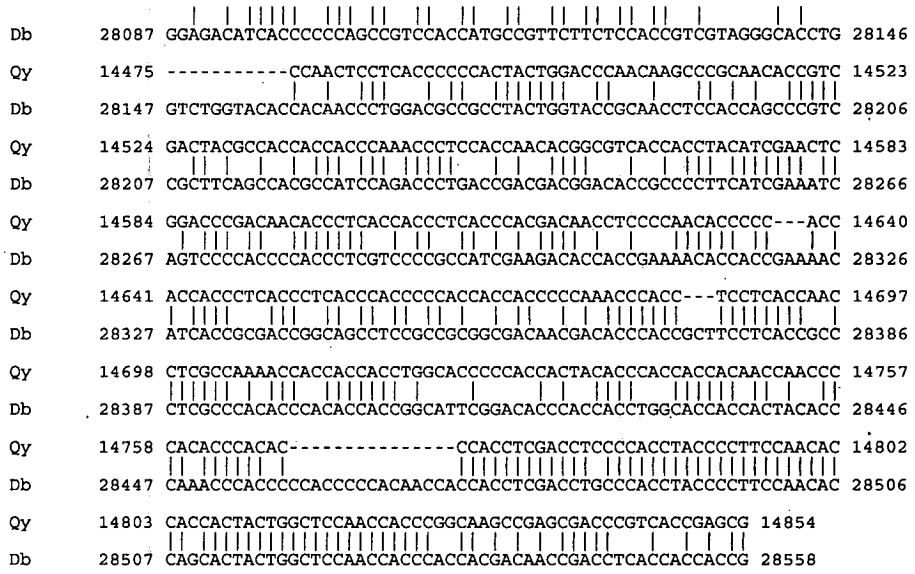
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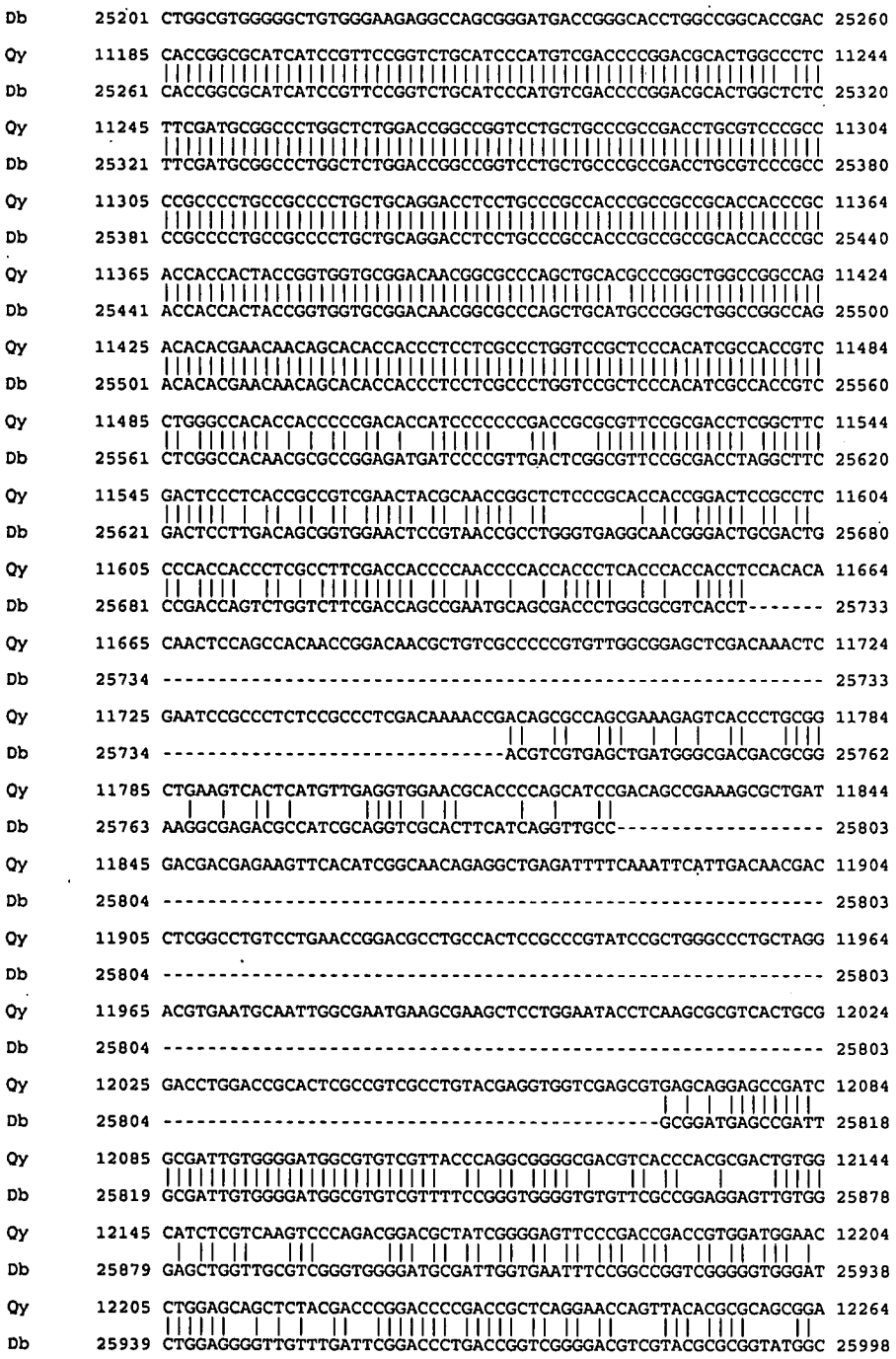
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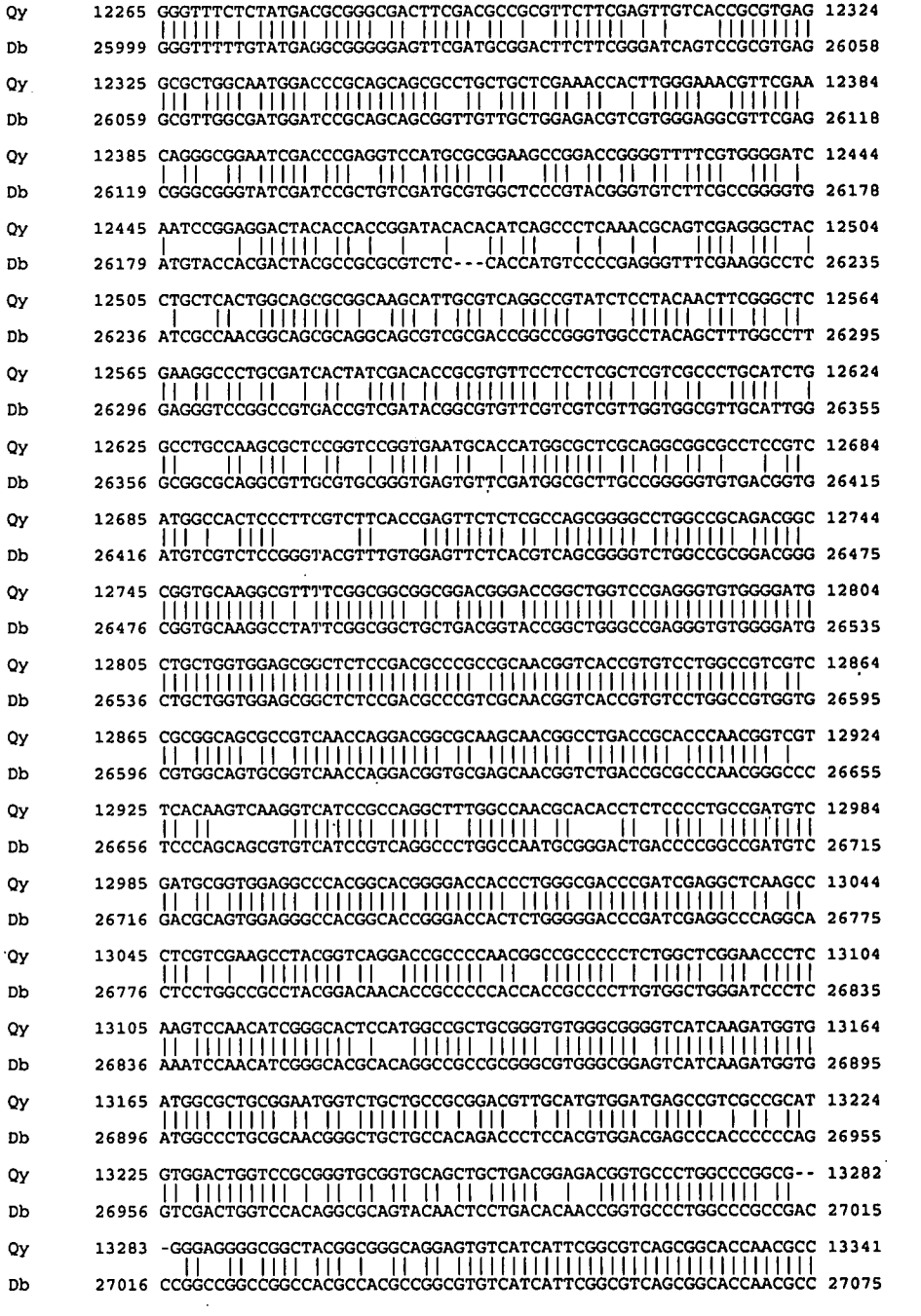
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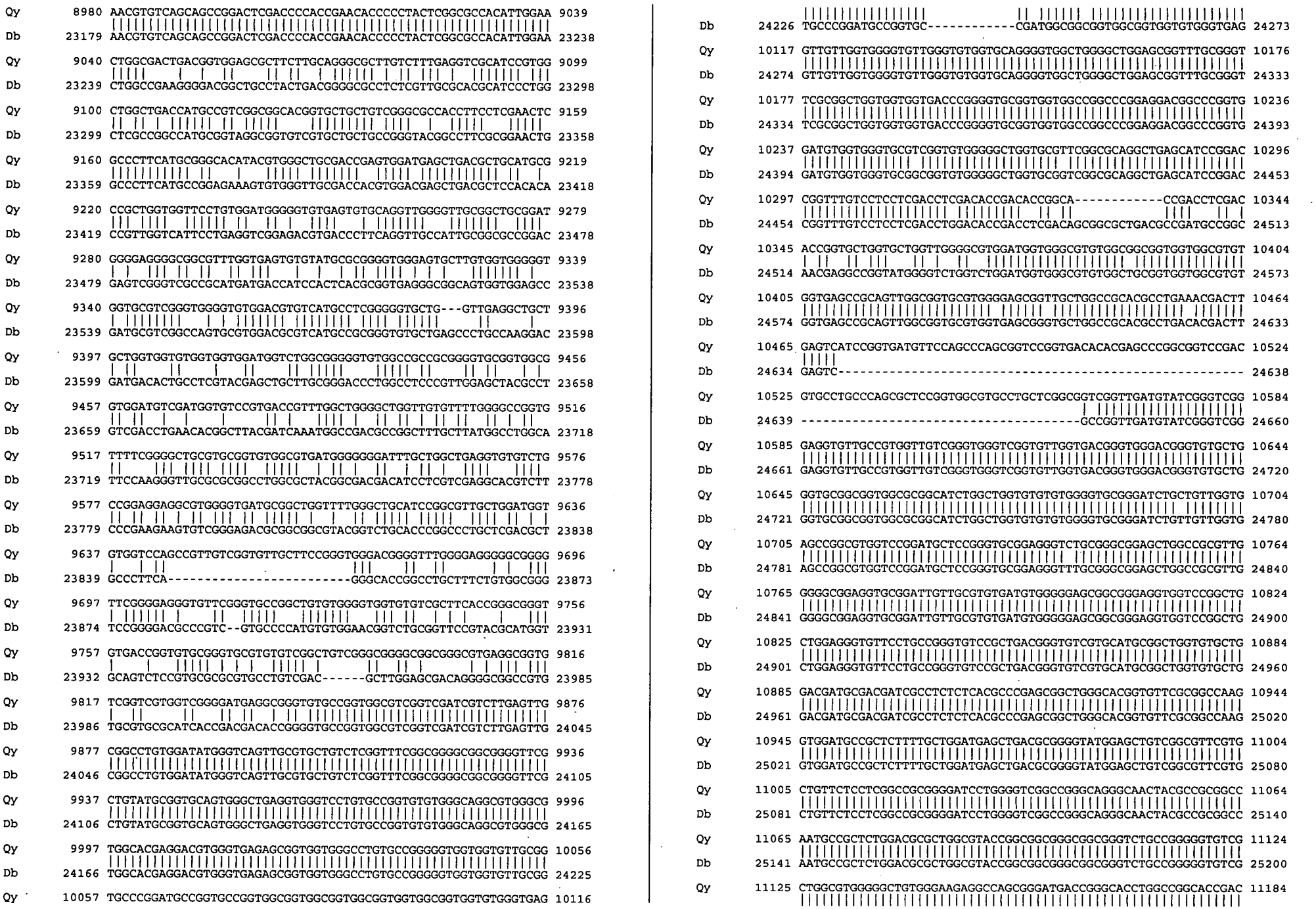


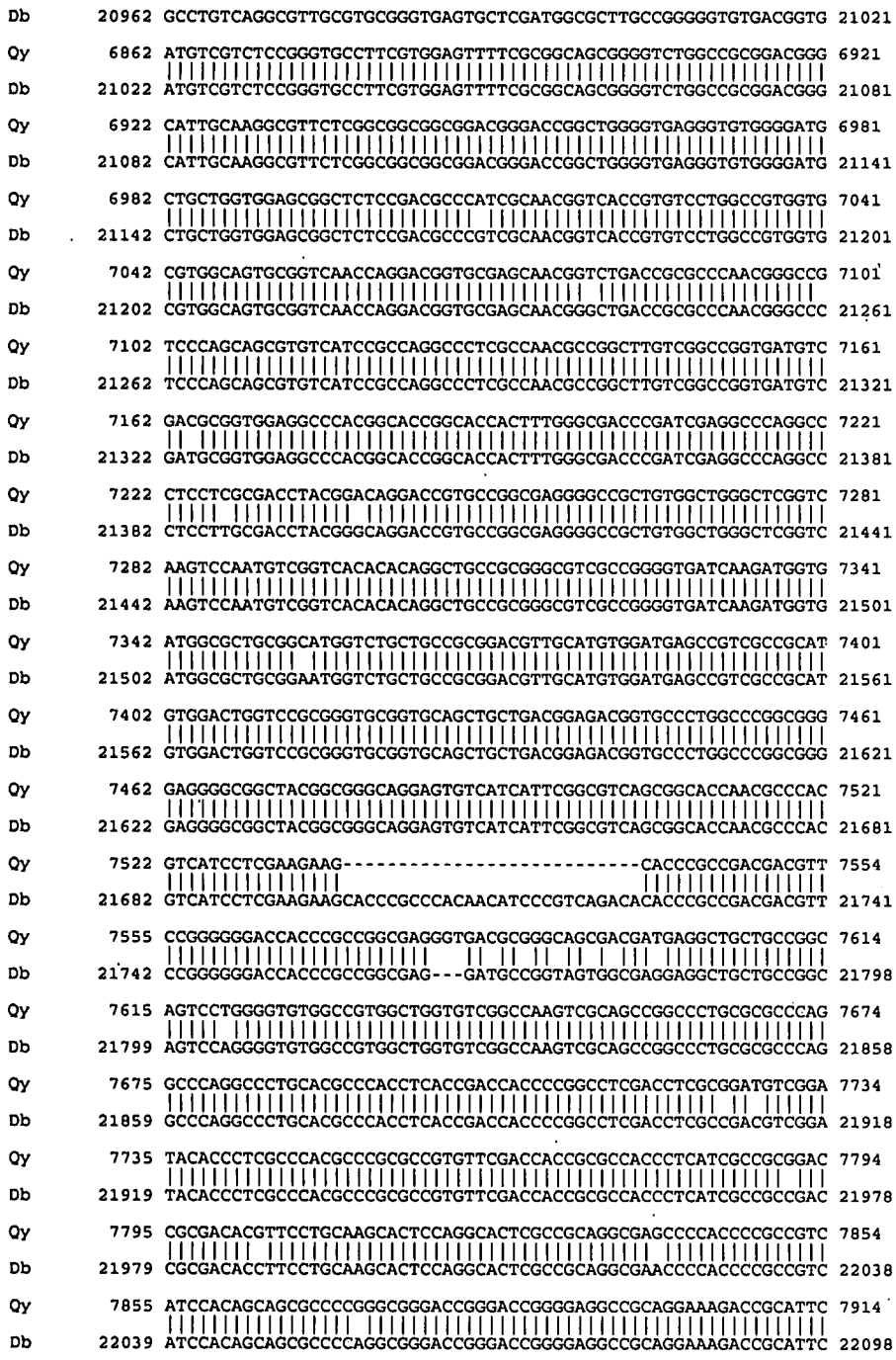


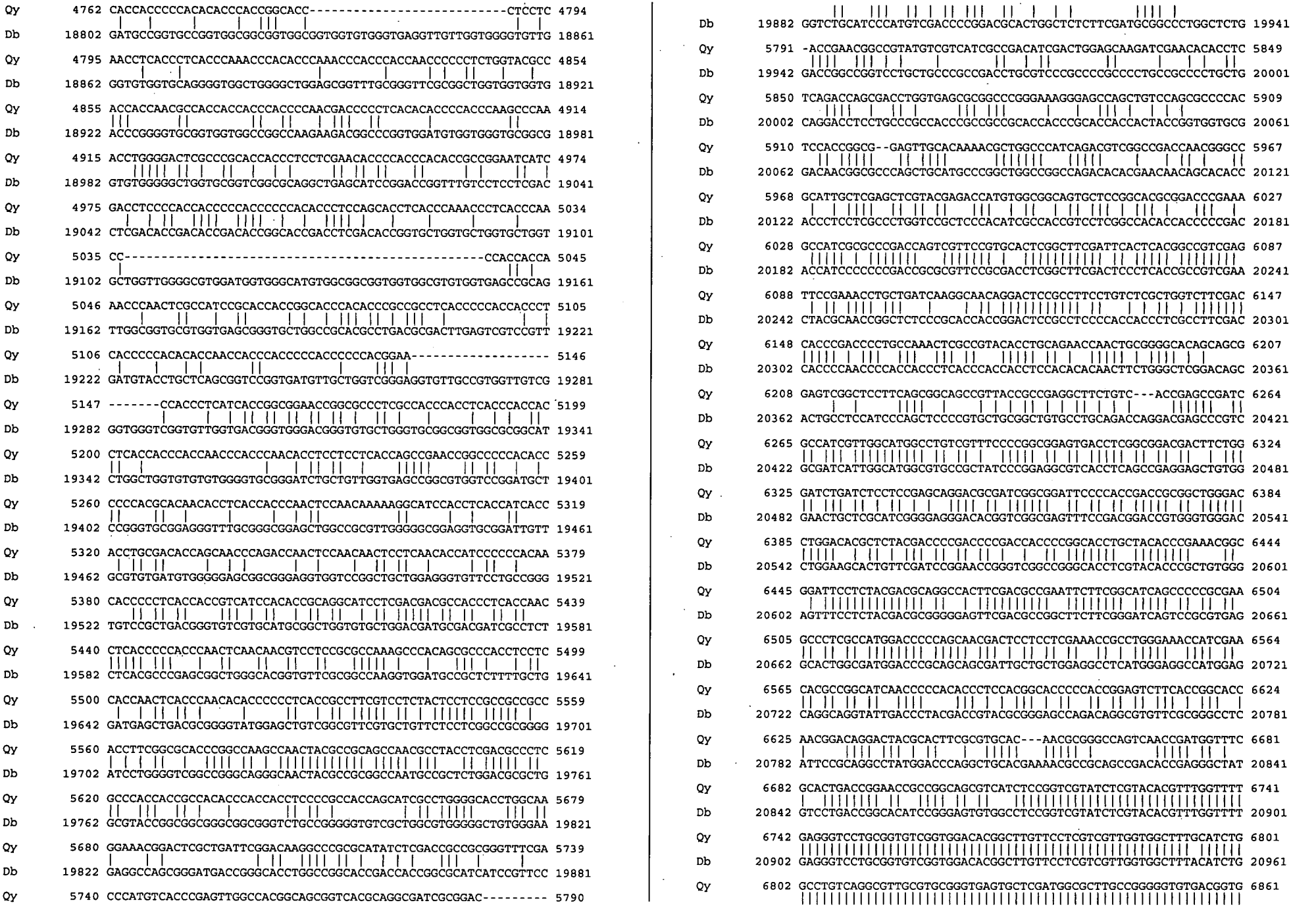
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ACCESSION   AB032367
VERSION     AB032367.1  GI:5902890
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  AUTHORS   Ikeda,H., Nonomiya,T., Usami,M., Ohta,T. and Omura,S.
  TITLE     Organization of the biosynthetic gene cluster for the polyketide
            anthelmintic macrolide avermectin in Streptomyces avermitilis
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9509-9514 (1999)
  MEDLINE   99380548
REFERENCE   2  (bases 1 to 64957)
  AUTHORS   Ikeda,H., Nonomiya,T., Usami,M., Ohta,T. and Omura,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-1999) Haruo Ikeda, School of Pharmaceutical
            Sciences, Kitasato University, Microbial chemistry; 5-9-1
            Shirokane, Minato-ku, Tokyo 108-8641, Japan
            (E-mail:ikeda@mc.pharm.kitasato-u.ac.jp, Tel:+81-3-5791-6242,
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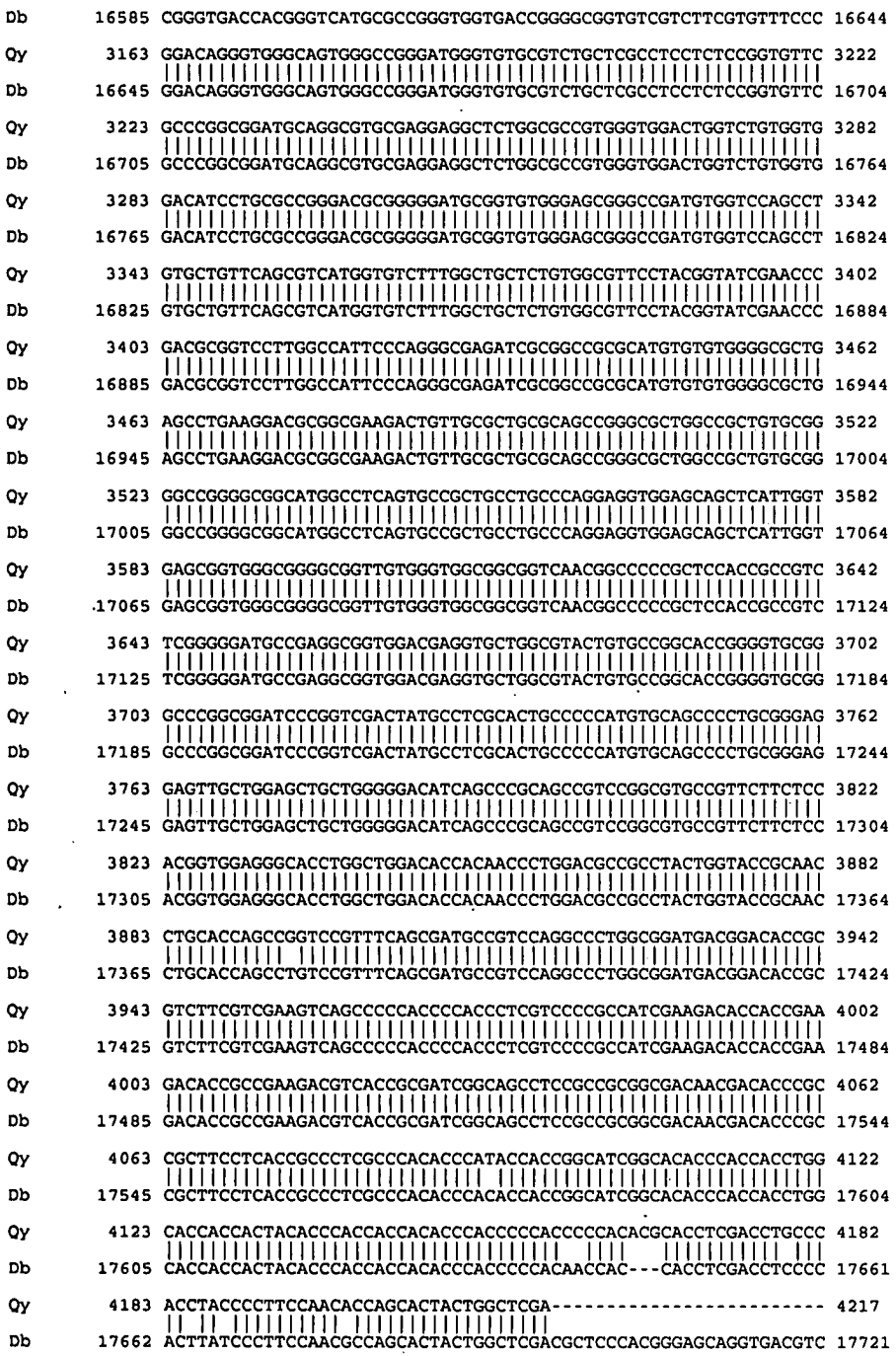


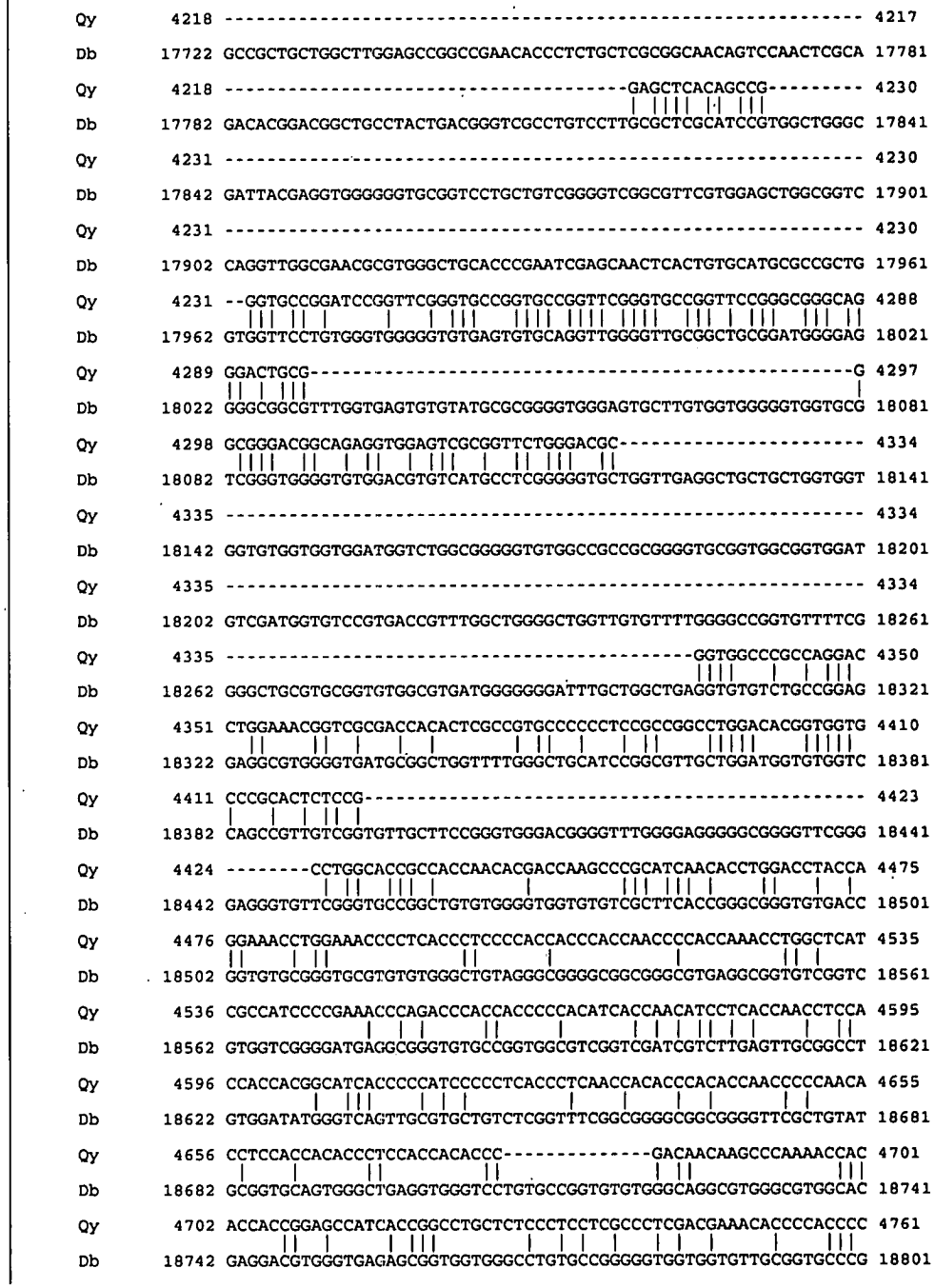





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REFERENCE   1  (bases 1 to 31422)
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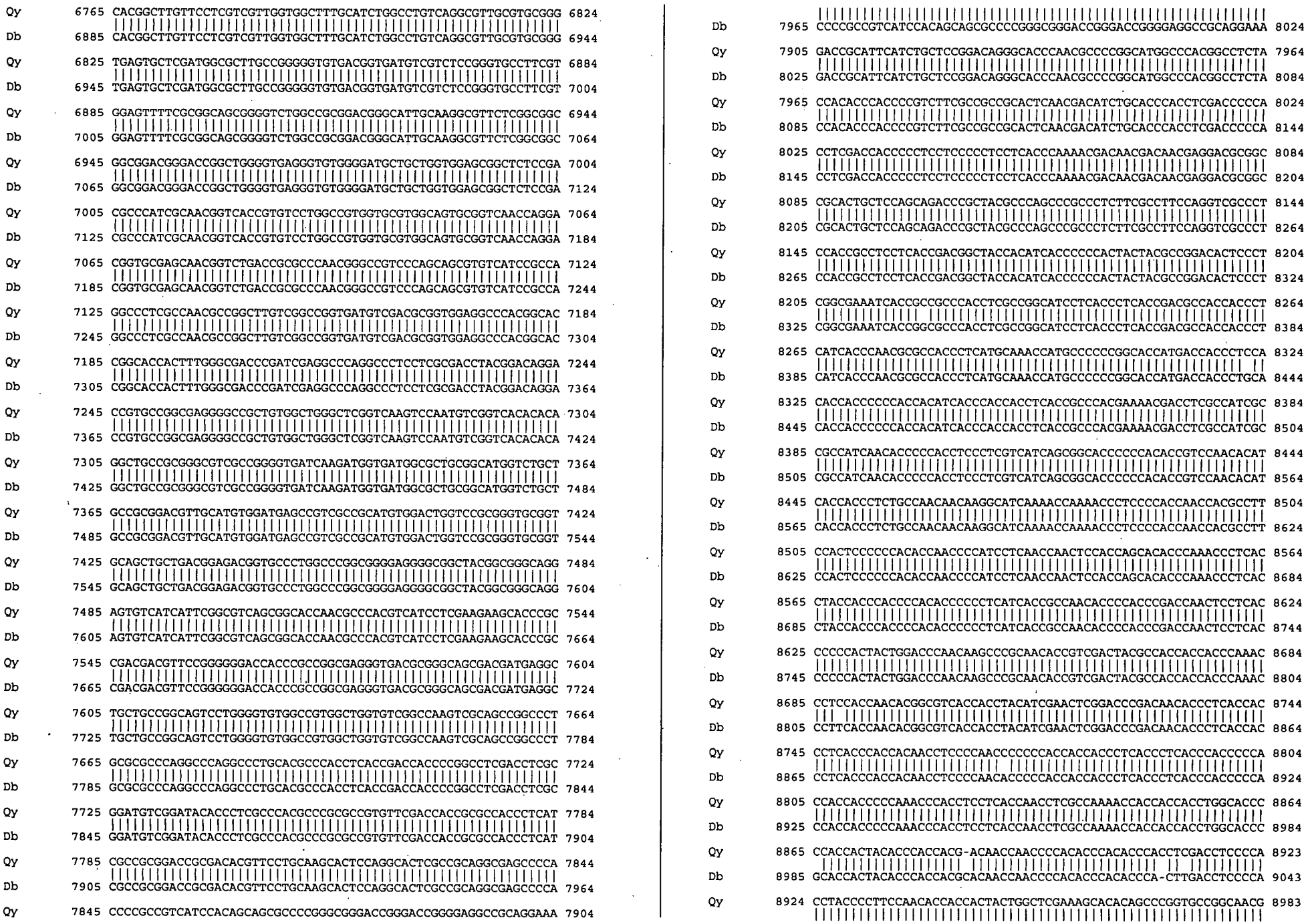
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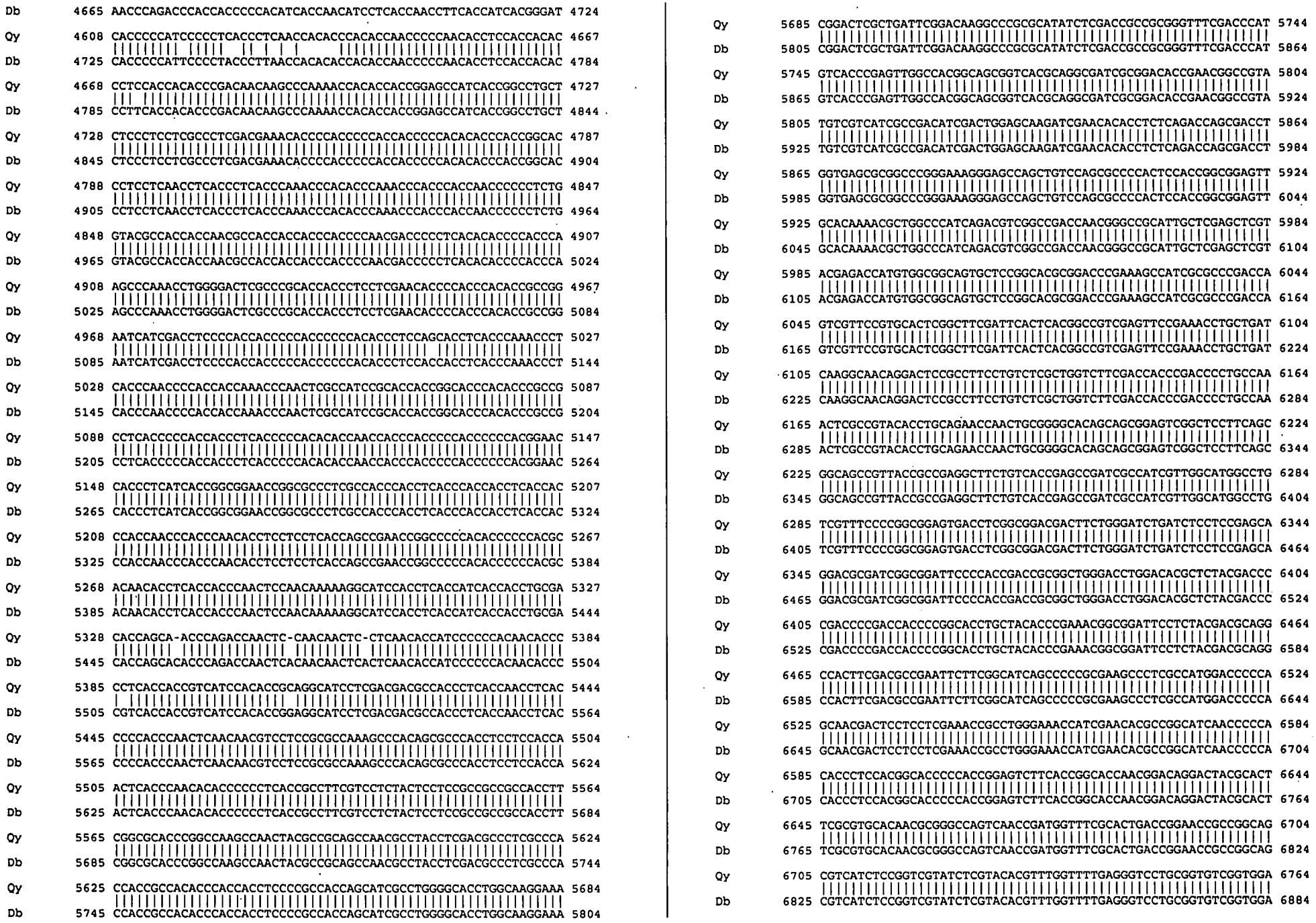
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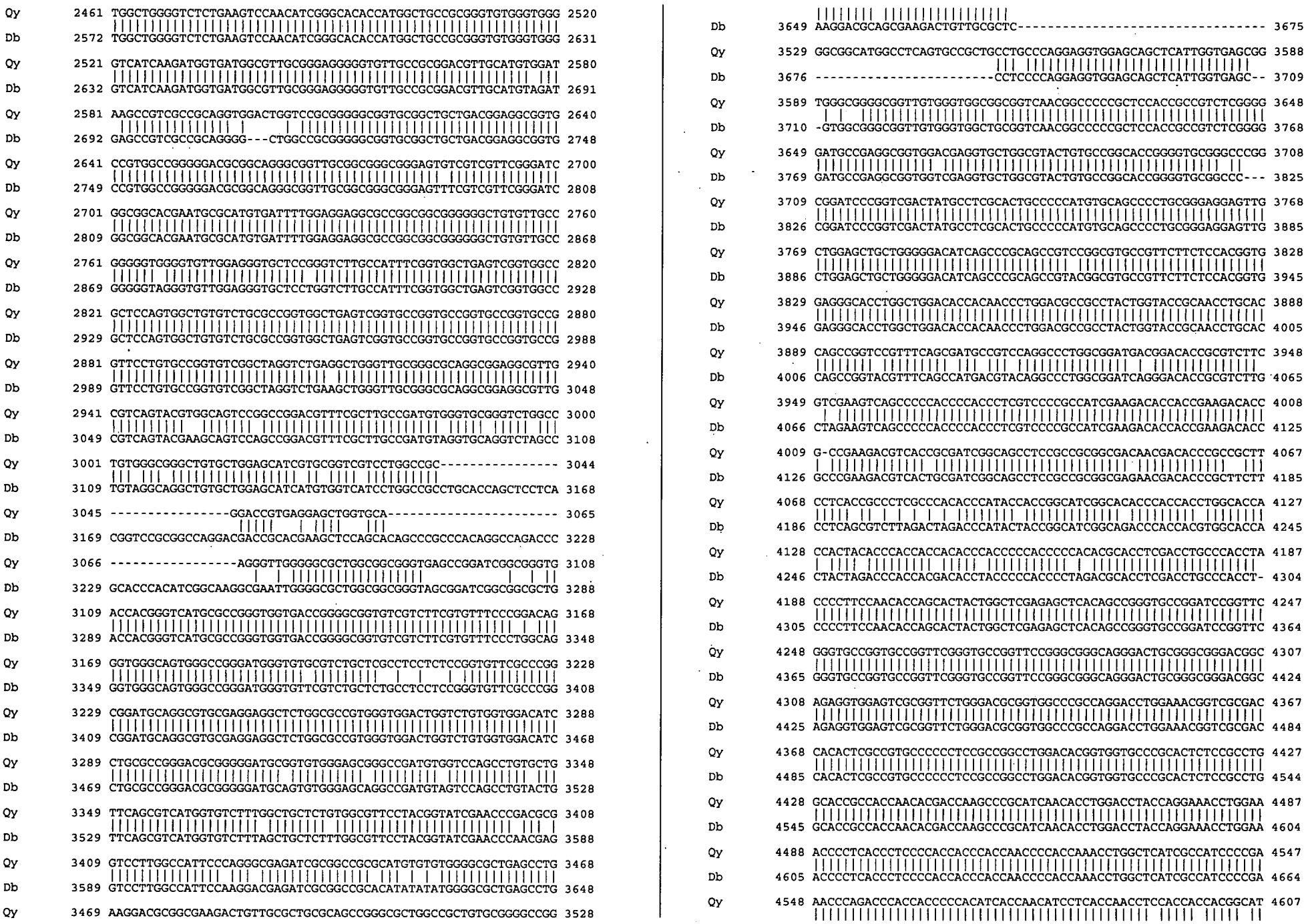
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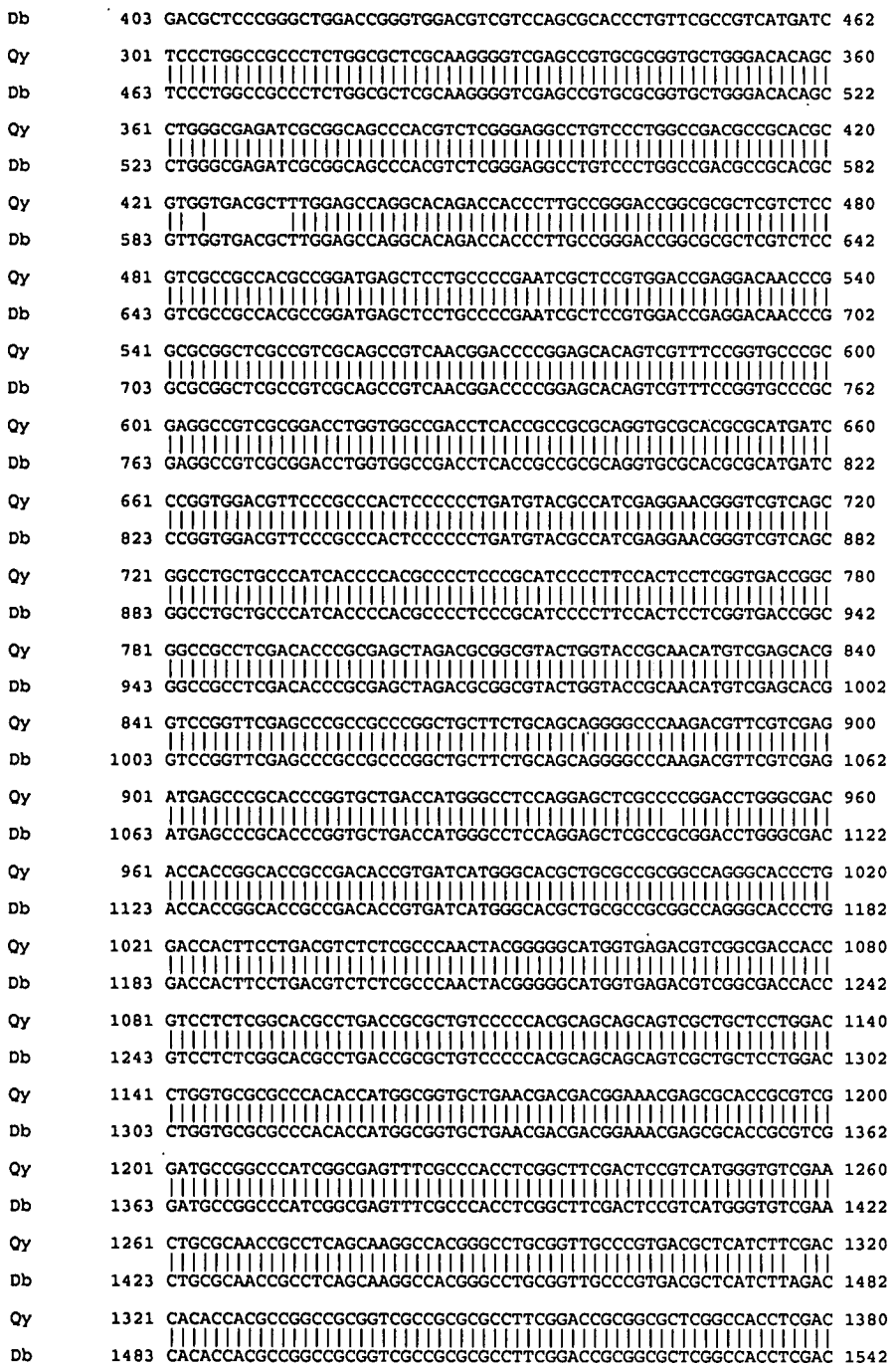
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DEFINITION Avermectin aglycon synthase gene.
ACCESSION E38021
VERSION E38021.1 GI:18626910
KEYWORDS JP 2000245457-A/2.








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DEFINITION Streptomyces avermitilis avermectin polyketide synthase gene, partial cds.
ACCESSION AF275943
VERSION AF275943.1 GI:9964075
KEYWORDS .
SOURCE Streptomyces avermitilis.
ORGANISM Streptomyces avermitilis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE 1 (bases 1 to 11096)
AUTHORS Hong,Y.-S. and Lee,J.J.
TITLE Targeted Gene Disruption of the avermectin O-methyltransferase gene and polyketide synthase gene from Streptomyces avermitilis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 11096)
AUTHORS Hong,Y.-S. and Lee,J.J.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-2000) Anticancer Agent Research Laboratory, Korea Research Institute of Bioscience and Biotechnology, P.O. Box 116, YuSong-Gu, Taejon 305-600, South Korea
FEATURES Location/Qualifiers
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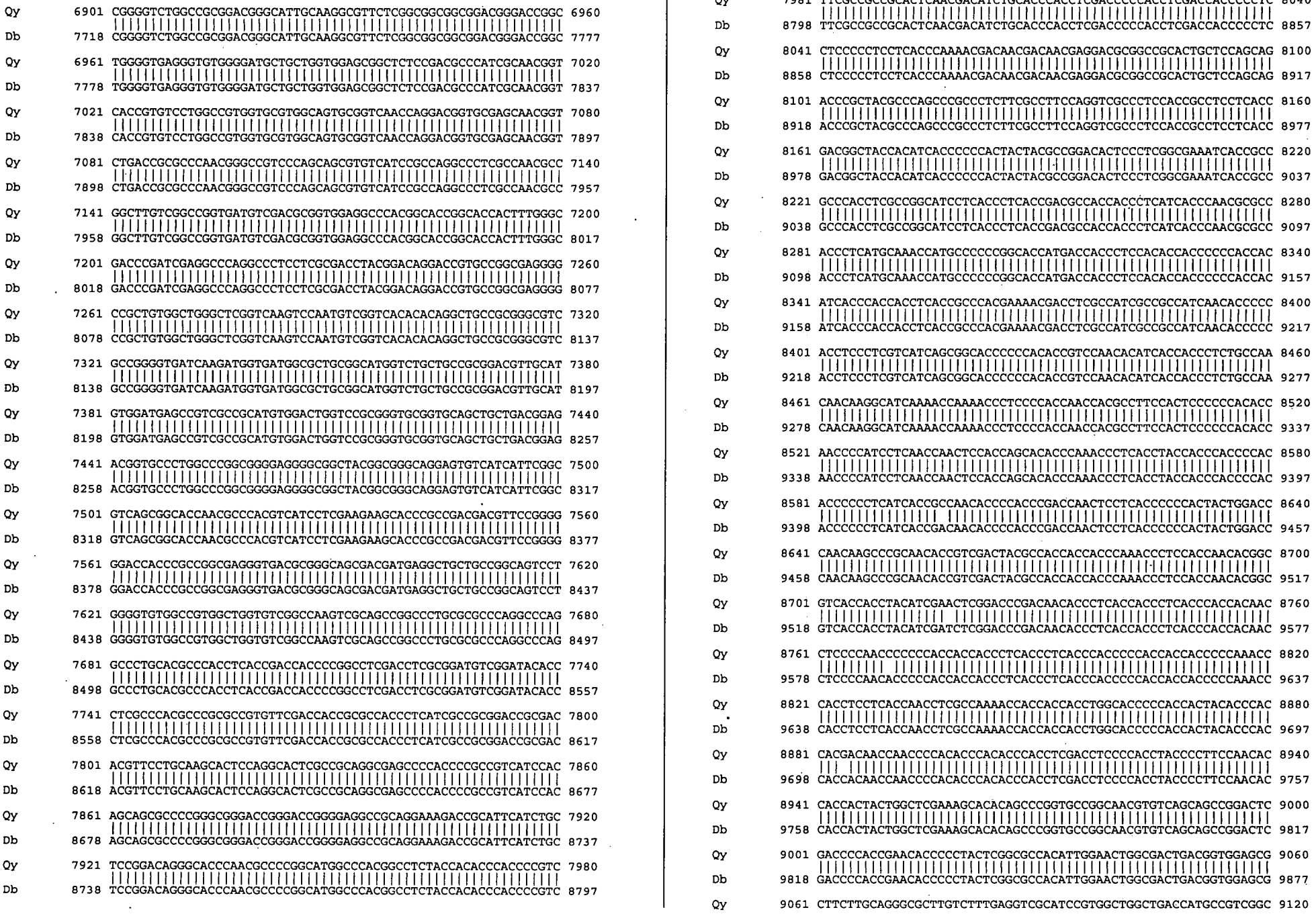
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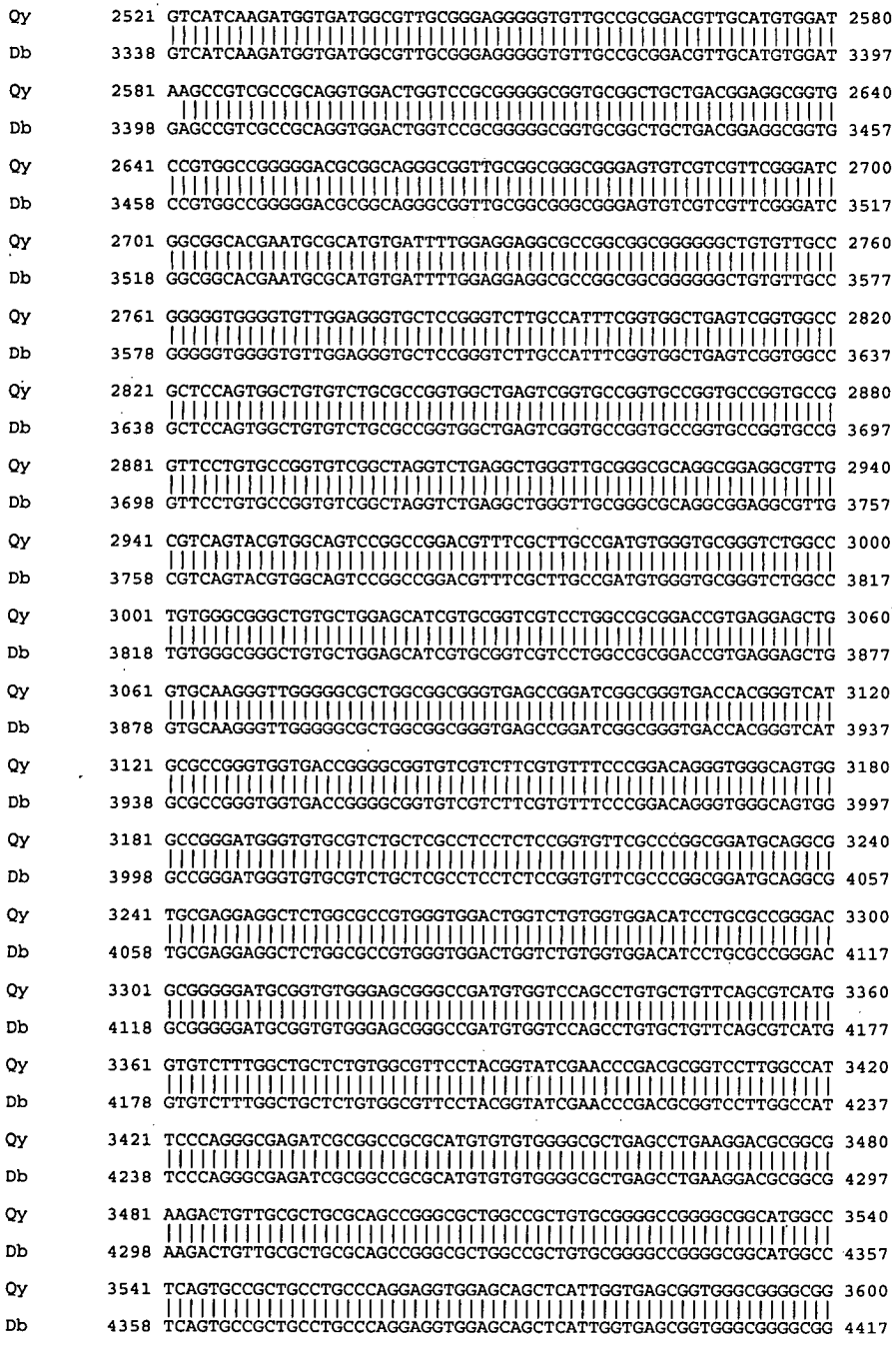
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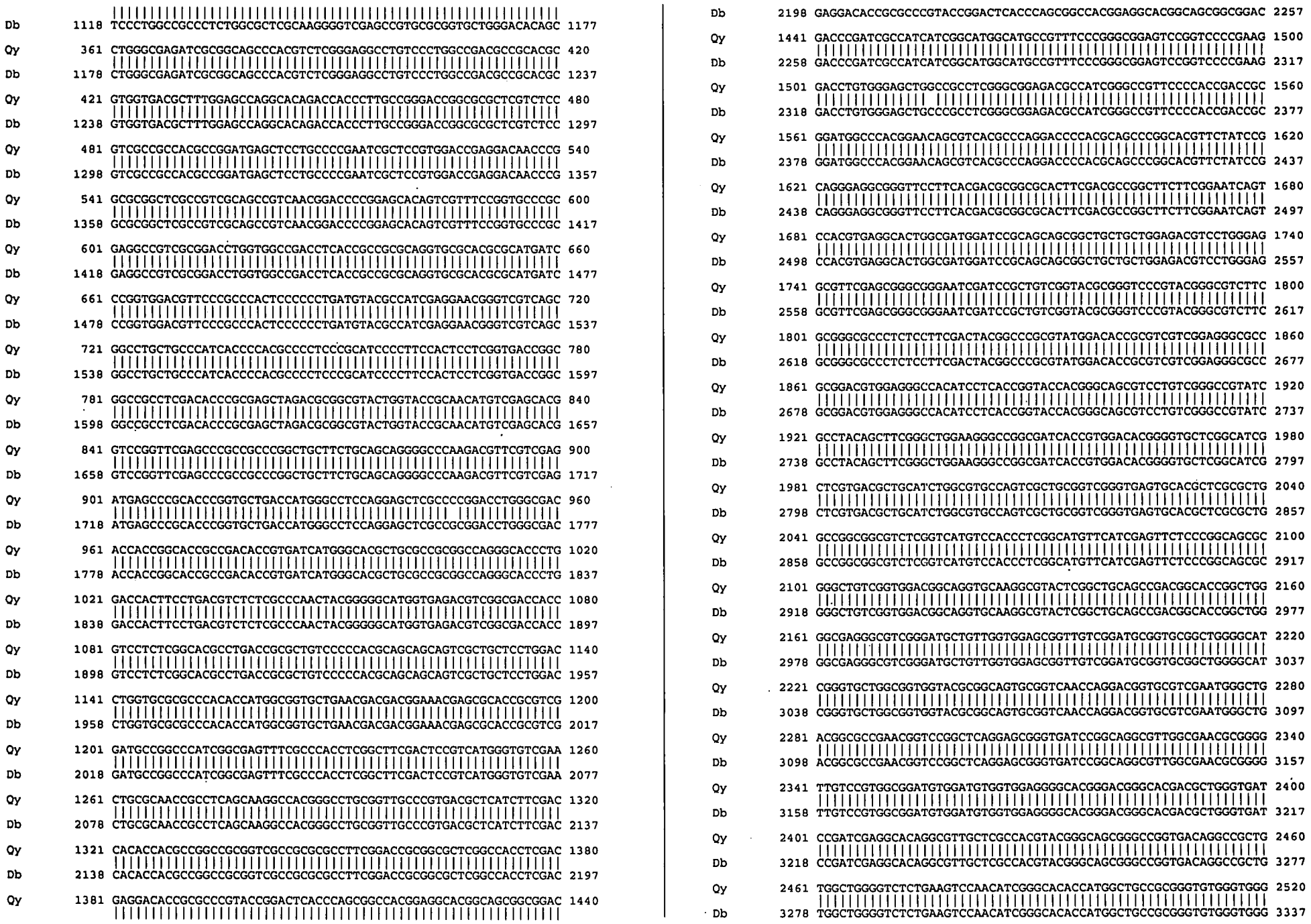
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Qy      5041 CACCAAACCCAACTCGCCATCCGCACCACCGGCACCCACACCCGCCGCCTCACCCCCACC 5100
Db      5858 CACCAAACCCAACTCGCCATCCGCACCACCGGCACCCACACCCGCCGCCTCACCCCCACC 5917
Qy      5101 ACCCTCACCCCCACACACCAACCACCCACCCCCACCCCCCACGGAACCACCCTCATCACC 5160
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Qy      5341 GACCAACTCCAACAACTCCTCAACACCATCCCCCCACAACACCCCCTCACCACCGTCATC 5400
Db      6158 GACCAACTCCAACATCTCCTCAACACCATCCCCCCACAACACCCCCTCACCACCGTCATC 6217
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Qy      5521 CCCCTCACCGCCTTCGTCCTCTACTCCTCCGCCGCCGCCACCTTCGGCGCACCCGGCCAA 5580
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Qy      6001 GCAGTGCTCCGGCACGCGGACCCGAAAGCCATCGCGCCCGACCAGTCGTTCCGTGCACTC 6060
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Qy      6121 CGCCTTCCTGTCTCGCTGGTCTTCGACCACCCGACCCCTGCCAAACTCGCCGTACACCTG 6180
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Qy      6181 CAGAACCAACTGCGGGGCACAGCAGCGGAGTCGGCTCCTTCAGCGGCAGCCGTTACCGCC 6240
Db      6998 CAGAACCAACTGCGGGGCACAGCAGCGGAGTCGGCTCCTTCAGCGGCAGCCGTTACCGCC 7057
Qy      6241 GAGGCTTCTGTCACCGAGCCGATCGCCATCGTTGGCATGGCCTGTCGTTTCCCCGGCGGA 6300
Db      7058 GAGGCTTCTGTCACCGAGCCGATCGCCATCGTTGGCATGGCCTGTCGTTTCCCCGGCGGA 7117
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Db      7118 GTGACCTCGGCGGACGACTTCTGGGATCTGATCTCCTCCGAGCAGGACGCGATCGGCGGA 7177
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Db      7178 TTCCCCACCGACCGCGGCTGGGACCTGGACACGCTCTACGACCCCGACCCCGACCACCCC 7237
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Qy      6841 CTTGCCGGGGGTGTGACGGTGATGTCGTCTCCGGGTGCCTTCGTGGAGTTTTCGCGGCAG 6900
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Qy      29461 GATCGGCCGCTGACCGGTGTCGTGCACAGTGCGGGCATCCTGGACGACGGCGTGATCACG 29520
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Qy      29701 CTTGCTCATCGCCGCCGCGCCGAGGGGCTGCCCGCCGTCTCTCTCGCCTGGGGCCTGTGG 29760
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RESULT 3
AX006889

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LOCUS       AX006889               12381 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 1 from Patent WO0001827.
ACCESSION   AX006889
VERSION     AX006889.1  GI:9994904
KEYWORDS    .
SOURCE      Streptomyces avermitilis.
  ORGANISM  Streptomyces avermitilis
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE   1  (bases 1 to 12381)
  AUTHORS   Kellenberger,J.L., Leadlay,P.F., Staunton,J., Mcarthur,H.A. and
            Stutzman-Engwall,K.J.
  TITLE     Polyketides, their preparation, and materials for use therein
  JOURNAL   Patent: WO 0001827-A 1 13-JAN-2000;
            KELLENBERGER JOHANNES LAURENZ (CH); LEADLAY PETER FRANCIS (GB);
            STAUNTON JAMES (GB); BIOTICA TECH LTD (GB); PFIZER (US); MCARTHUR
            HAMISH ALASTAIR IRVIN (US); STUTZMAN ENGWALL KIM JONELLE (US)
FEATURES             Location/Qualifiers
     source          1. .12381
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BASE COUNT     1884 a   4561 c   4005 g   1931 t
ORIGIN
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Query Match 37.6%; Score 11548; DB 6; Length 12381;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 11554; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy      27421 AACCCCCACACCCACCTCGACCTGCCCACCTACCCCTTCCAACACCAGCACTACTGGCTC 27480
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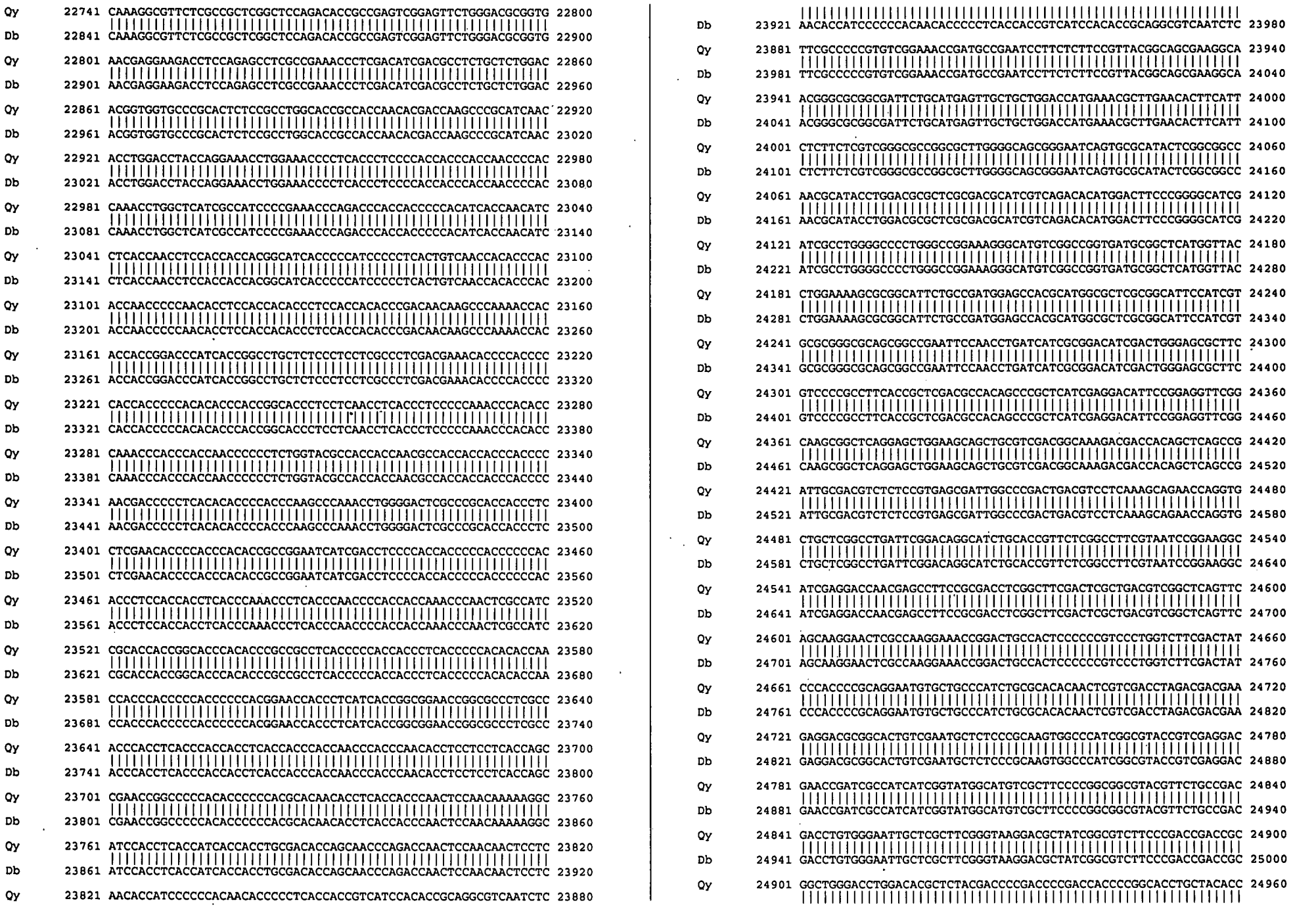
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Qy      25621 CCCAACGGGCCCTCCCAGCAGCGTGTCATCCGTCAGGCCCTGGCCAATGCGGGACTGACC 25680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25721 CCCAACGGGCCCTCCCAGCAGCGTGTCATCCGTCAGGCCCTGGCCAATGCGGGACTGACC 25780
Qy      25681 CCGGCCGATGTCGACGCAGTGGAGGGCCACGGCACCGGGACCACTCTGGGGGACCCGATC 25740
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Db      25781 CCGGCCGATGTCGACGCAGTGGAGGGCCACGGCACCGGGACCACTCTGGGGGACCCGATC 25840
Qy      25741 GAGGCCCAGGCACTCCTGGCCGCCTACGGACAACACCGCCCCCACCACCGCCCCTTGTGG 25800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25841 GAGGCCCAGGCACTCCTGGCCGCCTACGGACAACACCGCCCCCACCACCGCCCCTTGTGG 25900
Qy      25801 CTGGGATCCCTCAAATCCAACATCGGGCACGCACAGGCCGCCGCGGGCGTGGGCGGAGTC 25860
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Db      25901 CTGGGATCCCTCAAATCCAACATCGGGCACGCACAGGCCGCCGCGGGCGTGGGCGGAGTC 25960
Qy      25861 ATCAAGATGGTGATGGCCCTGCGCAACGGGCTGCTGCCACAGACCCTCCACGTGGACGAG 25920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25961 ATCAAGATGGTGATGGCCCTGCGCAACGGGCTGCTGCCACAGACCCTCCACGTGGACGAG 26020
Qy      25921 CCCACCCCCCAGGTCGACTGGTCCACAGGCGCAGTACAACTCCTGACACAACCGGTGCCC 25980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26021 CCCACCCCCCAGGTCGACTGGTCCACAGGCGCAGTACAACTCCTGACACAACCGGTGCCC 26080
Qy      25981 TGGCCCGCCGACCCGGCCGGCCGGCCACGCCACGCCGGCGTGTCATCATTCGGCGTCAGC 26040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26081 TGGCCCGCCGACCCGGCCGGCCGGCCACGCCACGCCGGCGTGTCATCATTCGGCGTCAGC 26140
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Qy      26041 GGCACCAACGCCCACATCATCCTCGAAGAAGCACCCACTCCCCAGGACAGCGATACCGAC 26100
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Db      26141 GGCACCAACGCCCACATCATCCTCGAAGAAGCACCCACTCCCCAGGACAGCGATACCGAC 26200
Qy      26101 GACGAACCGCCTGCCAACGCACCAGCCCTGCCCCATCCCCTCCCTCTTCCCGTGCCGGTG 26160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26201 GACGAACCGCCTGCCAACGCACCAGCCCTGCCCCATCCCCTCCCTCTTCCCGTGCCGGTG 26260
Qy      26161 TCGGCGAGGTCTGAGGCCGGGTTGCGGGCGCAGGCACAGGCGTTGCGCCAGTACGTGGCA 26220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26261 TCGGCGAGGTCTGAGGCCGGGTTGCGGGCGCAGGCACAGGCGTTGCGCCAGTACGTGGCA 26320
Qy      26221 GCCCGCCCGGACATGTCACCTGCCGACATTGGTGCGGGTCTGGCCCGCGGCCGGGCCGTA 26280
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Db      26321 GCCCGCCCGGACATGTCACCTGCCGACATTGGTGCGGGTCTGGCCCGCGGCCGGGCCGTA 26380
Qy      26281 CTGGAACACCGCGCCGTCATCCTGGCCGCGGACCGCGAGGAACTGGCGCAGGCACTGACA 26340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26381 CTGGAACACCGCGCCGTCATCCTGGCCGCGGACCGCGAGGAACTGGCGCAGGCACTGACA 26440
Qy      26341 GCCCTGGCAGCCGGCGAACCCCACCCCCACATCACCACAGGCCACACCCGGGGCGGTGAC 26400
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Db      26441 GCCCTGGCAGCCGGCGAACCCCACCCCCACATCACCACAGGCCACACCCGGGGCGGTGAC 26500
Qy      26401 CGCGGCGGCGTCGTCTTCGTCTTCCCCGGACAGGGCGGCCAGTGGGCCGGGATGGGCCTG 26460
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Db      26501 CGCGGCGGCGTCGTCTTCGTCTTCCCCGGACAGGGCGGCCAGTGGGCCGGGATGGGCCTG 26560
Qy      26461 ACCCTGCTCACCTCCTCACCCGTGTTCGCCGAACACATCGACGCATGCGAGAAAGCCCTC 26520
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Db      26561 ACCCTGCTCACCTCCTCACCCGTGTTCGCCGAACACATCGACGCATGCGAGAAAGCCCTC 26620
Qy      26521 ACCCCCTGGGTGCCCTGGTCCCTGACCGACATCCTGCACCGCGACCCCGACGACCCCGCA 26580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26621 ACCCCCTGGGTGCCCTGGTCCCTGACCGACATCCTGCACCGCGACCCCGACGACCCCGCA 26680
Qy      26581 TGGCAACAAGCCGACGTGGTCCAGCCCGTGCTCTTCAGCATCATGGTCTCCCTCGCCGCC 26640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26681 TGGCAACAAGCCGACGTGGTCCAGCCCGTGCTCTTCAGCATCATGGTCTCCCTCGCCGCC 26740
Qy      26641 CTGTGGCGCTCCTACGGCATCGAACCCGACGCGGTCCTCGGCCACTCCCAGGGAGAAATC 26700
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Db      26741 CTGTGGCGCTCCTACGGCATCGAACCCGACGCGGTCCTCGGCCACTCCCAGGGAGAAATC 26800
Qy      26701 GCCGCCGCCCACATCTGCGGCGCACTCAGCCTGAAAGACGCCGCCAAAACCGTTGCACTG 26760
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Db      26801 GCCGCCGCCCACATCTGCGGCGCACTCAGCCTGAAAGACGCCGCCAAAACCGTTGCACTG 26860
Qy      26761 CGCAGCCGCGCACTGGCCGCCGTACGAGGCCGGGGCGCCATGGCCTCACTGCCCCTGCCC 26820
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Db      26861 CGCAGCCGCGCACTGGCCGCCGTACGAGGCCGGGGCGCCATGGCCTCACTGCCCCTGCCC 26920
Qy      26821 GCCCAGGACGTGCAGCAGCTCATTTCCGAACGGTGGGAAGGGCAGTTGTGGGTGGCAGCC 26880
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Db      26921 GCCCAGGACGTGCAGCAGCTCATTTCCGAACGGTGGGAAGGGCAGTTGTGGGTGGCAGCC 26980
Qy      26881 CTCAACGGCCCCCACTCCACCACCGTCTCCGGCGACACCAAGGCGGTGGATGAGGTGCTG 26940
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Db      26981 CTCAACGGCCCCCACTCCACCACCGTCTCCGGCGACACCAAGGCGGTGGATGAGGTGCTG 27040
Qy      26941 GCGCACTGCACCGACACCGGCCTACGGGCCAAACGCATCCCCGTCGACTACGCCTCCCAC 27000
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Db      27041 GCGCACTGCACCGACACCGGCCTACGGGCCAAACGCATCCCCGTCGACTACGCCTCCCAC 27100
Qy      27001 TGCCCCCACGTCCAACCCCTCCACGACGAACTCCTGCACCTGCTGGGAGACATCACCCCC 27060
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Db      27101 TGCCCCCACGTCCAACCCCTCCACGACGAACTCCTGCACCTGCTGGGAGACATCACCCCC 27160
Qy      27061 CAGCCGTCCACCGTGCCGTTCTTCTCCACCGTGGAAGGCACCTGGCTGGACACCACAACC 27120
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Db      27161 CAGCCGTCCACCGTGCCGTTCTTCTCCACCGTGGAAGGCACCTGGCTGGACACCACAACC 27220
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Db      20621 GCGTGTTCCTCCTCGCTCGTCGCCCTGCACCTCGCCTGCCAGTCCCTCAGGTCCGGTGAA 20680

Qy      20581 TGCACCATGGCCTTGGCCGGCGGGGCCACGGTCATGACCACCCCGATCACCTTCACCGAA 20640
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Db      20681 TGCACCATGGCCTTGGCCGGCGGGGCCACGGTCATGACCACCCCGATCACCTTCACCGAA 20740

Qy      20641 TTCGCCCGCCAACGCGGACTCGCCCCCGACGGGCGTTGCAAGGCGTTCTCGGCGGCGGCT 20700
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Db      20741 TTCGCCCGCCAACGCGGACTCGCCCCCGACGGGCGTTGCAAGGCGTTCTCGGCGGCGGCT 20800

Qy      20701 GACGGTACCGGCTGGGGTGAGGGTGTGGGGATGCTGCTGGTGGAGCGGCTCTCCGACGCC 20760
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Db      20801 GACGGTACCGGCTGGGGTGAGGGTGTGGGGATGCTGCTGGTGGAGCGGCTCTCCGACGCC 20860

Qy      20761 CGCCGCAACGGTCACCGTGTCCTGGCCGTGGTGCGTGGCAGTGCGGTCAACCAGGACGGT 20820
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Db      20861 CGCCGCAACGGTCACCGTGTCCTGGCCGTGGTGCGTGGCAGTGCGGTCAACCAGGACGGT 20920

Qy      20821 GCGAGCAACGGTCTGACCGCGCCCAACGGGCCCTCCCAGCAGCGCGTCATCCGCCAGGCC 20880
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Db      20921 GCGAGCAACGGTCTGACCGCGCCCAACGGGCCCTCCCAGCAGCGCGTCATCCGCCAGGCC 20980

Qy      20881 CTCGCCAACGCGGACCTGACCCCCGCCGACGTCGATGCGGTGGAGGCCCACGGCACCGGC 20940
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Db      20981 CTCGCCAACGCGGACCTGACCCCCGCCGACGTCGATGCGGTGGAGGCCCACGGCACCGGC 21040

Qy      20941 ACCACTTTGGGCGACCCGATCGAGGCCCAGGCCATCCTCGCGACCTACGGACAGGACCGT 21000
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Db      21041 ACCACTTTGGGCGACCCGATCGAGGCCCAGGCCATCCTCGCGACCTACGGACAGGACCGT 21100

Qy      21001 CCCGGCAACGGGCCGTTGTGGCTGGGCTCCGTCAAGTCCAACGTCGGACACACACAGGCC 21060
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Db      21101 CCCGGCAACGGGCCGTTGTGGCTGGGCTCCGTCAAGTCCAACGTCGGACACACACAGGCC 21160

Qy      21061 GCGGCGGGCGTGGCCGGAGTGATCAAGATGGTGATGGCCCTCCGCCACCGGACACTCCCA 21120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21161 GCGGCGGGCGTGGCCGGAGTGATCAAGATGGTGATGGCCCTCCGCCACCGGACACTCCCA 21220

Qy      21121 CCGACTCTCCACGCGGATGAGCCGTCGCCGCATGTGGACTGGTCCGCGGGTGCGGTGCAG 21180
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Db      21221 CCGACTCTCCACGCGGATGAGCCGTCGCCGCATGTGGACTGGTCCGCGGGTGCGGTGCAG 21280

Qy      21181 CTGCTGACGGAGACGGTGCCCTGGCCCGGCGGGGAGGGGCGGCCGCGGCGGGCAGGAGTG 21240
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Db      21281 CTGCTGACGGAGACGGTGCCCTGGCCCGGCGGGGAGGGGCGGCCGCGGCGGGCAGGAGTG 21340

Qy      21241 TCATCATTCGGCGTCAGCGGCACCAACGCCCACGTCATCCTCGAAGAAGCACCCGCCGAC 21300
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Db      21341 TCATCATTCGGCGTCAGCGGCACCAACGCCCACGTCATCCTCGAAGAAGCACCCGCCGAC 21400

Qy      21301 GACGTTCCGGGGGGGACCACCCGCCGACGAGGATGCCGGTAGTGGCGAGGAGGCTGCTGCC 21360
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Db      21401 GACGTTCCGGGGGGGACCACCCGCCGACGAGGATGCCGGTAGTGGCGAGGAGGCTGCTGCC 21460

Qy      21361 GGCAGTCCTGGGGTGTGGCCGTGGCTGGTGTCGGCCAAGTCGCAGCCGGCCCTGCGCGCC 21420
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Db      21461 GGCAGTCCTGGGGTGTGGCCGTGGCTGGTGTCGGCCAAGTCGCAGCCGGCCCTGCGCGCC 21520

Qy      21421 CAGGCCCAGGCCCTGCACGCCCACCTCACCGACCACCCCGGCCTCGACCTCGCCGACGTC 21480
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Db      21521 CAGGCCCAGGCCCTGCACGCCCACCTCACCGACCACCCCGGCCTCGACCTCGCCGACGTC 21580

Qy      21481 GGATACACCCTCGCCCACGCCCGCGCCGTGTTCGACCACCGCGCCACCCTCATCGCCGCC 21540
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Db      21581 GGATACACCCTCGCCCACGCCCGCGCCGTGTTCGACCACCGCGCCACCCTCATCGCCGCC 21640

Qy      21541 GACCGCGACACCTTCCTGCAAGCACTCCAGGCACTCGCCGCAGGCGAACCCCACCCCGCC 21600
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Db      21641 GACCGCGACACCTTCCTGCAAGCACTCCAGGCACTCGCCGCAGGCGAACCCCACCCCGCC 21700

Qy      21601 GTCATCCACAGCAGCGCCCCAGGCGGGACCGGGACCGGGGAGGCCGCAGGAAAGACCGCA 21660
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Db      21701 GTCATCCACAGCAGCGCCCCAGGCGGGACCGGGACCGGGGAGGCCGCAGGAAAGACCGCA 21760

Qy      21661 TTCATCTGCTCCGGACAGGGCACCCAACGCCCCGGCATGGCCCACGGCCTCTACCACACC 21720
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Db      21761 TTCATCTGCTCCGGACAGGGCACCCAACGCCCCGGCATGGCCCACGGCCTCTACCACACC 21820

Qy      21721 CACCCCGTCTTCGCCGCCGCACTCAACGACATCTGCACCCACCTCGACCCCCACCTCGAC 21780
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Db      21821 CACCCCGTCTTCGCCGCCGCACTCAACGACATCTGCACCCACCTCGACCCCCACCTCGAC 21880

Qy      21781 CACCCCCTCCTCCCCCTCCTCACCCAAAACGACAACGACAACGACAACGAGGACGCGGCC 21840
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Db      21881 CACCCCCTCCTCCCCCTCCTCACCCAAAACGACAACGACAACGACAACGAGGACGCGGCC 21940

Qy      21841 GCACTGCTCCAGCAGACCCCGTACGCCCAGCCCGCCCTCTTCGCCTTCCAGGTCGCCCTC 21900
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Db      21941 GCACTGCTCCAGCAGACCCCGTACGCCCAGCCCGCCCTCTTCGCCTTCCAGGTCGCCCTC 22000

Qy      21901 CACCGCCTCCTCACCGACGGCTACCACATCACCCCCCACTACTACGCCGGACACTCCCTC 21960
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Db      22001 CACCGCCTCCTCACCGACGGCTACCACATCACCCCCCACTACTACGCCGGACACTCCCTC 22060

Qy      21961 GGCGAAATCACCGCCGCCCACCTCGCCGGCATCCTCACCCTCACCGACGCCACCACCCTC 22020
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Db      22061 GGCGAAATCACCGCCGCCCACCTCGCCGGCATCCTCACCCTCACCGACGCCACCACCCTC 22120

Qy      22021 ATCACCCAACGCGCCACCCTCATGCAAACCATGCCCCCCGGCACCATGACCACCCTCCAC 22080
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Db      22121 ATCACCCAACGCGCCACCCTCATGCAAACCATGCCCCCCGGCACCATGACCACCCTCCAC 22180

Qy      22081 ACCACCCCACACCACATCACCCACCACCTCACCGCCCACGAAAACGACCTCGCCATCGCC 22140
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Db      22181 ACCACCCCACACCACATCACCCACCACCTCACCGCCCACGAAAACGACCTCGCCATCGCC 22240

Qy      22141 GCCATCAACACCCCCACCTCCCTCGTCATCAGCGGCACCCCCCACACCGTCCAACACATC 22200
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Db      22241 GCCATCAACACCCCCACCTCCCTCGTCATCAGCGGCACCCCCCACACCGTCCAACACATC 22300

Qy      22201 ACCACCCTCTGCCAACAACAAGGCATCAAAACCAAAACCCTCCCCACCAACCACGCCTTC 22260
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Db      22301 ACCACCCTCTGCCAACAACAAGGCATCAAAACCAAAACCCTCCCCACCAACCACGCCTTC 22360

Qy      22261 CACTCCCCCCACACCAACCCCATCCTCAACCAACTCCACCAGCACACCCAAACCCTCACC 22320
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Db      22361 CACTCCCCCCACACCAACCCCATCCTCAACCAACTCCACCAGCACACCCAAACCCTCACC 22420

Qy      22321 TACCACCCACCCCACACCCCCCTCATCACCGCCAACACCCCACCCGACCAACTCCTCACC 22380
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Db      22421 TACCACCCACCCCACACCCCCCTCATCACCGCCAACACCCCACCCGACCAACTCCTCACC 22480

Qy      22381 CCCCACTACTGGACCCAACAAGCCCGCAACACCGTCGACTACGCCACCACCACCCAAACC 22440
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Db      22481 CCCCACTACTGGACCCAACAAGCCCGCAACACCGTCGACTACGCCACCACCACCCAAACC 22540

Qy      22441 CTCCACCAACACGGCGTCACCACCTACATCGAACTCGGACCCGACAACACCCTCACCACC 22500
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Db      22541 CTCCACCAACACGGCGTCACCACCTACATCGAACTCGGACCCGACAACACCCTCACCACC 22600

Qy      22501 CTCACCCACCACAACCTCCCCAACACCCCCACCACCACCCTCACCCTCACCCACCCCCAC 22560
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Db      22601 CTCACCCACCACAACCTCCCCAACACCCCCACCACCACCCTCACCCTCACCCACCCCCAC 22660

Qy      22561 CACCACCCCCAAACCCACCTCCTCACCAACCTCGCCAAAACCACCACCACCTGGCACCCC 22620
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Qy      22621 CACCACTACACCCACCACCACAACCAACCCCACACCCACACCCACCTCGACCTCCCCACC 22680
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Db      22721 CACCACTACACCCACCACCACAACCAACCCCACACCCACACCCACCTCGACCTCCCCACC 22780

Qy      22681 TACCCCTTCCAACACCACCACTACTGGCTCGAACTACCCAGCGCCCAAACCAGCCCCGGT 22740
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Db      22781 TACCCCTTCCAACACCACCACTACTGGCTCGAACTACCCAGCGCCCAAACCAGCCCCGGT 22840
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Qy      18361 ATCACCCCCATCCCCCTCACCCTCAACCACACCCACACCAACCCCCAACACCTCCACCAC 18420
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Db      18461 ATCACCCCCATCCCCCTCACCCTCAACCACACCCACACCAACCCCCAACACCTCCACCAC 18520

Qy      18421 ACCCGACAACAAGCCCAAAACCACACCACCGGACCCATCACCGGCCTGCTCTCCCTCCTC 18480
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Db      18521 ACCCGACAACAAGCCCAAAACCACACCACCGGACCCATCACCGGCCTGCTCTCCCTCCTC 18580

Qy      18481 GCCCTCGACGAAACACCCCACCCCCACCACCCCCACACACCCACCGGCACCCTCCTCAAC 18540
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Db      18581 GCCCTCGACGAAACACCCCACCCCCACCACCCCCACACACCCACCGGCACCCTCCTCAAC 18640

Qy      18541 CTCACCCTCACCCAAACCCACACCCAAACCCACCCACCAACCCCCCTCTGGTACGCCACC 18600
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Db      18641 CTCACCCTCACCCAAACCCACACCCAAACCCACCCACCAACCCCCCTCTGGTACGCCACC 18700

Qy      18601 ACCAACGCCACCACCACCCACCCCAACGACCCCCTCACACACCCCACCCAAGCCCAAACC 18660
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Db      18701 ACCAACGCCACCACCACCCACCCCAACGACCCCCTCACACACCCCACCCAAGCCCAAACC 18760

Qy      18661 TGGGGACTCGCCCGCACCACCCTCCTCGAACACCCCACCCACACCGCCGGAATCATCGAC 18720
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Db      18761 TGGGGACTCGCCCGCACCACCCTCCTCGAACACCCCACCCACACCGCCGGAATCATCGAC 18820

Qy      18721 CTCCCCACCACCCCCACCCCCCACACCCTCCACCACCTCACCCAAACCCTCACCCAACCC 18780
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Db      18821 CTCCCCACCACCCCCACCCCCCACACCCTCCACCACCTCACCCAAACCCTCACCCAACCC 18880

Qy      18781 CACCACCAAACCCAACTCGCCATCCGCACCACCGGCACCCACACCCGCCGCCTCACCCCC 18840
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Db      18881 CACCACCAAACCCAACTCGCCATCCGCACCACCGGCACCCACACCCGCCGCCTCACCCCC 18940

Qy      18841 ACCACCCTCACCCCCACACACCAACCACCCACCCCCACCCCCCACGGAACCACCCTCATC 18900
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Db      18941 ACCACCCTCACCCCCACACACCAACCACCCACCCCCACCCCCCACGGAACCACCCTCATC 19000

Qy      18901 ACCGGCGGAACCGGCGCCCTCGCCACCCACCTCACCCACCACCTCACCACCCACCAACCC 18960
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Db      19001 ACCGGCGGAACCGGCGCCCTCGCCACCCACCTCACCCACCACCTCACCACCCACCAACCC 19060

Qy      18961 ACCCAACACCTCCTCCTCACCAGCCGAACCGGCCCCCACACCCCCCACGCACAACACCTC 19020
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Db      19061 ACCCAACACCTCCTCCTCACCAGCCGAACCGGCCCCCACACCCCCCACGCACAACACCTC 19120

Qy      19021 ACCACCCAACTCCAACAAAAAGGCATCCACCTCACCATCACCACCTGCGACACCAGCAAC 19080
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Db      19121 ACCACCCAACTCCAACAAAAAGGCATCCACCTCACCATCACCACCTGCGACACCAGCAAC 19180

Qy      19081 CCAGACCAACTCCAACAACTCCTCAACACCATCCCCCCACAACACCCCCTCACCACCGTC 19140
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Db      19181 CCAGACCAACTCCAACAACTCCTCAACACCATCCCCCCACAACACCCCCTCACCACCGTC 19240

Qy      19141 ATCCACACCGCAGGCATCCTCGACGACGCCACCCTCACCAACCTCACCCCCACCCAACTC 19200
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Db      19241 ATCCACACCGCAGGCATCCTCGACGACGCCACCCTCACCAACCTCACCCCCACCCAACTC 19300

Qy      19201 AACAACGTCCTCCGCGCCAAAGCCCACAGCGCCCACCTCCTCCACCAACTCACCCAACAC 19260
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Db      19301 AACAACGTCCTCCGCGCCAAAGCCCACAGCGCCCACCTCCTCCACCAACTCACCCAACAC 19360

Qy      19261 ACCCCCCTCAACGCCTTCGTCCTCTACTCCTCCGCCGCCGCCACCTTCGGCGCACCCGGC 19320
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Db      19361 ACCCCCCTCAACGCCTTCGTCCTCTACTCCTCCGCCGCCGCCACCTTCGGCGCACCCGGC 19420

Qy      19321 CAAGCCAACTACGCCGCAGCCAACGCCTACCTCGACGCCCTCGCCCACCACCGCCACACC 19380
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Db      19421 CAAGCCAACTACGCCGCAGCCAACGCCTACCTCGACGCCCTCGCCCACCACCGCCACACC 19480

Qy      19381 CACCACCTCCCCGCCACCAGCATCGCCTGGGGCACCTGGCAAGGAAACGGACTGGCGACT 19440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19481 CACCACCTCCCCGCCACCAGCATCGCCTGGGGCACCTGGCAAGGAAACGGACTGGCGACT 19540

Qy      19441 GGTCAAGTCAGCGAACATCTCCGCCGCCGCGGGATGTTCGCCATGCCGCCCGAGTTGGCG 19500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19541 GGTCAAGTCAGCGAACATCTCCGCCGCCGCGGGATGTTCGCCATGCCGCCCGAGTTGGCG 19600

Qy      19501 GTCACAGCTGTTGACGGCGCGATCGCGAGCGGGCGCCCGAGTCTCCTCGTCGCCGATATC 19560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19601 GTCACAGCTGTTGACGGCGCGATCGCGAGCGGGCGCCCGAGTCTCCTCGTCGCCGATATC 19660

Qy      19561 GACTGGAAGAAATTGGGACCGGTTCTCTCCAGCAAGTCGTCGGTCTTGCTCGAGGACCTT 19620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19661 GACTGGAAGAAATTGGGACCGGTTCTCTCCAGCAAGTCGTCGGTCTTGCTCGAGGACCTT 19720

Qy      19621 CCCCAGGCACAGGGAACTGAGGAGGCGCGCAGTACCGTTGAGCAGACGGAGAGCACAAAC 19680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19721 CCCCAGGCACAGGGAACTGAGGAGGCGCGCAGTACCGTTGAGCAGACGGAGAGCACAAAC 19780

Qy      19681 CTCCGGCAACTCCTCATGGGTCGGTCACGTTCCGAGCAGGAAGAAGAGCTGCTCAGCCTC 19740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19781 CTCCGGCAACTCCTCATGGGTCGGTCACGTTCCGAGCAGGAAGAAGAGCTGCTCAGCCTC 19840

Qy      19741 GTCCGCATCCACTCCGCGGCAGTGCTCGGGCGCGACGACTCCGAGGCCATCCCGCCCGGT 19800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19841 GTCCGCATCCACTCCGCGGCAGTGCTCGGGCGCGACGACTCCGAGGCCATCCCGCCCGGT 19900

Qy      19801 CGGCTGTTCAGGGATCTAGGGTTCGACTCGCTTGCGGCGGTGGAGCTTCGCAACCACCTC 19860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19901 CGGCTGTTCAGGGATCTAGGGTTCGACTCGCTTGCGGCGGTGGAGCTTCGCAACCACCTC 19960

Qy      19861 GCAGCACAGACGGAGCTGGCTCTGCCGACGACTCTCGTCTTCGATTACCCCAGCCCCACC 19920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19961 GCAGCACAGACGGAGCTGGCTCTGCCGACGACTCTCGTCTTCGATTACCCCAGCCCCACC 20020

Qy      19921 AAGCTCGCCCAATTTCTGCTCTCCGAGATCGCGGAGTTCCAGCCCGACAACTCAACTCCG 19980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20021 AAGCTCGCCCAATTTCTGCTCTCCGAGATCGCGGAGTTCCAGCCCGACAACTCAACTCCG 20080

Qy      19981 CTTCCGCGACCCCGGGCAGAGCTCGATGAGCCGATCGCCATCGTTGGCATGGCCTGTCGC 20040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20081 CTTCCGCGACCCCGGGCAGAGCTCGATGAGCCGATCGCCATCGTTGGCATGGCCTGTCGC 20140

Qy      20041 TTCCCCGGCGGAGTGACCTCGGCGGACGACTTCTGGGATCTGATCTCCTCCGAGCAGGAC 20100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20141 TTCCCCGGCGGAGTGACCTCGGCGGACGACTTCTGGGATCTGATCTCCTCCGAGCAGGAC 20200

Qy      20101 GCGATCGGCGGATTCCCCACCGACCGCGGCTGGGACCTGGACACGCTCTACGACCCCGAC 20160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20201 GCGATCGGCGGATTCCCCACCGACCGCGGCTGGGACCTGGACACGCTCTACGACCCCGAC 20260

Qy      20161 CCCGACCACCCCGGCACCTGCTACACCCGAAACGGCGGATTCCTCTACGACGCAGGCCAC 20220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20261 CCCGACCACCCCGGCACCTGCTACACCCGAAACGGCGGATTCCTCTACGACGCAGGCCAC 20320

Qy      20221 TTCGACGCCGAATTCTTCGGCATCAGCCCCCGCGAAGCCCTCGCCATGGACCCCCAGCAA 20280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20321 TTCGACGCCGAATTCTTCGGCATCAGCCCCCGCGAAGCCCTCGCCATGGACCCCCAGCAA 20380

Qy      20281 CGACTCCTCCTCGAAACCGCCTGGGAAACCATCGAACACGCCGGCATCAACCCCCACACC 20340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20381 CGACTCCTCCTCGAAACCGCCTGGGAAACCATCGAACACGCCGGCATCAACCCCCACACC 20440

Qy      20341 CTCCACGGCACCCCCACCGGAGTCTTCACCGGCACCAACGGACAGGACCACGCGGCACAC 20400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20441 CTCCACGGCACCCCCACCGGAGTCTTCACCGGCACCAACGGACAGGACCACGCGGCACAC 20500

Qy      20401 ATCCGTCAGGCCCCGAGCGGTACCGAGGGATTCGTCCTGACCGGGGCAGCCACCAGCATC 20460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20501 ATCCGTCAGGCCCCGAGCGGTACCGAGGGATTCGTCCTGACCGGGGCAGCCACCAGCATC 20560

Qy      20461 GCCTCCGGCCGAATCTCCTACATCCTCGGGTTGGAAGGGCCTGCGGTCACCCTCGACACA 20520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20561 GCCTCCGGCCGAATCTCCTACATCCTCGGGTTGGAAGGGCCTGCGGTCACCCTCGACACA 20620

Qy      20521 GCGTGTTCCTCCTCGCTCGTCGCCCTGCACCTCGCCTGCCAGTCCCTCAGGTCCGGTGAA 20580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      16241 GGCACCGGCACCACTTTGGGCGACCCGATCGAGGCCCAGGCCCTCCTCGCCACCTACGGA 16300
Qy      16201 CAGGACCGCCCCGGCAACGAACCGCTGTGGCTGGGCTCGATGAAGTCGAACATCGGCCAC 16260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      16301 CAGGACCGCCCCGGCAACGAACCGCTGTGGCTGGGCTCGATGAAGTCGAACATCGGCCAC 16360

Qy      16261 GCGCAGGCTGCCGCAGGTGTGGGCGGGGTCATCAAGATGGTGATGGCGCTGCGGAATGGT 16320
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Db      16361 GCGCAGGCTGCCGCAGGTGTGGGCGGGGTCATCAAGATGGTGATGGCGCTGCGGAATGGT 16420

Qy      16321 CTGCTGCCGCGGACGTTGCATGTGGATGAGCCGTCGCCGCATGTGGACTGGTCCGCGGGG 16380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      16421 CTGCTGCCGCGGACGTTGCATGTGGATGAGCCGTCGCCGCATGTGGACTGGTCCGCGGGG 16480

Qy      16381 GCGGTGCAGCTGCTGACGGAGACGGTGCCCTGGCCCGGCGGGGAGGGGCGGCTGCGGCGG 16440
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Db      16481 GCGGTGCAGCTGCTGACGGAGACGGTGCCCTGGCCCGGCGGGGAGGGGCGGCTGCGGCGG 16540

Qy      16441 GCAGGAGTGTCATCGTTCGGCGTCAGCGGCACCAACGCCCACGTCATCCTCGAAGAAGCA 16500
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Db      16541 GCAGGAGTGTCATCGTTCGGCGTCAGCGGCACCAACGCCCACGTCATCCTCGAAGAAGCA 16600

Qy      16501 CCCGCCCACAACATCCCGTCAGACACACCCGCCGACGACGCCCCGGGAGAAGCAGCCGCC 16560
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Db      16601 CCCGCCCACAACATCCCGTCAGACACACCCGCCGACGACGCCCCGGGAGAAGCAGCCGCC 16660

Qy      16561 GACGATGTTCCGGGGGAAGCGGCCGGCGACGACGCCGGTACCGGCGGGGAAGCGACTGGT 16620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      16661 GACGATGTTCCGGGGGAAGCGGCCGGCGACGACGCCGGTACCGGCGGGGAAGCGACTGGT 16720

Qy      16621 CCTGCTGCCGGCAGTCCAGGGGTGTGGCCGTGGCTGGTGTCGGCCAAGTCGCAGCCGGCC 16680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      16721 CCTGCTGCCGGCAGTCCAGGGGTGTGGCCGTGGCTGGTGTCGGCCAAGTCGCAGCCGGCC 16780

Qy      16681 CTGCGCGCCCAGGCCCAGGCCCTGCACGCCCACCTCACCGACCACCCCGGCCTCGACCTC 16740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      16781 CTGCGCGCCCAGGCCCAGGCCCTGCACGCCCACCTCACCGACCACCCCGGCCTCGACCTC 16840

Qy      16741 GCCGACGTCGGGTACACCCTCGCCCACGCCCGCGCCGTGTTCGACCACCGCGCCACCCTC 16800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      16841 GCCGACGTCGGGTACACCCTCGCCCACGCCCGCGCCGTGTTCGACCACCGCGCCACCCTC 16900

Qy      16801 ATCGCCGCCGACCGCGACACCTTCCTGCAAGCACTCCAGGCACTCGCCGCAGGCGAACCC 16860
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Db      16901 ATCGCCGCCGACCGCGACACCTTCCTGCAAGCACTCCAGGCACTCGCCGCAGGCGAACCC 16960

Qy      16861 CACCCCGCCGTCATCCACAGCAGCGCCCCAGGCGGGACCGGGACCGGGGAGGCCGCAGGA 16920
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Db      16961 CACCCCGCCGTCATCCACAGCAGCGCCCCAGGCGGGACCGGGACCGGGGAGGCCGCAGGA 17020

Qy      16921 AAGACCGCATTCATCTGCTCCGGACAGGGCACCCAACGCCCCGGCATGGCCCACGGCCTC 16980
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Db      17021 AAGACCGCATTCATCTGCTCCGGACAGGGCACCCAACGCCCCGGCATGGCCCACGGCCTC 17080

Qy      16981 TACCACACCCACCCCGTCTTCGCCGCCGCACTCAACGACATCTGCACCCACCTCGACCCC 17040
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Db      17081 TACCACACCCACCCCGTCTTCGCCGCCGCACTCAACGACATCTGCACCCACCTCGACCCC 17140

Qy      17041 CACCTCGACCACCCCCTCCTCCCCCTCCTCACCCAGGACCCCAACACCCAGGACACCACC 17100
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Qy      17101 ACCCTCGAAGAAGCGGCCGCACTGCTCCAGCAGACCCCGTACGCCCAGCCCGCCCTCTTC 17160
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Db      17201 ACCCTCGAAGAAGCGGCCGCACTGCTCCAGCAGACCCCGTACGCCCAGCCCGCCCTCTTC 17260

Qy      17161 GCCTTCCAGGTCGCCCTCCACCGCCTCCTCACCGACGGCTACCACATCACCCCCCACTAC 17220
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Db      17261 GCCTTCCAGGTCGCCCTCCACCGCCTCCTCACCGACGGCTACCACATCACCCCCCACTAC 17320

Qy      17221 TACGCCGGACACTCCCTCGGCGAAATCACCGCCGCCCACCTCGCCGGCATCCTCACCCTC 17280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17321 TACGCCGGACACTCCCTCGGCGAAATCACCGCCGCCCACCTCGCCGGCATCCTCACCCTC 17380

Qy      17281 ACCGACGCCACCACCCTCATCACCCAACGCGCCACCCTCATGCAAACCATGCCCCCCGGC 17340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17381 ACCGACGCCACCACCCTCATCACCCAACGCGCCACCCTCATGCAAACCATGCCCCCCGGC 17440

Qy      17341 ACCATGACCACCCTCCACACCACCCCCCACCACATCACCCACCACCTCACCGCCCACGAA 17400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17441 ACCATGACCACCCTCCACACCACCCCCCACCACATCACCCACCACCTCACCGCCCACGAA 17500

Qy      17401 AACGACCTCGCCATCGCCGCCATCAACACCCCCACCTCCCTCGTCATCAGCGGCACCCCC 17460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17501 AACGACCTCGCCATCGCCGCCATCAACACCCCCACCTCCCTCGTCATCAGCGGCACCCCC 17560

Qy      17461 CACACCGTCCAACACATCACCACCCTCTGCCAACAACAAGGCATCAAAACCAAAACCCTC 17520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17561 CACACCGTCCAACACATCACCACCCTCTGCCAACAACAAGGCATCAAAACCAAAACCCTC 17620

Qy      17521 CCCACCAAAAACGCCTTCCACTCCCCCCACACCAACCCCATCCTCAACCAACTCCACCAG 17580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      17621 CCCACCAAAAACGCCTTCCACTCCCCCCACACCAACCCCATCCTCAACCAACTCCACCAG 17680

Qy      17581 CACACCCAAACCCTCACCTACCACCCACCCCACACCCCCCTCATCACCGCCAACACCCCA 17640
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Db      17681 CACACCCAAACCCTCACCTACCACCCACCCCACACCCCCCTCATCACCGCCAACACCCCA 17740

Qy      17641 CCCGACCAACTCCTCACCCCCCACTACTGGACCCAACAAGCCCGCAACACCGTCGACTAC 17700
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Db      17741 CCCGACCAACTCCTCACCCCCCACTACTGGACCCAACAAGCCCGCAACACCGTCGACTAC 17800

Qy      17701 GCCACCACCACCCAAACCCTCCACCAACACGGCGTCACCACCTACATCGAACTCGGACCC 17760
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Db      17801 GCCACCACCACCCAAACCCTCCACCAACACGGCGTCACCACCTACATCGAACTCGGACCC 17860

Qy      17761 GACAACACCCTCACCACCCTCACCCACCACAACCTCCCCAACACCCCCACCACCACCCTC 17820
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Db      17861 GACAACACCCTCACCACCCTCACCCACCACAACCTCCCCAACACCCCCACCACCACCCTC 17920

Qy      17821 ACCCTCACCCACCCCCACCACCACCCCCAAACCCACCTCCTCACCAACCTCGCCAAAACC 17880
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Db      17921 ACCCTCACCCACCCCCACCACCACCCCCAAACCCACCTCCTCACCAACCTCGCCAAAACC 17980

Qy      17881 ACCACCACCTGGCACCCCCACCACTACACCCACCACCACAACCAACCCCACACCCACACC 17940
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Db      17981 ACCACCACCTGGCACCCCCACCACTACACCCACCACCACAACCAACCCCACACCCACACC 18040

Qy      17941 CACCTCGACCTCCCCACCTACCCCTTCCAACACCAGCACTACTGGCTCGAAAGCACACAG 18000
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Db      18041 CACCTCGACCTCCCCACCTACCCCTTCCAACACCAGCACTACTGGCTCGAAAGCACACAG 18100

Qy      18001 CCGGGTGCCGGATCCGGTTCGGGTTCCGGTTCCGGGCGGGCAGGGACTGCGGGCGGGACG 18060
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Db      18101 CCGGGTGCCGGATCCGGTTCGGGTTCCGGTTCCGGGCGGGCAGGGACTGCGGGCGGGACG 18160

Qy      18061 GCAGAGGTGGAGTCGCGGTTCTGGGACGCGGTGGCCCGCCAGGACCTGGAAACGGTCGCG 18120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      18161 GCAGAGGTGGAGTCGCGGTTCTGGGACGCGGTGGCCCGCCAGGACCTGGAAACGGTCGCG 18220

Qy      18121 ACCACGCTCGCCGTGCCCCCCTCCGCCGGCCTGGACACGGTGGTGCCCGCACTCTCCGCC 18180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      18221 ACCACGCTCGCCGTGCCCCCCTCCGCCGGCCTGGACACGGTGGTGCCCGCACTCTCCGCC 18280

Qy      18181 TGGCACCGCCACCAACACGACCAAGCCCGCATCAACACCTGGACCTACCAGGAAACCTGG 18240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      18281 TGGCACCGCCACCAACACGACCAAGCCCGCATCAACACCTGGACCTACCAGGAAACCTGG 18340

Qy      18241 AAACCCCTCACCCTCCCCACCACCCACCAACCCCACCAAACCTGGCTCATCGCCATCCCC 18300
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Db      18341 AAACCCCTCACCCTCCCCACCACCCACCAACCCCACCAAACCTGGCTCATCGCCATCCCC 18400

Qy      18301 GAAACCCAGACCCACCACCCCCACATCACCAACATCCTCACCAACCTCCACCACCACGGC 18360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      18401 GAAACCCAGACCCACCACCCCCACATCACCAACATCCTCACCAACCTCCACCACCACGGC 18460
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Qy      13981 GCCCTCTTCGCCTTCCAGGTCGCCCTCCACCGCCTCCTCACCGACGGCTACCACATCACC 14040
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Db      14081 GCCCTCTTCGCCTTCCAGGTCGCCCTCCACCGCCTCCTCACCGACGGCTACCACATCACC 14140

Qy      14041 CCCCACTACTACGCCGGACACTCCCTCGGCGAAATCACCGCCGCCCACCTCGCCGGCATC 14100
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Db      14141 CCCCACTACTACGCCGGACACTCCCTCGGCGAAATCACCGCCGCCCACCTCGCCGGCATC 14200

Qy      14101 CTCACCCTCACCGACGCCACCACCCTCATCACCCAACGCGCCACCCTCATGCAAACCATG 14160
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Db      14201 CTCACCCTCACCGACGCCACCACCCTCATCACCCAACGCGCCACCCTCATGCAAACCATG 14260

Qy      14161 CCCCCCGGCACCATGACCACCCTCCACACCACCCCCCACCACATCACCCACCACCTCACC 14220
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Db      14261 CCCCCCGGCACCATGACCACCCTCCACACCACCCCCCACCACATCACCCACCACCTCACC 14320

Qy      14221 GCCCACGAAAACGACCTCGCCATCGCCGCCATCAACACCCCCACCTCCCTCGTCATCAGC 14280
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Qy      14281 GGCACCCCCCCACACCGTCCAACACATCACCACCCTCTGCCAACAACAAGGCATCAAAACC 14340
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Db      14381 GGCACCCCCCCACACCGTCCAACACATCACCACCCTCTGCCAACAACAAGGCATCAAAACC 14440

Qy      14341 AAAACCCTCCCCACCAACCACGCCTTCCACTCCCCCCACACCAACCCCATCCTCAACCAA 14400
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Db      14441 AAAACCCTCCCCACCAACCACGCCTTCCACTCCCCCCACACCAACCCCATCCTCAACCAA 14500

Qy      14401 CTCCACCAGCACACCCAAACCCTCACCTACCACCCACCCCACACCCCCCTCATCACCGCC 14460
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Db      14501 CTCCACCAGCACACCCAAACCCTCACCTACCACCCACCCCACACCCCCCTCATCACCGCC 14560

Qy      14461 AACACCCCACCCGACCAACTCCTCACCCCCCCACTACTGGACCCAACAAGCCCGCAACACC 14520
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Db      14561 AACACCCCACCCGACCAACTCCTCACCCCCCCACTACTGGACCCAACAAGCCCGCAACACC 14620

Qy      14521 GTCGACTACGCCACCACCACCCAAACCCTCCACCAACACGGCGTCACCACCTACATCGAA 14580
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Qy      14581 CTCGGACCCGACAACACCCTCACCACCCTCACCCACGACAACCTCCCCAACACCCCCACC 14640
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Qy      14641 ACCACCCTCACCCTCACCCACCCCCACCACCACCCCCAAACCCACCTCCTCACCAACCTC 14700
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Qy      14701 GCCAAAACCACCACCACCTGGCACCCCCACCACTACACCCACCACCACAACCAACCCCAC 14760
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Qy      14761 ACCCACACCCACCTCGACCTCCCCACCTACCCCTTCCAACACCACCACTACTGGCTCCAA 14820
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Db      14861 ACCCACACCCACCTCGACCTCCCCACCTACCCCTTCCAACACCACCACTACTGGCTCCAA 14920

Qy      14821 CCACCCGGCAAGCCGAGCGACCCGTCACCGAGCGAAGGCCGTGAGCAAGCCACGACCCCA 14880
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Qy      14881 TCAACCCCGCTGCGTGATGTCCTCGTGGGCAAGTCTCCGCAGGAGCGAGACGAAGAGCTG 14940
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Db      14981 TCAACCCCGCTGCGTGATGTCCTCGTGGGCAAGTCTCCGCAGGAGCGAGACGAAGAGCTG 15040

Qy      14941 TTGCGCCTGGTGCGCACCCATGCGGCCGCTGTGCTGGGCCATGCCACTCCCGAAGTGATC 15000
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Db      15041 TTGCGCCTGGTGCGCACCCATGCGGCCGCTGTGCTGGGCCATGCCACTCCCGAAGTGATC 15100

Qy      15001 GTTCCGAACAAGGCCTTCAAAGAGCTGGGTTTTGATTCTCTCGCCGCAATTCAGCTTCGT 15060
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Qy      15061 AATCGACTGCTTGCTGACGTTGACCTGCCGCTTCCGGCCACGCTGATCTTCGATTACCCC 15120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      15161 AATCGACTGCTTGCTGACGTTGACCTGCCGCTTCCGGCCACGCTGATCTTCGATTACCCC 15220

Qy      15121 ACTCCGATGGCGCTTTGCCAGTTCCTCCGGGCGGCGATCGTCGGAGCGGACACAGGCACG 15180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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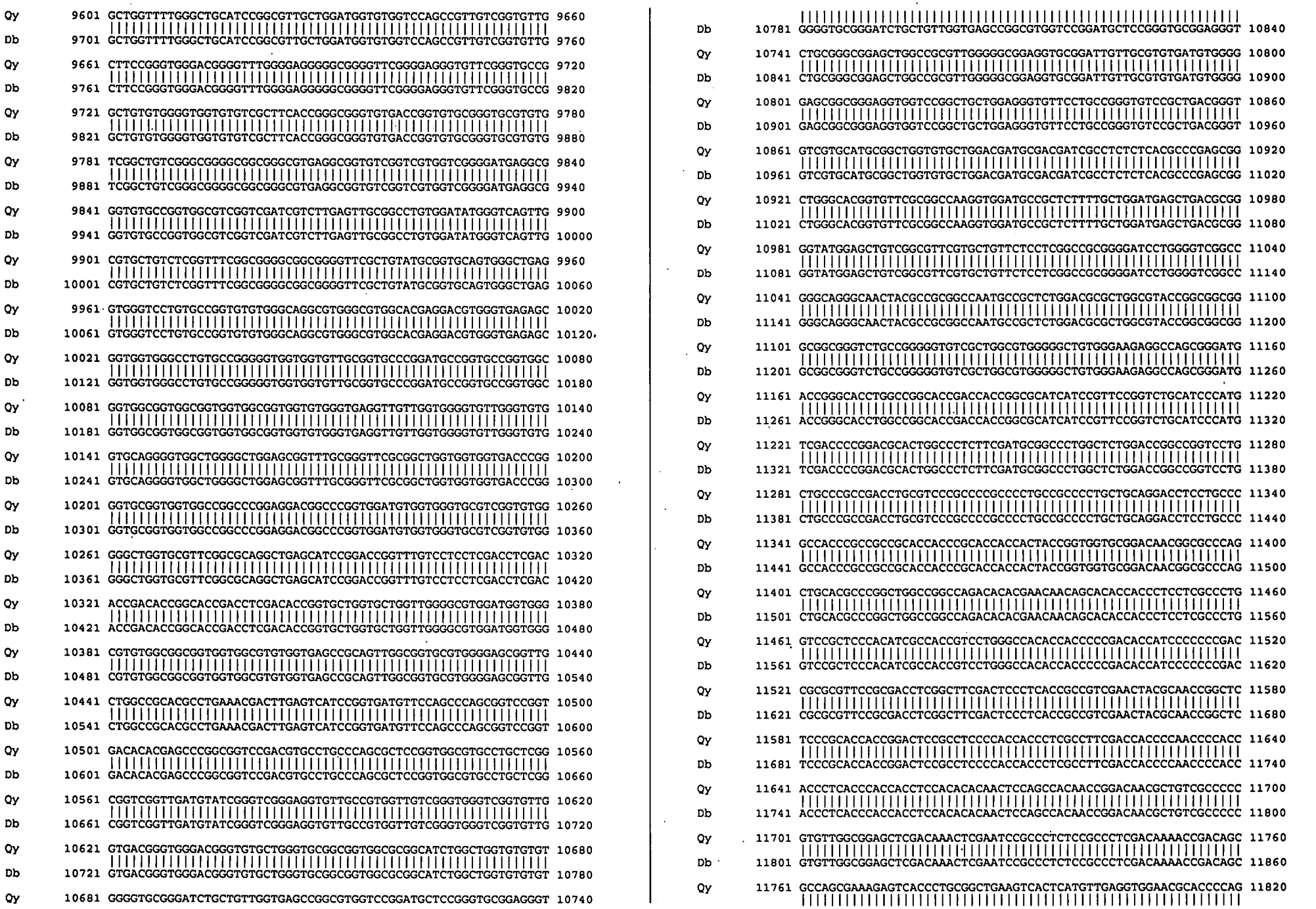
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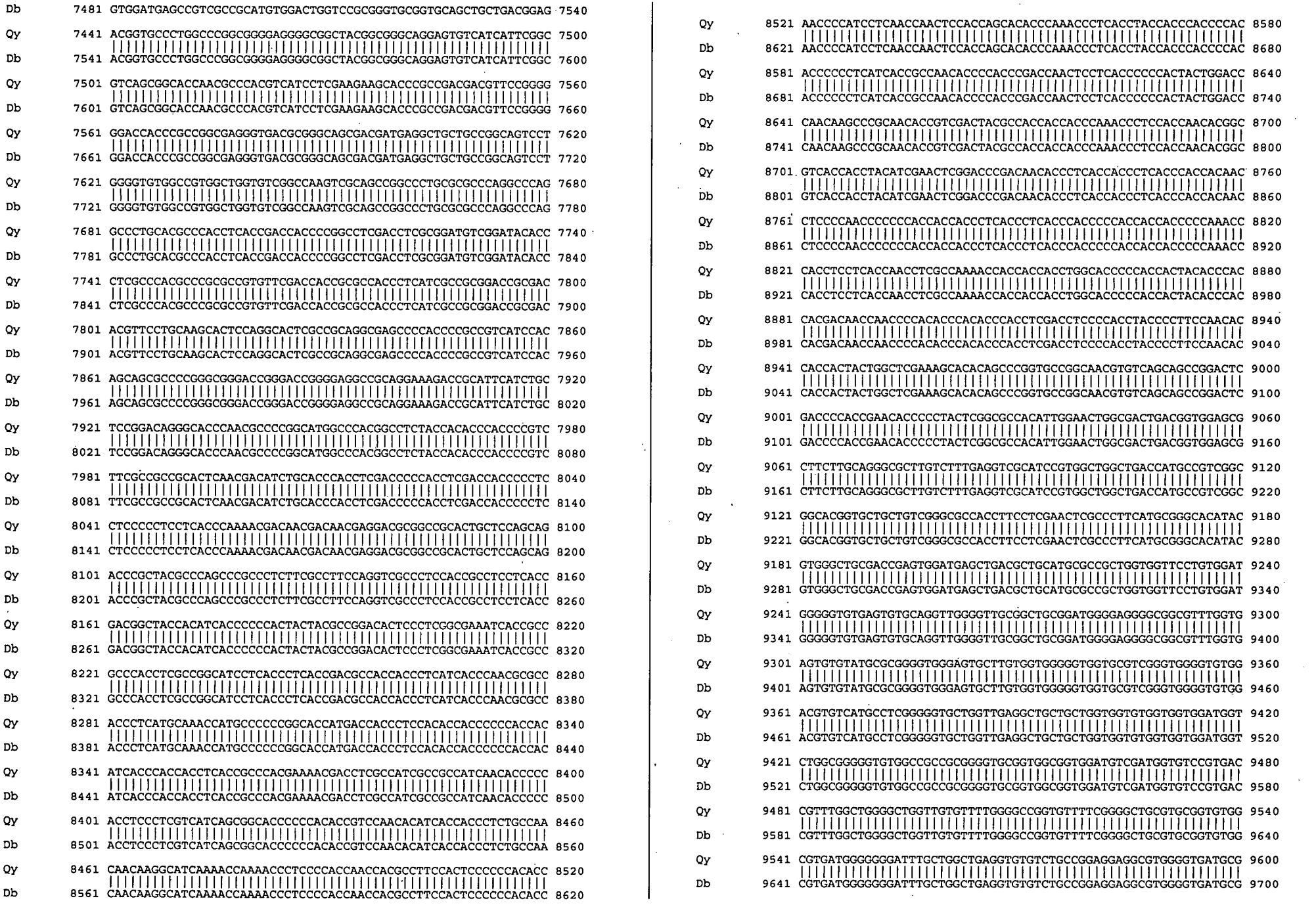
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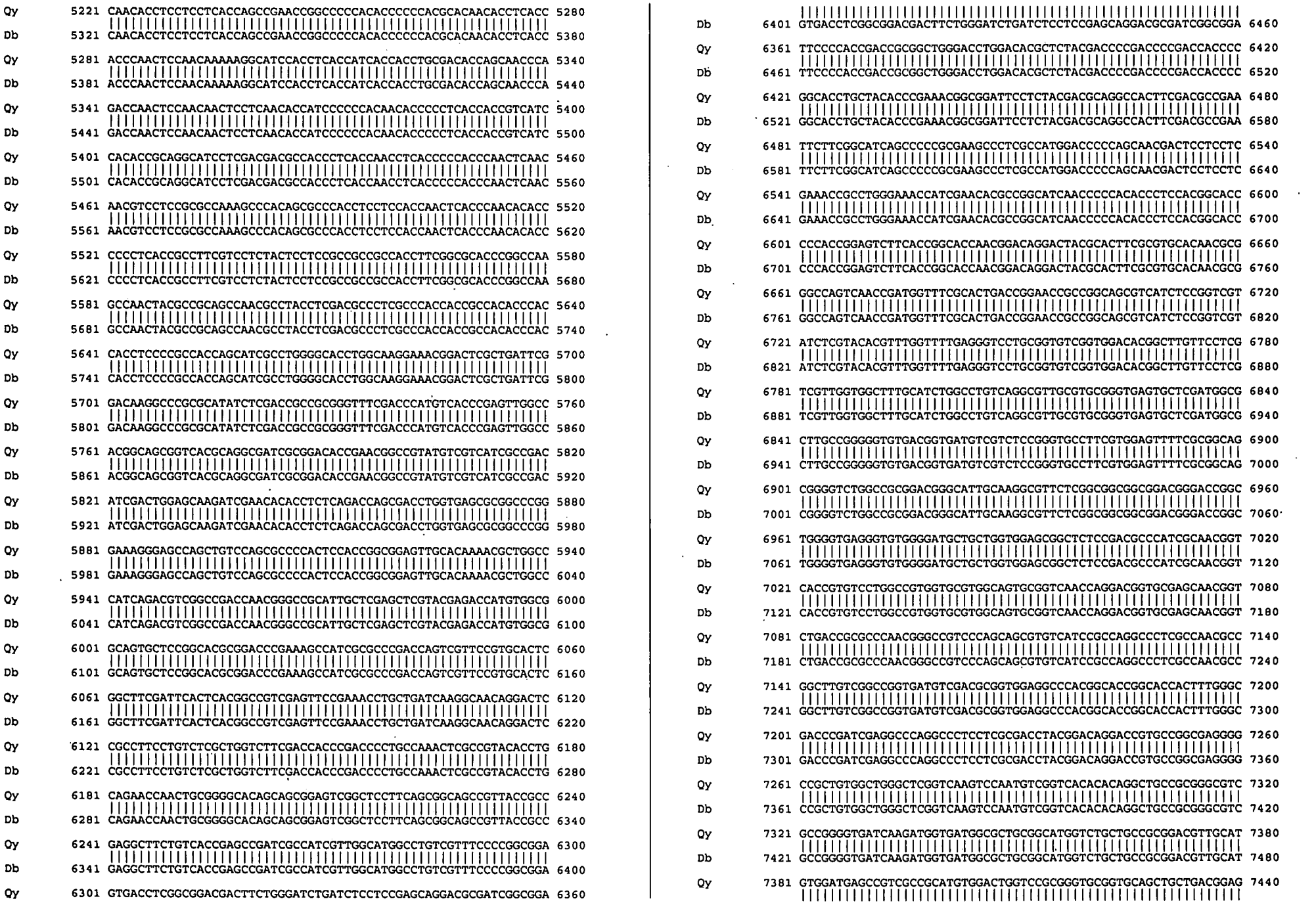
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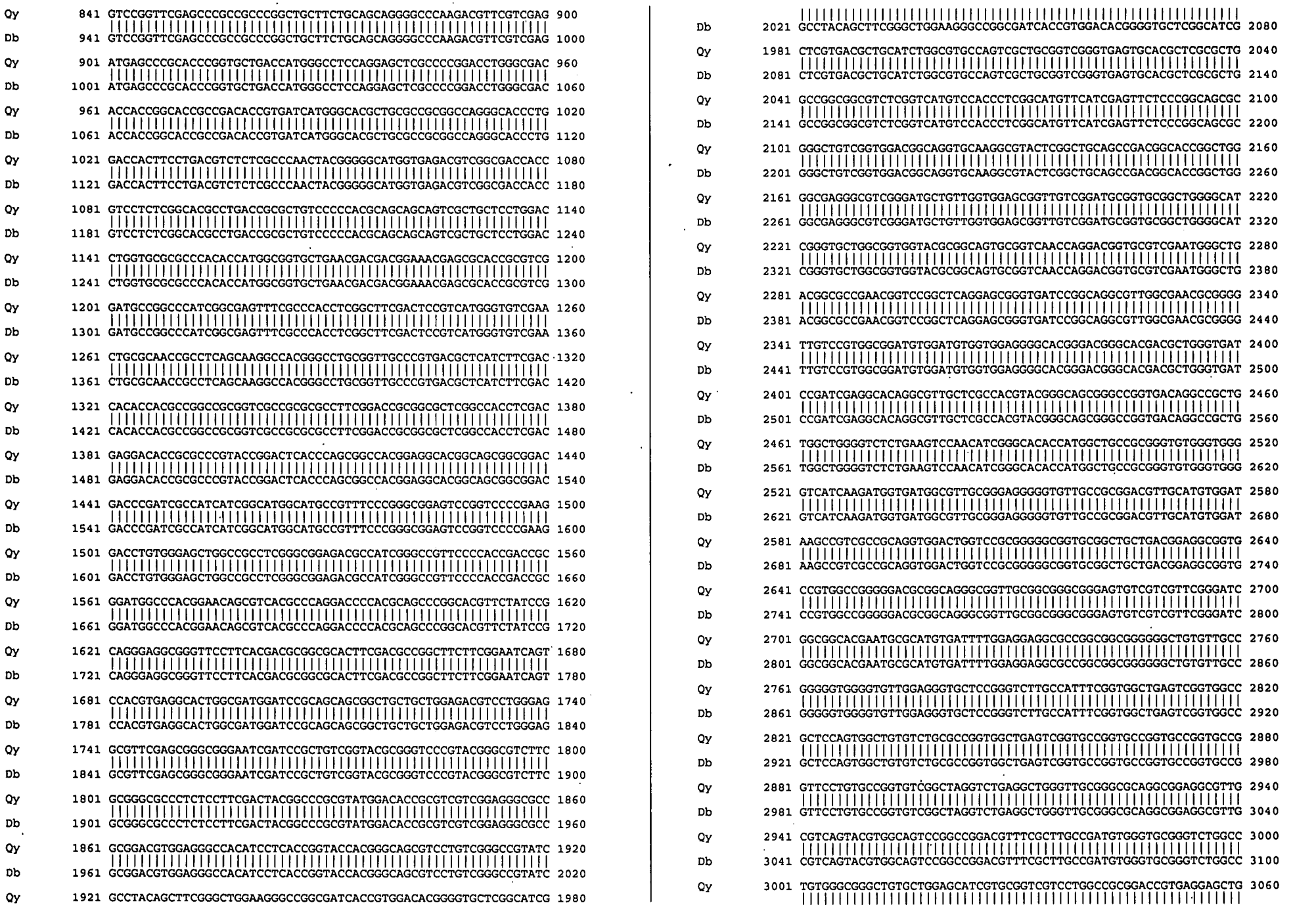






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RESULT 2
AB032367
LOCUS AB032367 64957 bp DNA linear BCT 18-SEP-1999
DEFINITION Streptomyces avermitilis polyketide synthase gene cluster (aveA1, aveA2, aveA3, aveA4) and aveC, aveE genes, complete cds.
ACCESSION AB032367
VERSION AB032367.1 GI:5902890
KEYWORDS AveC; cytochrome P450 hydroxylase; type I polyketide synthase AVES 4; type I polyketide synthase AVES 3; type I polyketide synthase AVES 2; type I polyketide synthase AVES 1.
SOURCE Streptomyces avermitilis DNA.
ORGANISM Streptomyces avermitilis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE 1 (bases 1 to 64957)
AUTHORS Ikeda,H., Nonomiya,T., Usami,M., Ohta,T. and Omura,S.
TITLE Organization of the biosynthetic gene cluster for the polyketide anthelmintic macrolide avermectin in Streptomyces avermitilis
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9509-9514 (1999)
MEDLINE 99380548
REFERENCE 2 (bases 1 to 64957)
AUTHORS Ikeda,H., Nonomiya,T., Usami,M., Ohta,T. and Omura,S.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-1999) Haruo Ikeda, School of Pharmaceutical Sciences, Kitasato University, Microbial chemistry; 5-9-1 Shirokane, Minato-ku, Tokyo 108-8641, Japan
(E-mail:ikeda@mc.pharm.kitasato-u.ac.jp, Tel:+81-3-5791-6242, Fax:+81-3-3444-6197)
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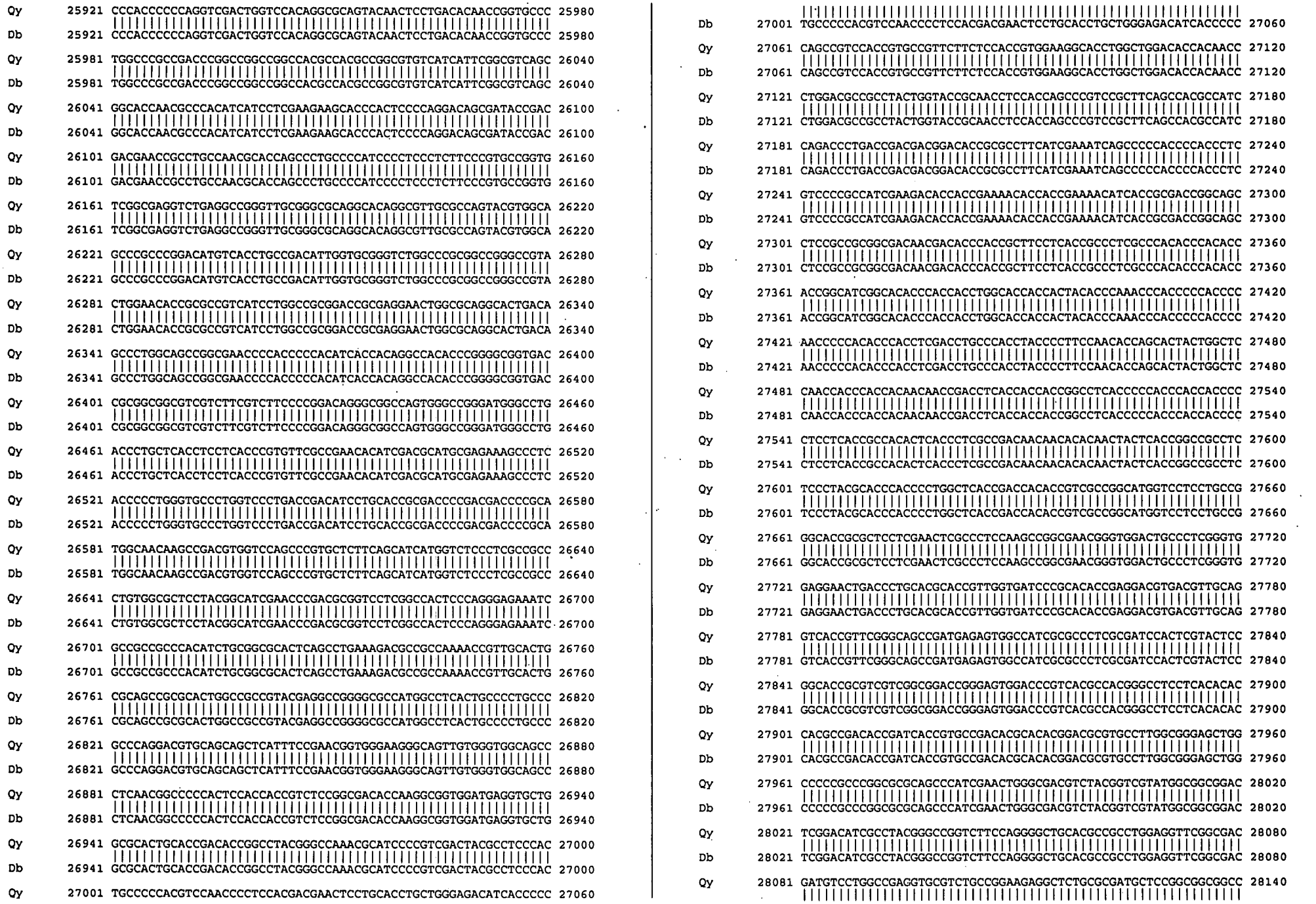
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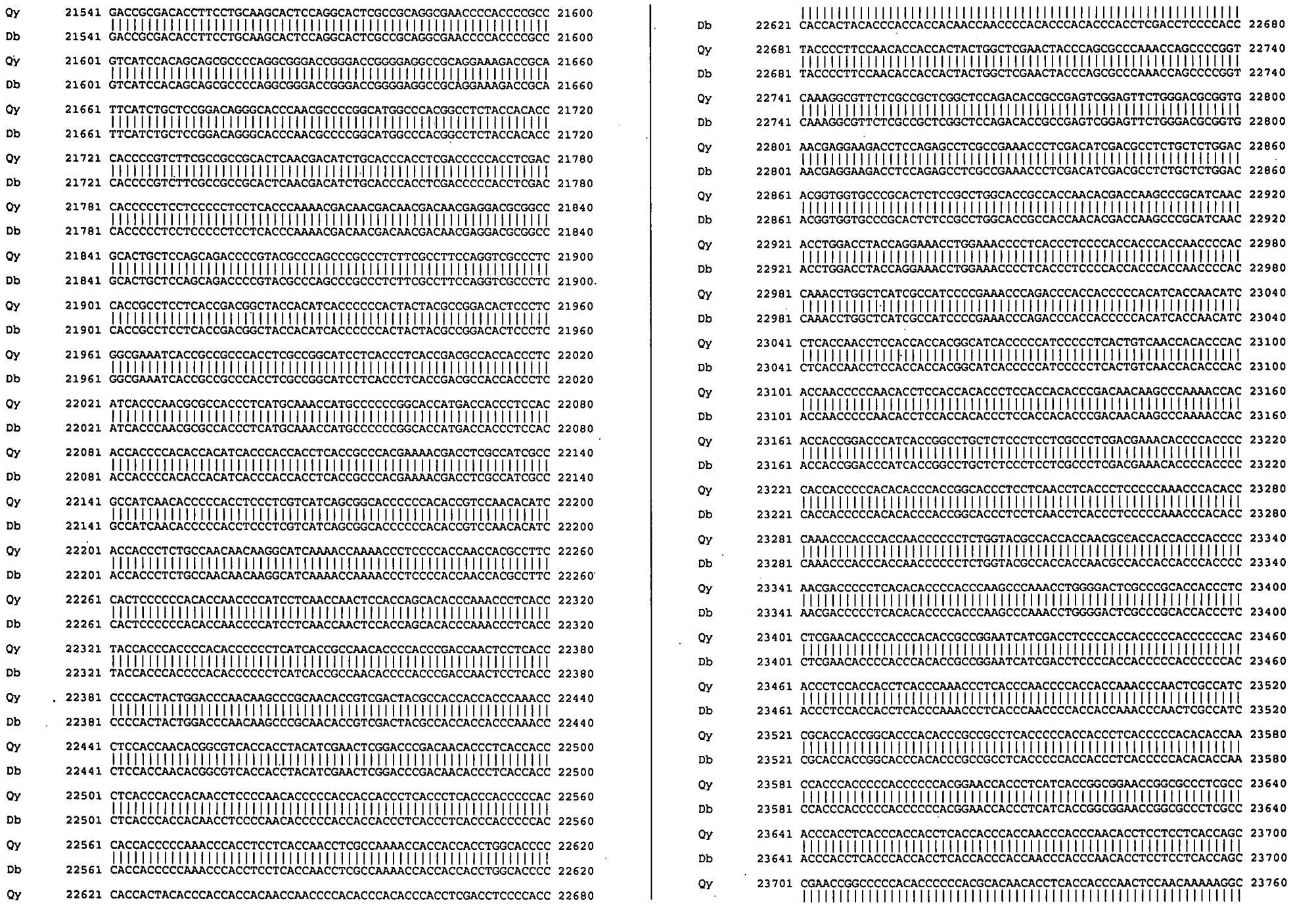
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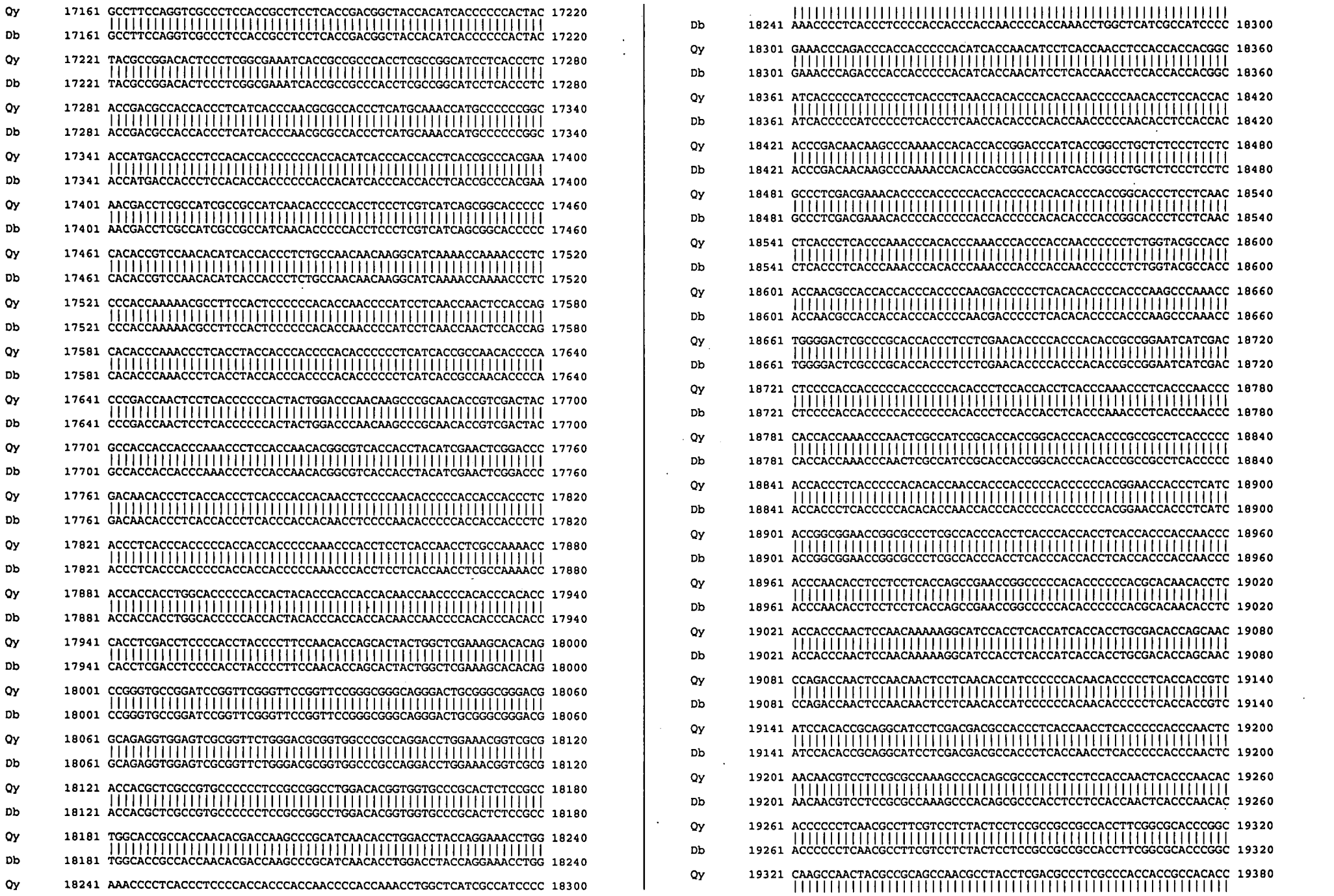
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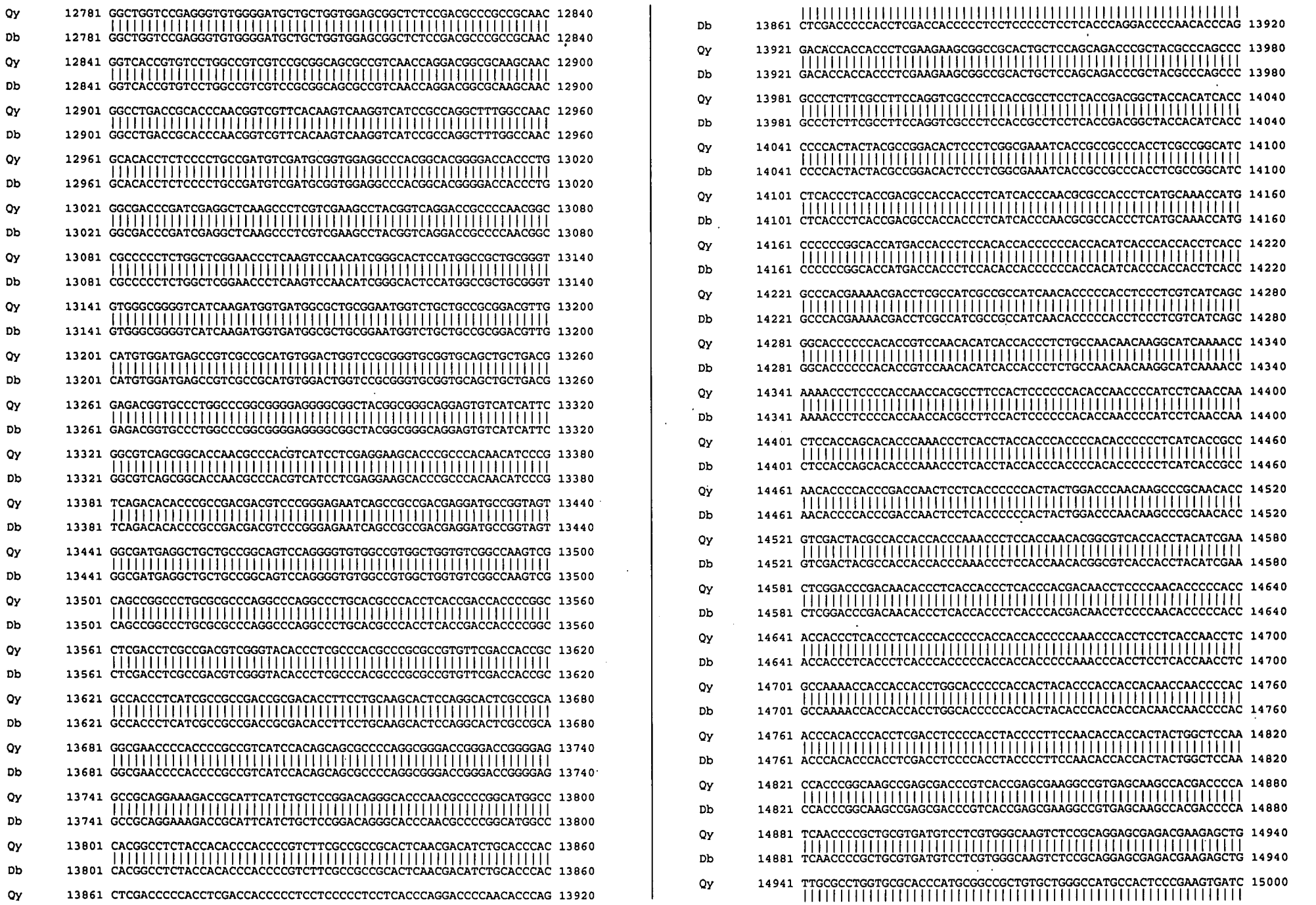
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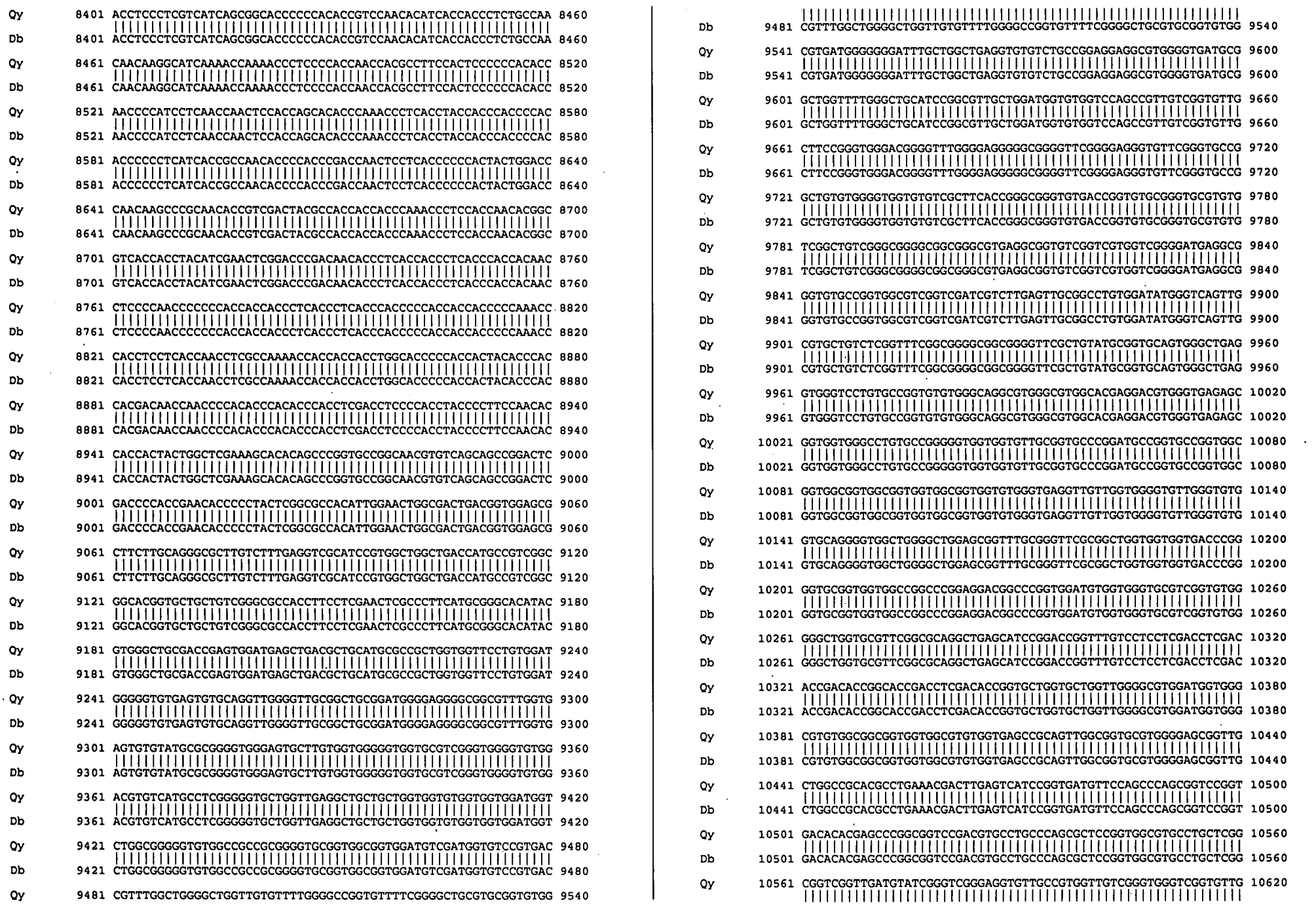
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Db      7321 GCCGGGGTGATCAAGATGGTGATGGCGCTGCGGCATGGTCTGCTGCCGCGGACGTTGCAT 7380
Qy      7381 GTGGATGAGCCGTCGCCGCATGTGGACTGGTCCGCGGGTGCGGTGCAGCTGCTGACGGAG 7440
Db      7381 GTGGATGAGCCGTCGCCGCATGTGGACTGGTCCGCGGGTGCGGTGCAGCTGCTGACGGAG 7440
Qy      7441 ACGGTGCCCTGGCCCGGCGGGGAGGGGCGGCTACGGCGGGCAGGAGTGTCATCATTCGGC 7500
Db      7441 ACGGTGCCCTGGCCCGGCGGGGAGGGGCGGCTACGGCGGGCAGGAGTGTCATCATTCGGC 7500
Qy      7501 GTCAGCGGCACCAACGCCCACGTCATCCTCGAAGAAGCACCCGCCGACGACGTTCCGGGG 7560
Db      7501 GTCAGCGGCACCAACGCCCACGTCATCCTCGAAGAAGCACCCGCCGACGACGTTCCGGGG 7560
Qy      7561 GGACCACCCGCCGGCGAGGGTGACGCGGGCAGCGACGATGAGGCTGCTGCCGGCAGTCCT 7620
Db      7561 GGACCACCCGCCGGCGAGGGTGACGCGGGCAGCGACGATGAGGCTGCTGCCGGCAGTCCT 7620
Qy      7621 GGGGTGTGGCCGTGGCTGGTGTCGGCCAAGTCGCAGCCGGCCCTGCGCGCCCAGGCCCAG 7680
Db      7621 GGGGTGTGGCCGTGGCTGGTGTCGGCCAAGTCGCAGCCGGCCCTGCGCGCCCAGGCCCAG 7680
Qy      7681 GCCCTGCACGCCCACCTCACCGACCACCCCGGCCTCGACCTCGCGGATGTCGGATACACC 7740
Db      7681 GCCCTGCACGCCCACCTCACCGACCACCCCGGCCTCGACCTCGCGGATGTCGGATACACC 7740
Qy      7741 CTCGCCCACGCCCGCGCCGTGTTCGACCACCGCGCCACCCTCATCGCCGCGGACCGCGAC 7800
Db      7741 CTCGCCCACGCCCGCGCCGTGTTCGACCACCGCGCCACCCTCATCGCCGCGGACCGCGAC 7800
Qy      7801 ACGTTCCTGCAAGCACTCCAGGCACTCGCCGCAGGCGAGCCCCACCCCGCCGTCATCCAC 7860
Db      7801 ACGTTCCTGCAAGCACTCCAGGCACTCGCCGCAGGCGAGCCCCACCCCGCCGTCATCCAC 7860
Qy      7861 AGCAGCGCCCCGGGCGGGACCGGGACCGGGGAGGCCGCAGGAAAGACCGCATTCATCTGC 7920
Db      7861 AGCAGCGCCCCGGGCGGGACCGGGACCGGGGAGGCCGCAGGAAAGACCGCATTCATCTGC 7920
Qy      7921 TCCGGACAGGGCACCCAACGCCCCGGCATGGCCCACGGCCTCTACCACACCCACCCCGTC 7980
Db      7921 TCCGGACAGGGCACCCAACGCCCCGGCATGGCCCACGGCCTCTACCACACCCACCCCGTC 7980
Qy      7981 TTCGCCGCCGCACTCAACGACATCTGCACCCACCTCGACCCCCACCTCGACCACCCCCTC 8040
Db      7981 TTCGCCGCCGCACTCAACGACATCTGCACCCACCTCGACCCCCACCTCGACCACCCCCTC 8040
Qy      8041 CTCCCCCTCCTCACCCAAAACGACAACGACAACGAGGACGCGGCCGCACTGCTCCAGCAG 8100
Db      8041 CTCCCCCTCCTCACCCAAAACGACAACGACAACGAGGACGCGGCCGCACTGCTCCAGCAG 8100
Qy      8101 ACCCGCTACGCCCAGCCCGCCCTCTTCGCCTTCCAGGTCGCCCTCCACCGCCTCCTCACC 8160
Db      8101 ACCCGCTACGCCCAGCCCGCCCTCTTCGCCTTCCAGGTCGCCCTCCACCGCCTCCTCACC 8160
Qy      8161 GACGGCTACCACATCACCCCCCACTACTACGCCGGACACTCCCTCGGCGAAATCACCGCC 8220
Db      8161 GACGGCTACCACATCACCCCCCACTACTACGCCGGACACTCCCTCGGCGAAATCACCGCC 8220
Qy      8221 GCCCACCTCGCCGGCATCCTCACCCTCACCGACGCCACCACCCTCATCACCCAACGCGCC 8280
Db      8221 GCCCACCTCGCCGGCATCCTCACCCTCACCGACGCCACCACCCTCATCACCCAACGCGCC 8280
Qy      8281 ACCCTCATGCAAACCATGCCCCCCGGCACCATGACCACCCTCCACACCACCCCCCACCAC 8340
Db      8281 ACCCTCATGCAAACCATGCCCCCCGGCACCATGACCACCCTCCACACCACCCCCCACCAC 8340
Qy      8341 ATCACCCACCACCTCACCGCCCACGAAAACGACCTCGCCATCGCCGCCATCAACACCCCC 8400
Db      8341 ATCACCCACCACCTCACCGCCCACGAAAACGACCTCGCCATCGCCGCCATCAACACCCCC 8400
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Qy      4021 ACCGCGATCGGCAGCCTCCGCCGCGGCGACAACGACACCCGCCGCTTCCTCACCGCCCTC 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 ACCGCGATCGGCAGCCTCCGCCGCGGCGACAACGACACCCGCCGCTTCCTCACCGCCCTC 4080

Qy      4081 GCCCACACCCATACCACCGGCATCGGCACACCCACCACCTGGCACCACCACTACACCCAC 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 GCCCACACCCATACCACCGGCATCGGCACACCCACCACCTGGCACCACCACTACACCCAC 4140

Qy      4141 CACCACACCCACCCCCACCCCCACACGCACCTCGACCTGCCCACCTACCCCTTCCAACAC 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 CACCACACCCACCCCCACCCCCACACGCACCTCGACCTGCCCACCTACCCCTTCCAACAC 4200

Qy      4201 CAGCACTACTGGCTCGAGAGCTCACAGCCGGGTGCCGGATCCGGTTCGGGTGCCGGTGCC 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 CAGCACTACTGGCTCGAGAGCTCACAGCCGGGTGCCGGATCCGGTTCGGGTGCCGGTGCC 4260

Qy      4261 GGTTCGGGTGCCGGTTCCGGGCGGGCAGGGACTGCGGGCGGGACGGCAGAGGTGGAGTCG 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 GGTTCGGGTGCCGGTTCCGGGCGGGCAGGGACTGCGGGCGGGACGGCAGAGGTGGAGTCG 4320

Qy      4321 CGGTTCTGGGACGCGGTGGCCCGCCAGGACCTGGAAACGGTCGCGACCACACTCGCCGTG 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 CGGTTCTGGGACGCGGTGGCCCGCCAGGACCTGGAAACGGTCGCGACCACACTCGCCGTG 4380

Qy      4381 CCCCCCTCCGCCGGCCTGGACACGGTGGTGCCCGCACTCTCCGCCTGGCACCGCCACCAA 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||.
Db      4381 CCCCCCTCCGCCGGCCTGGACACGGTGGTGCCCGCACTCTCCGCCTGGCACCGCCACCAA 4440

Qy      4441 CACGACCAAGCCCGCATCAACACCTGGACCTACCAGGAAACCTGGAAACCCCTCACCCTC 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 CACGACCAAGCCCGCATCAACACCTGGACCTACCAGGAAACCTGGAAACCCCTCACCCTC 4500

Qy      4501 CCCACCACCCACCAACCCCACCAAACCTGGCTCATCGCCATCCCCGAAACCCAGACCCAC 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 CCCACCACCCACCAACCCCACCAAACCTGGCTCATCGCCATCCCCGAAACCCAGACCCAC 4560

Qy      4561 CACCCCCACATCACCAACATCCTCACCAACCTCCACCACCACGGCATCACCCCCATCCCC 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 CACCCCCACATCACCAACATCCTCACCAACCTCCACCACCACGGCATCACCCCCATCCCC 4620

Qy      4621 CTCACCCTCAACCACACCCACACCAACCCCCAACACCTCCACCACACCCTCCACCACACC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 CTCACCCTCAACCACACCCACACCAACCCCCAACACCTCCACCACACCCTCCACCACACC 4680

Qy      4681 CGACAACAAGCCCAAAACCACACCACCGGAGCCATCACCGGCCTGCTCTCCCTCCTCGCC 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      4741 CTCGACGAAACACCCCACCCCCACCACCCCCACACACCCACCGGCACCCTCCTCAACCTC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4741 CTCGACGAAACACCCCACCCCCACCACCCCCACACACCCACCGGCACCCTCCTCAACCTC 4800

Qy      4801 ACCCTCACCCAAACCCACACCCAAACCCACCCACCAACCCCCCTCTGGTACGCCACCACC 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4801 ACCCTCACCCAAACCCACACCCAAACCCACCCACCAACCCCCCTCTGGTACGCCACCACC 4860

Qy      4861 AACGCCACCACCACCCACCCCAACGACCCCCTCACACACCCCACCCAAGCCCAAACCTGG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4861 AACGCCACCACCACCCACCCCAACGACCCCCTCACACACCCCACCCAAGCCCAAACCTGG 4920

Qy      4921 GGACTCGCCCGCACCACCCTCCTCGAACACCCCACCCACACCGCCGGAATCATCGACCTC 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4921 GGACTCGCCCGCACCACCCTCCTCGAACACCCCACCCACACCGCCGGAATCATCGACCTC 4980

Qy      4981 CCCACCACCCCCACCCCCCACACCCTCCAGCACCTCACCCAAACCCTCACCCAACCCCAC 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      5041 CACCAAACCCAACTCGCCATCCGCACCACCGGCACCCACACCCGCCGCCTCACCCCCACC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      5101 ACCCTCACCCCCACACACCAACCACCCACCCCCACCCCCCACGGAACCACCCTCATCACC 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5101 ACCCTCACCCCCACACACCAACCACCCACCCCCACCCCCCACGGAACCACCCTCATCACC 5160

Qy      5161 GGCGGAACCGGCGCCCTCGCCACCCACCTCACCCACCACCTCACCACCCACCAACCCACC 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5161 GGCGGAACCGGCGCCCTCGCCACCCACCTCACCCACCACCTCACCACCCACCAACCCACC 5220

Qy      5221 CAACACCTCCTCCTCACCAGCCGAACCGGCCCCCACACCCCCCACGCACAACACCTCACC 5280
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Db      5221 CAACACCTCCTCCTCACCAGCCGAACCGGCCCCCACACCCCCCACGCACAACACCTCACC 5280

Qy      5281 ACCCAACTCCAACAAAAAGGCATCCACCTCACCATCACCACCTGCGACACCAGCAACCCA 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5281 ACCCAACTCCAACAAAAAGGCATCCACCTCACCATCACCACCTGCGACACCAGCAACCCA 5340

Qy      5341 GACCAACTCCAACAACTCCTCAACACCATCCCCCCACAACACCCCCTCACCACCGTCATC 5400
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Db      5341 GACCAACTCCAACAACTCCTCAACACCATCCCCCCACAACACCCCCTCACCACCGTCATC 5400

Qy      5401 CACACCGCAGGCATCCTCGACGACGCCACCCTCACCAACCTCACCCCCACCCAACTCAAC 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401 CACACCGCAGGCATCCTCGACGACGCCACCCTCACCAACCTCACCCCCACCCAACTCAAC 5460

Qy      5461 AACGTCCTCCGCGCCAAAGCCCACAGCGCCCACCTCCTCCACCAACTCACCCAACACACC 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 AACGTCCTCCGCGCCAAAGCCCACAGCGCCCACCTCCTCCACCAACTCACCCAACACACC 5520

Qy      5521 CCCCTCACCGCCTTCGTCCTCTACTCCTCCGCCGCCGCCACCTTCGGCGCACCCGGCCAA 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 CCCCTCACCGCCTTCGTCCTCTACTCCTCCGCCGCCGCCACCTTCGGCGCACCCGGCCAA 5580

Qy      5581 GCCAACTACGCCGCAGCCAACGCCTACCTCGACGCCCTCGCCCACCACCGCCACACCCAC 5640
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Db      5581 GCCAACTACGCCGCAGCCAACGCCTACCTCGACGCCCTCGCCCACCACCGCCACACCCAC 5640

Qy      5641 CACCTCCCCGCCACCAGCATCGCCTGGGGCACCTGGCAAGGAAACGGACTCGCTGATTCG 5700
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Db      5641 CACCTCCCCGCCACCAGCATCGCCTGGGGCACCTGGCAAGGAAACGGACTCGCTGATTCG 5700

Qy      5701 GACAAGGCCCGCGCATATCTCGACCGCCGCGGGTTTCGACCCATGTCACCCGAGTTGGCC 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5701 GACAAGGCCCGCGCATATCTCGACCGCCGCGGGTTTCGACCCATGTCACCCGAGTTGGCC 5760

Qy      5761 ACGGCAGCGGTCACGCAGGCGATCGCGGACACCGAACGGCCGTATGTCGTCATCGCCGAC 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5761 ACGGCAGCGGTCACGCAGGCGATCGCGGACACCGAACGGCCGTATGTCGTCATCGCCGAC 5820

Qy      5821 ATCGACTGGAGCAAGATCGAACACACCTCTCAGACCAGCGACCTGGTGAGCGCGGCCCGG 5880
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Db      5821 ATCGACTGGAGCAAGATCGAACACACCTCTCAGACCAGCGACCTGGTGAGCGCGGCCCGG 5880

Qy      5881 GAAAGGGAGCCAGCTGTCCAGCGCCCCACTCCACCGGCGGAGTTGCACAAAACGCTGGCC 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5881 GAAAGGGAGCCAGCTGTCCAGCGCCCCACTCCACCGGCGGAGTTGCACAAAACGCTGGCC 5940

Qy      5941 CATCAGACGTCGGCCGACCAACGGGCCGCATTGCTCGAGCTCGTACGAGACCATGTGGCG 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5941 CATCAGACGTCGGCCGACCAACGGGCCGCATTGCTCGAGCTCGTACGAGACCATGTGGCG 6000

Qy      6001 GCAGTGCTCCGGCACGCGGACCCGAAAGCCATCGCGCCCGACCAGTCGTTCCGTGCACTC 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6001 GCAGTGCTCCGGCACGCGGACCCGAAAGCCATCGCGCCCGACCAGTCGTTCCGTGCACTC 6060

Qy      6061 GGCTTCGATTCACTCACGGCCGTCGAGTTCCGAAACCTGCTGATCAAGGCAACAGGACTC 6120
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Db      6061 GGCTTCGATTCACTCACGGCCGTCGAGTTCCGAAACCTGCTGATCAAGGCAACAGGACTC 6120

Qy      6121 CGCCTTCCTGTCTCGCTGGTCTTCGACCACCCGACCCCTGCCAAACTCGCCGTACACCTG 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6121 CGCCTTCCTGTCTCGCTGGTCTTCGACCACCCGACCCCTGCCAAACTCGCCGTACACCTG 6180

Qy      6181 CAGAACCAACTGCGGGGCACAGCAGCGGAGTCGGCTCCTTCAGCGGCAGCCGTTACCGCC 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1801 GCGGGCGCCCTCTCCTTCGACTACGGCCCGCGTATGGACACCGCGTCGTCGGAGGGCGCC 1860
Qy       1861 GCGGACGTGGAGGGCCACATCCTCACCGGTACCACGGGCAGCGTCCTGTCGGGCCGTATC 1920
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Db       1861 GCGGACGTGGAGGGCCACATCCTCACCGGTACCACGGGCAGCGTCCTGTCGGGCCGTATC 1920
Qy       1921 GCCTACAGCTTCGGGCTGGAAGGGCCGGCGATCACCGTGGACACGGGGTGCTCGGCATCG 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GCCTACAGCTTCGGGCTGGAAGGGCCGGCGATCACCGTGGACACGGGGTGCTCGGCATCG 1980
Qy       1981 CTCGTGACGCTGCATCTGGCGTGCCAGTCGCTGCGGTCGGGTGAGTGCACGCTCGCGCTG 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CTCGTGACGCTGCATCTGGCGTGCCAGTCGCTGCGGTCGGGTGAGTGCACGCTCGCGCTG 2040
Qy       2041 GCCGGCGGCGTCTCGGTCATGTCCACCCTCGGCATGTTCATCGAGTTCTCCCGGCAGCGC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GCCGGCGGCGTCTCGGTCATGTCCACCCTCGGCATGTTCATCGAGTTCTCCCGGCAGCGC 2100
Qy       2101 GGGCTGTCGGTGGACGGCAGGTGCAAGGCGTACTCGGCTGCAGCCGACGGCACCGGCTGG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GGGCTGTCGGTGGACGGCAGGTGCAAGGCGTACTCGGCTGCAGCCGACGGCACCGGCTGG 2160
Qy       2161 GGCGAGGGCGTCGGGATGCTGTTGGTGGAGCGGTTGTCGGATGCGGTGCGGCTGGGGCAT 2220
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Db       2161 GGCGAGGGCGTCGGGATGCTGTTGGTGGAGCGGTTGTCGGATGCGGTGCGGCTGGGGCAT 2220
Qy       2221 CGGGTGCTGGCGGTGGTACGCGGCAGTGCGGTCAACCAGGACGGTGCGTCGAATGGGCTG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CGGGTGCTGGCGGTGGTACGCGGCAGTGCGGTCAACCAGGACGGTGCGTCGAATGGGCTG 2280
Qy       2281 ACGGCGCCGAACGGTCCGGCTCAGGAGCGGGTGATCCGGCAGGCGTTGGCGAACGCGGGG 2340
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Db       2281 ACGGCGCCGAACGGTCCGGCTCAGGAGCGGGTGATCCGGCAGGCGTTGGCGAACGCGGGG 2340
Qy       2341 TTGTCCGTGGCGGATGTGGATGTGGTGGAGGGGCACGGGACGGGCACGACGCTGGGTGAT 2400
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Db       2341 TTGTCCGTGGCGGATGTGGATGTGGTGGAGGGGCACGGGACGGGCACGACGCTGGGTGAT 2400
Qy       2401 CCGATCGAGGCACAGGCGTTGCTCGCCACGTACGGGCAGCGGGCCGGTGACAGGCCGCTG 2460
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Db       2401 CCGATCGAGGCACAGGCGTTGCTCGCCACGTACGGGCAGCGGGCCGGTGACAGGCCGCTG 2460
Qy       2461 TGGCTGGGGTCTCTGAAGTCCAACATCGGGCACACCATGGCTGCCGCGGGTGTGGGTGGG 2520
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Qy       2521 GTCATCAAGATGGTGATGGCGTTGCGGGAGGGGGTGTTGCCGCGGACGTTGCATGTGGAT 2580
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Qy       2581 AAGCCGTCGCCGCAGGTGGACTGGTCCGCGGGGGCGGTGCGGCTGCTGACGGAGGCGGTG 2640
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Db       2581 AAGCCGTCGCCGCAGGTGGACTGGTCCGCGGGGGCGGTGCGGCTGCTGACGGAGGCGGTG 2640
Qy       2641 CCGTGGCCGGGGGACGCGGCAGGGCGGTTGCGGCGGGCGGGAGTGTCGTCGTTCGGGATC 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CCGTGGCCGGGGGACGCGGCAGGGCGGTTGCGGCGGGCGGGAGTGTCGTCGTTCGGGATC 2700
Qy       2701 GGCGGCACGAATGCGCATGTGATTTTGGAGGAGGCGCCGGCGGCGGGGGGCTGTGTTGCC 2760
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Db       2701 GGCGGCACGAATGCGCATGTGATTTTGGAGGAGGCGCCGGCGGCGGGGGGCTGTGTTGCC 2760
Qy       2761 GGGGGTGGGGTGTTGGAGGGTGCTCCGGGTCTTGCCATTTCGGTGGCTGAGTCGGTGGCC 2820
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Db       2761 GGGGGTGGGGTGTTGGAGGGTGCTCCGGGTCTTGCCATTTCGGTGGCTGAGTCGGTGGCC 2820
Qy       2821 GCTCCAGTGGCTGTGTCTGCGCCGGTGGCTGAGTCGGTGCCGGTGCCGGTGCCGGTGCCG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 GCTCCAGTGGCTGTGTCTGCGCCGGTGGCTGAGTCGGTGCCGGTGCCGGTGCCGGTGCCG 2880
Qy       2881 GTTCCTGTGCCGGTGTCGGCTAGGTCTGAGGCTGGGTTGCGGGCGCAGGCGGAGGCGTTG 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GTTCCTGTGCCGGTGTCGGCTAGGTCTGAGGCTGGGTTGCGGGCGCAGGCGGAGGCGTTG 2940

Qy       2941 CGTCAGTACGTGGCAGTCCGGCCGGACGTTTCGCTTGCCGATGTGGGTGCGGGTCTGGCC 3000
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Db       2941 CGTCAGTACGTGGCAGTCCGGCCGGACGTTTCGCTTGCCGATGTGGGTGCGGGTCTGGCC 3000
Qy       3001 TGTGGGCGGGCTGTGCTGGAGCATCGTGCGGTCGTCCTGGCCGCGGACCGTGAGGAGCTG 3060
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Qy       3061 GTGCAAGGGTTGGGGGCGCTGGCGGCGGGTGAGCCGGATCGGCGGGTGACCACGGGTCAT 3120
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Qy       3121 GCGCCGGGTGGTGACCGGGGCGGTGTCGTCTTCGTGTTTCCCGGACAGGGTGGGCAGTGG 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GCGCCGGGTGGTGACCGGGGCGGTGTCGTCTTCGTGTTTCCCGGACAGGGTGGGCAGTGG 3180
Qy       3181 GCCGGGATGGGTGTGCGTCTGCTCGCCTCCTCTCCGGTGTTCGCCCGGCGGATGCAGGCG 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 GCCGGGATGGGTGTGCGTCTGCTCGCCTCCTCTCCGGTGTTCGCCCGGCGGATGCAGGCG 3240
Qy       3241 TGCGAGGAGGCTCTGGCGCCGTGGGTGGACTGGTCTGTGGTGGACATCCTGCGCCGGGAC 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3301 GCGGGGGATGCGGTGTGGGAGCGGGCCGATGTGGTCCAGCCTGTGCTGTTCAGCGTCATG 3360
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Qy       3361 GTGTCTTTGGCTGCTCTGTGGCGTTCCTACGGTATCGAACCCGACGCGGTCCTTGGCCAT 3420
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Qy       3421 TCCCAGGGCGAGATCGCGGCCGCGCATGTGTGTGGGGCGCTGAGCCTGAAGGACGCGGCG 3480
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            THE KITASATO INSTITUTE
COMMENT     OS   Streptomyces avermitilis
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            PD   12-SEP-2000
            PF   24-FEB-1999 JP 1999046961
            PR
            PI   SATOSHI OMURA,HARUO IKEDA
            PC   C12N15/00,A61K31/70,C12N1/15,C12N9/88,C12P19/62, PC
            C12Q1/68//C07D493/22,
            PC   (C12N1/15,C12R1:465),(C12N9/88,C12R1:465),C12N15/00 CC
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                    /db_xref="taxon:33903"
BASE COUNT     5355 a  12455 c   8617 g   4263 t
ORIGIN

  Query Match           100.0%;  Score 30690;  DB 6;  Length 30690;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 30690;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        181 GAAGCCGCGTTCGCGCCCTACGTCGACTGGTCGGTGGAGCAGGTGTTGCGGGACTCGCCG 240
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 22:17:14 ; Search time 49787 Seconds
(without alignments)
17939.725 Million cell updates/sec

Title: US-09-914-286-1
Perfect score: 30690
Sequence: 1 gtgcagaggatggacggcgg.....acgaaggtgagacagcgtga 30690

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1		30690	100.0	30690	6	E38020	E38020 Avermectin
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7		4852.2	15.8	113193	1	AF357202	AF357202 Streptomy
8		4455.8	14.5	78210	1	AB070949	AB070949 Streptomy
9		4347.6	14.2	123580	1	AF263912	AF263912 Streptomy
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15		3403	11.1	90445	1	AF040570	AF040570 Amycolato
16		3399.8	11.1	53784	1	AMM223012	AJ223012 Amycolato
17		3399.8	11.1	53789	6	A69720	A69720 Sequence 3
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19		3242.8	10.6	67523	1	SCU24241	U24241 Sorangium c
20		3194.8	10.4	49377	6	I88042	I88042 Sequence 1
21		3142	10.2	50000	6	AX089417	AX089417 Sequence
22		3142	10.2	50000	6	AX089420	AX089420 Sequence
23		3142	10.2	80161	1	AY007564	AY007564 Saccharop
24		3142	10.2	80161	6	AR165018	AR165018 Sequence
25		3140.6	10.2	28958	6	AR044578	AR044578 Sequence
26		3140.6	10.2	28958	6	I47768	I47768 Sequence 6
27		3140.6	10.2	28958	6	I50958	I50958 Sequence 6
28		3140.6	10.2	28958	6	I63356	I63356 Sequence 6
29		3140.6	10.2	28958	6	I70387	I70387 Sequence 6
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36		2847.2	9.3	20394	6	AX067996	AX067996 Sequence
37		2841.8	9.3	41097	1	AF016585	AF016585 Streptomy
38		2691.6	8.8	17101	1	AB017641	AB017641 Micromono
39	c	2550.2	8.3	77534	1	AF235504	AF235504 Streptomy
40	c	2371.4	7.7	39314	1	SGR300302	AJ300302 Streptomy
41	c	2366.2	7.7	30000	6	AX250263	AX250263 Sequence
42		2304.2	7.5	24568	1	AF220951	AF220951 Streptomy
43		2304.2	7.5	50937	6	AR159871	AR159871 Sequence
44		2237	7.3	32870	1	AF007101	AF007101 Streptomy
45		2179.4	7.1	47981	1	AF263245	AF263245 Micromono

ALIGNMENTS

RESULT 1
E38020
LOCUS E38020 30690 bp DNA linear PAT 31-JAN-2002
DEFINITION Avermectin aglycon synthase gene.
ACCESSION E38020
VERSION E38020.1 GI:18626909
KEYWORDS JP 2000245457-A/1.
SOURCE Streptomyces avermitilis.
ORGANISM Streptomyces avermitilis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE 1 (bases 1 to 30690)
AUTHORS Omura,S. and Ikeda,H.
TITLE Avermectin aglycon synthase gene
JOURNAL Patent: JP 2000245457-A 1 12-SEP-2000;

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  Query Match          12.2%;  Score 3732.4;  DB 1;  Length 84985;
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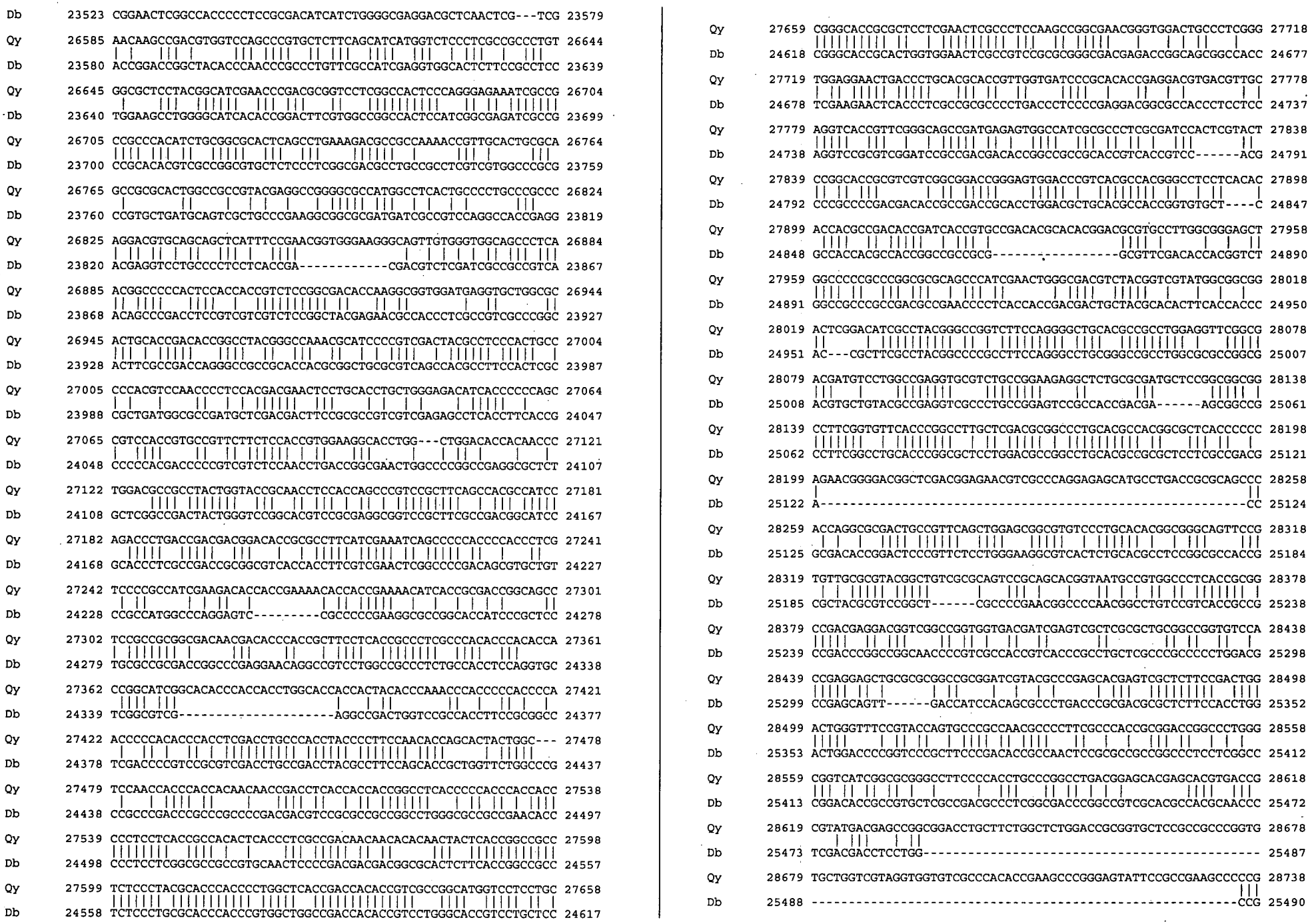
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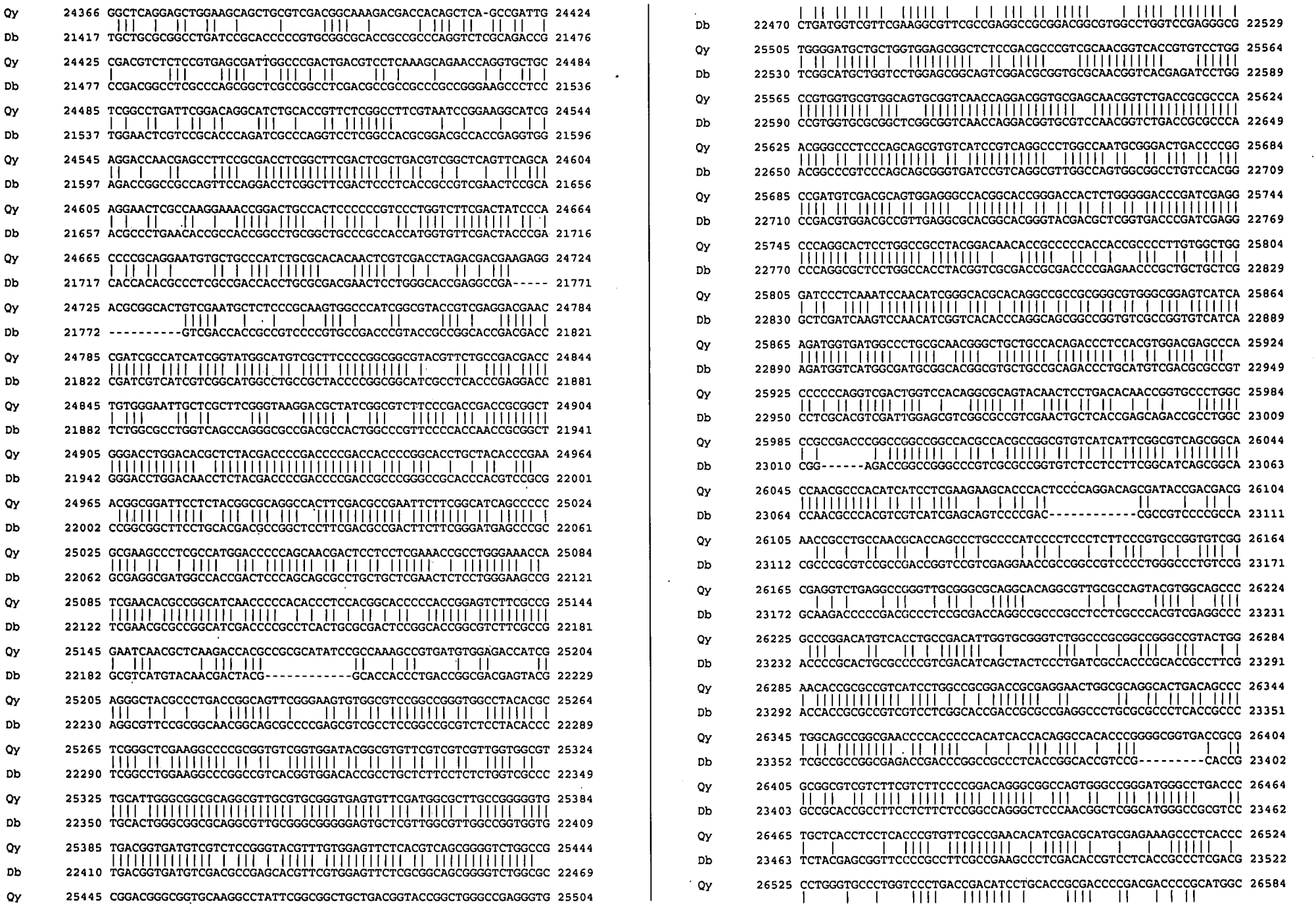
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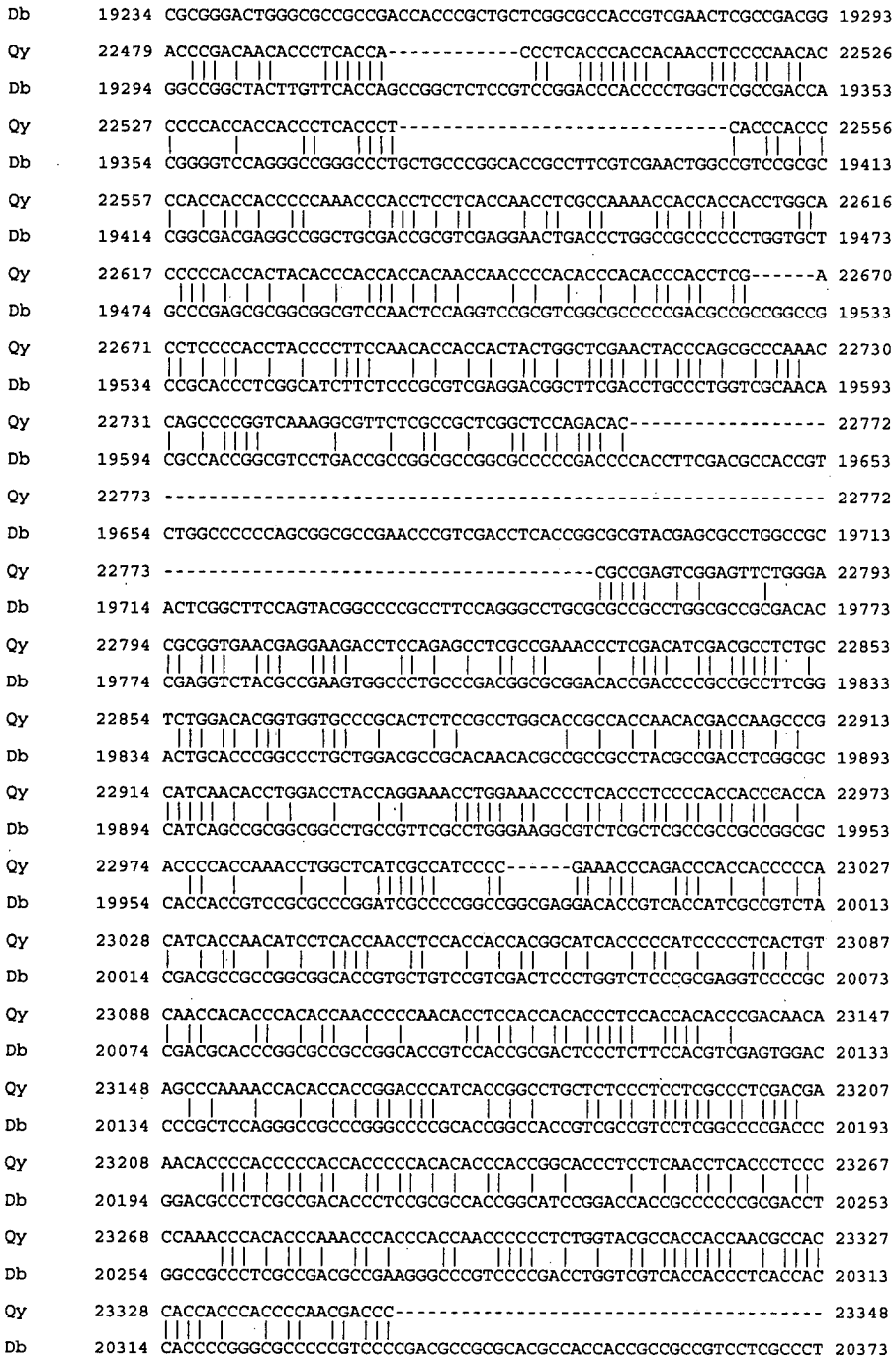
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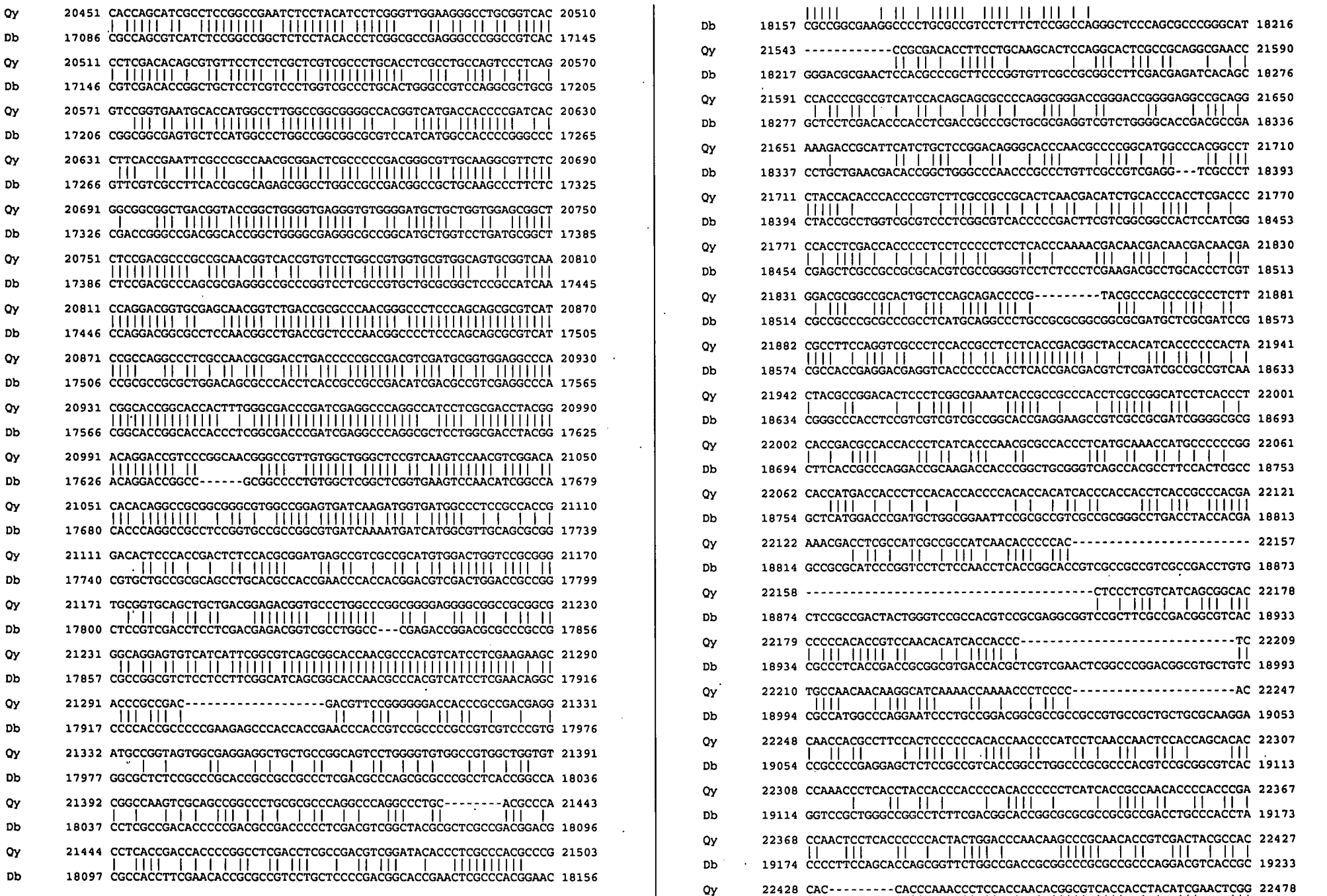
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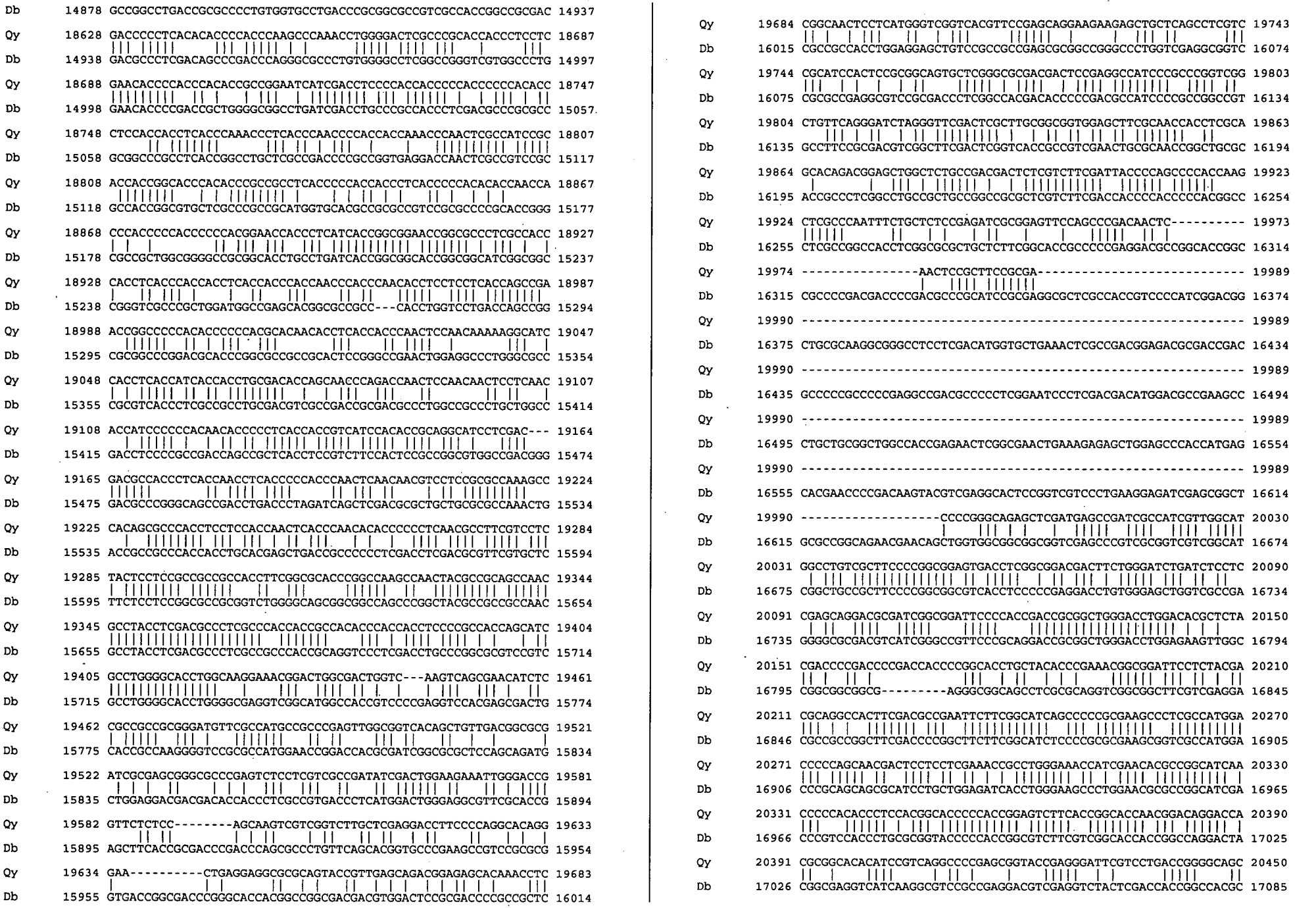
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  AUTHORS   Aparicio,J.F., Fouces,R., Mendes,M.V., Olivera,N. and Martin,J.F.
  TITLE     A complex multienzyme system encoded by five polyketide synthase
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  JOURNAL   Chem. Biol. 7 (11), 895-905 (2000)
  MEDLINE   20547809
   PUBMED   11094342
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  AUTHORS   Aparicio,J.F.
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  JOURNAL   Submitted (27-JUN-2000) Aparicio J.F., Molecular Genetics,
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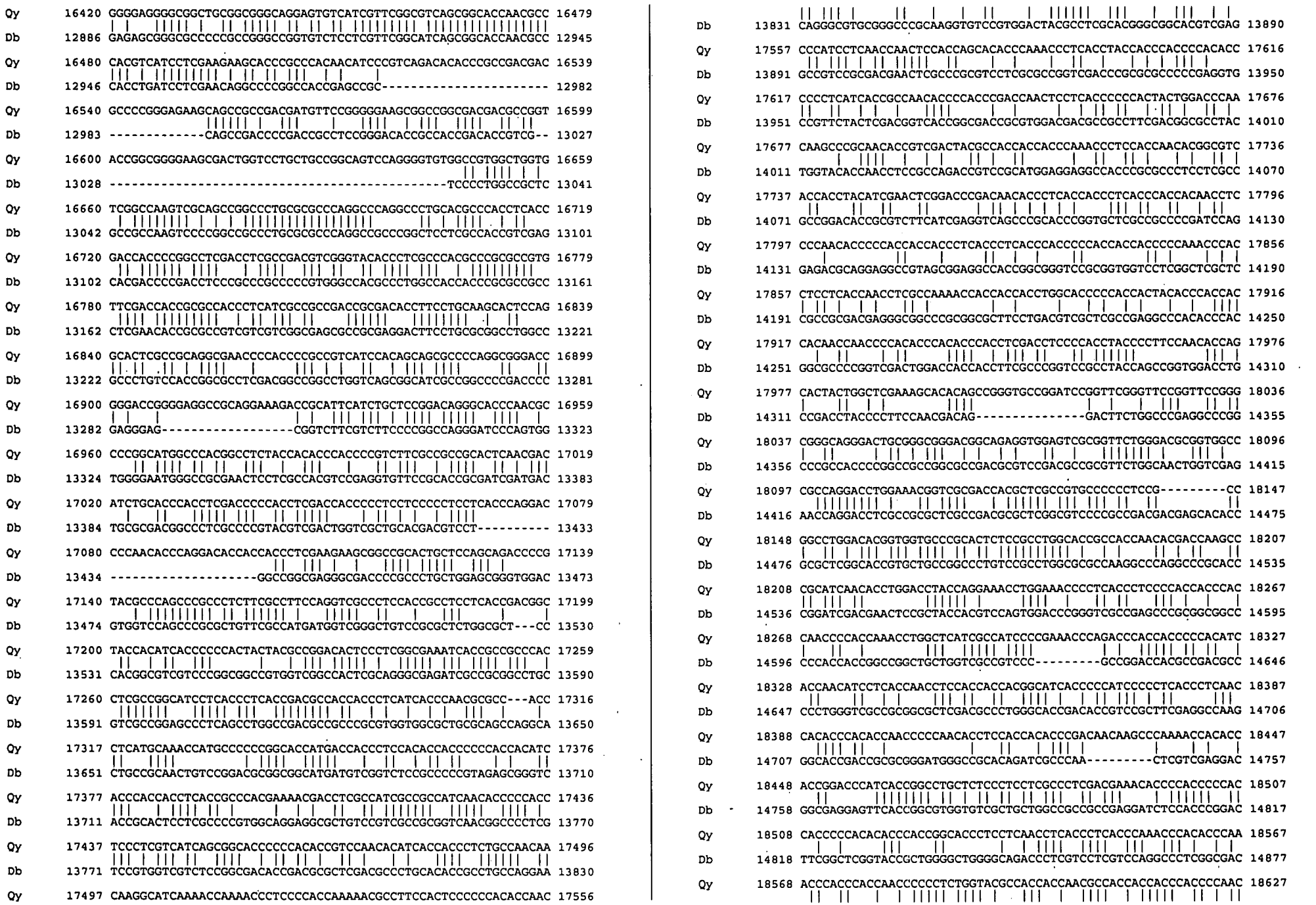


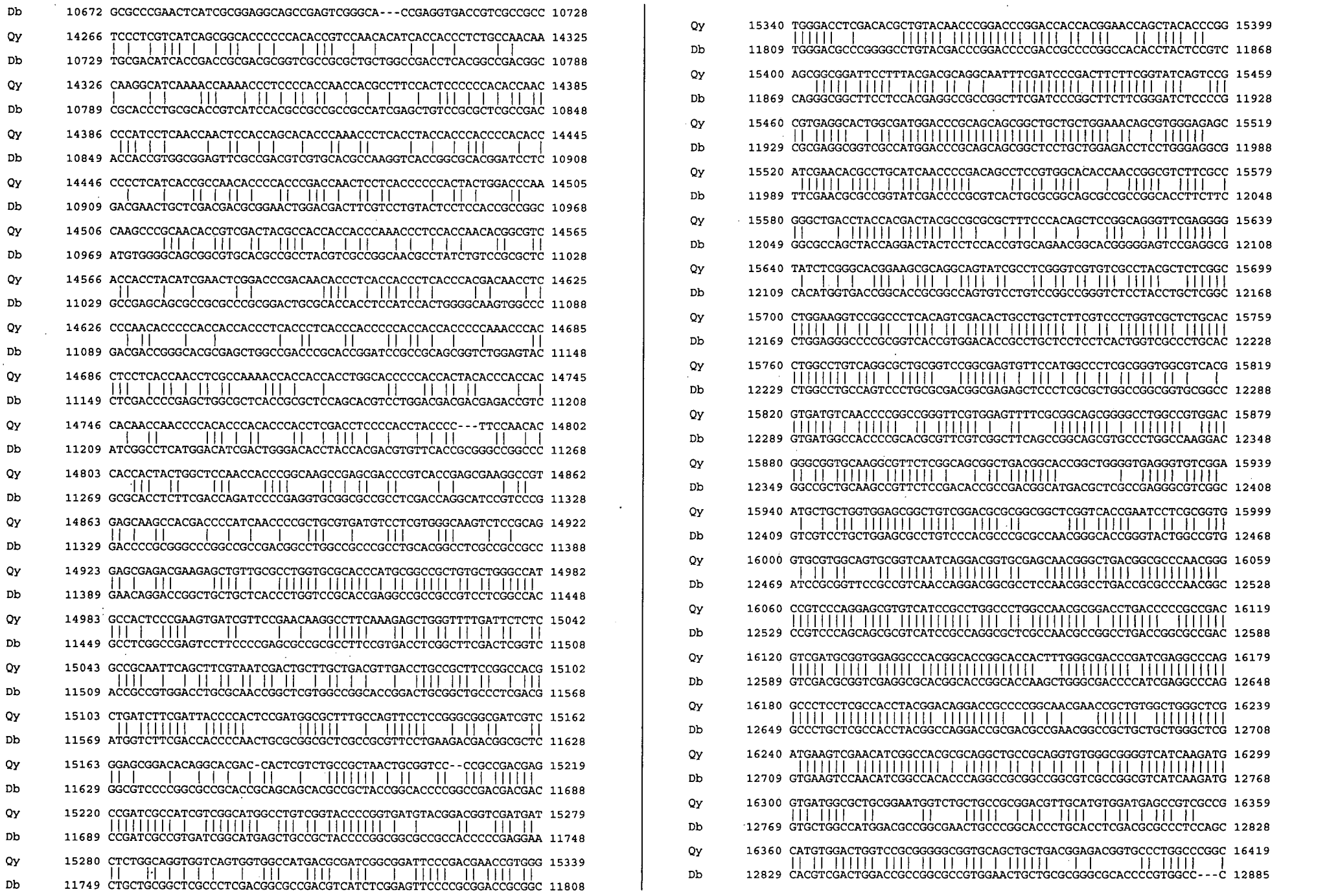


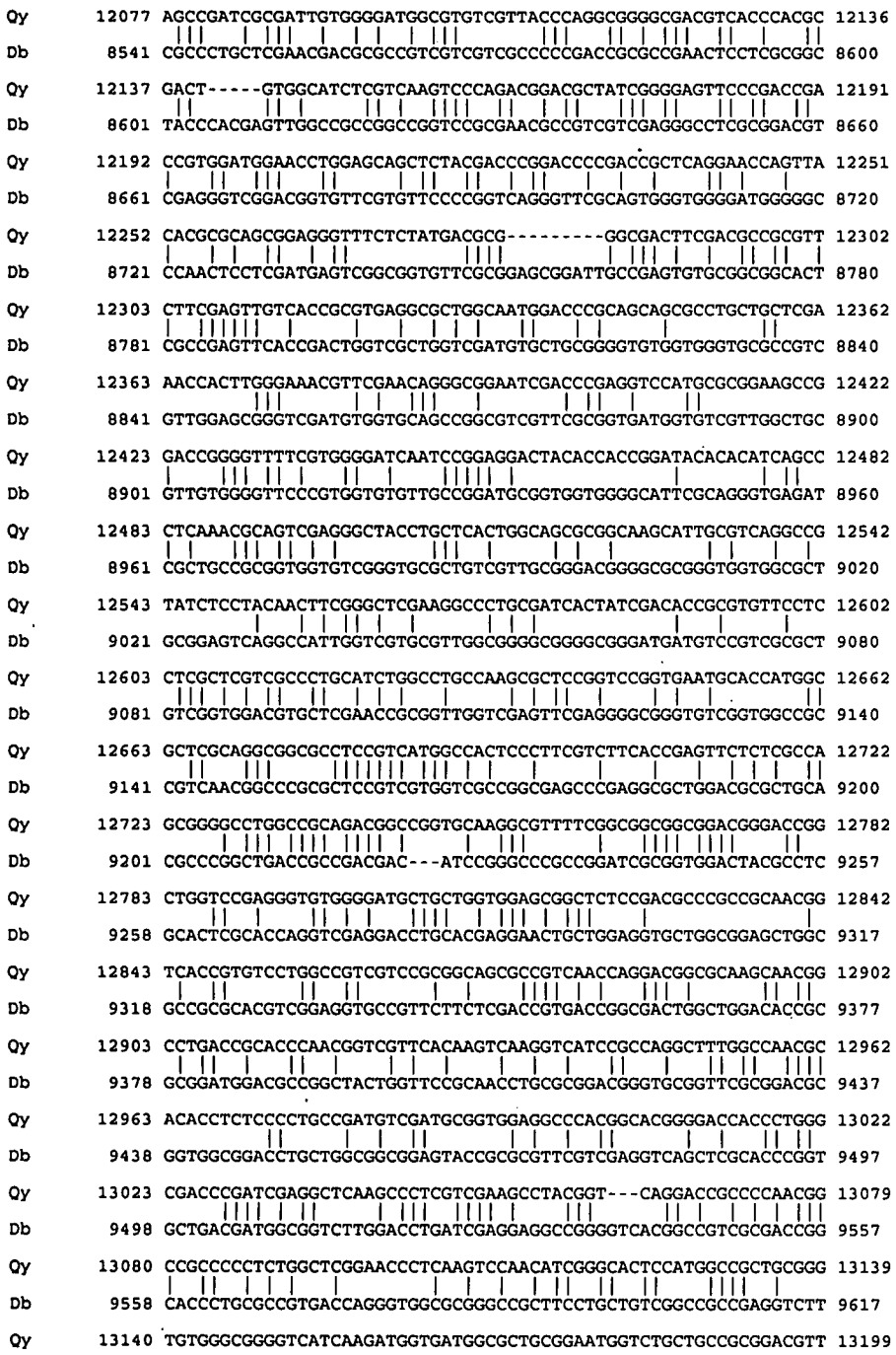

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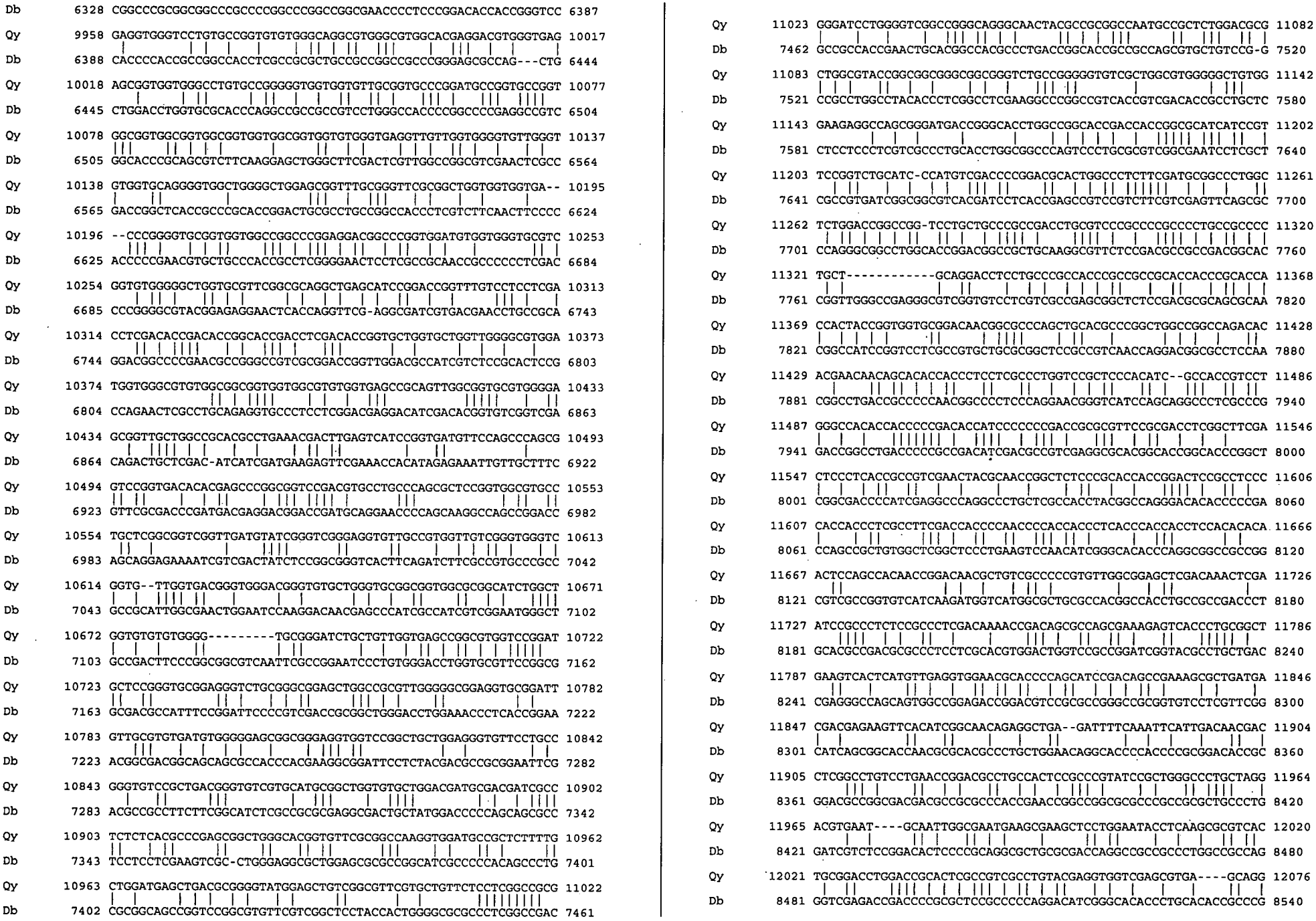


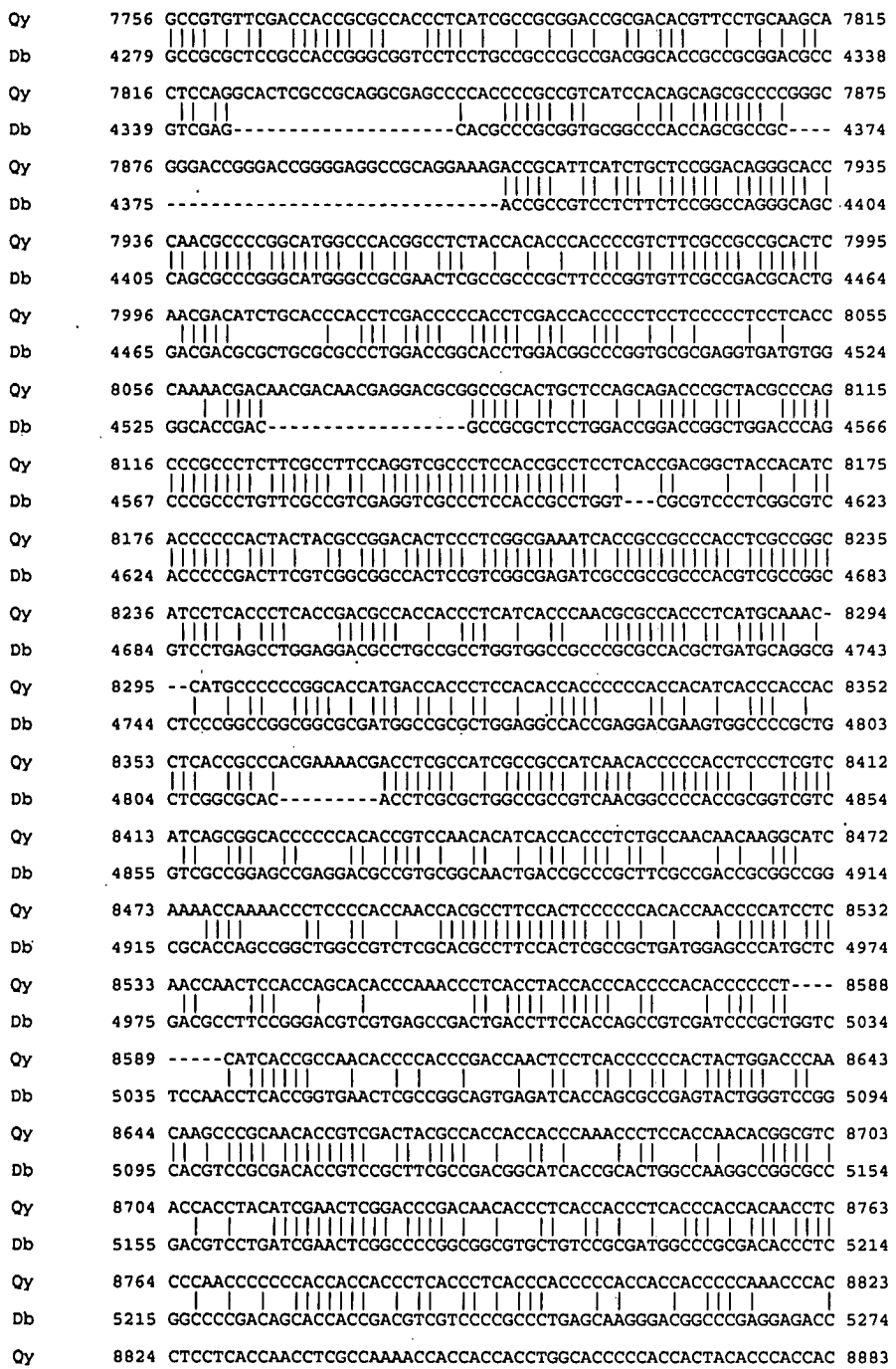


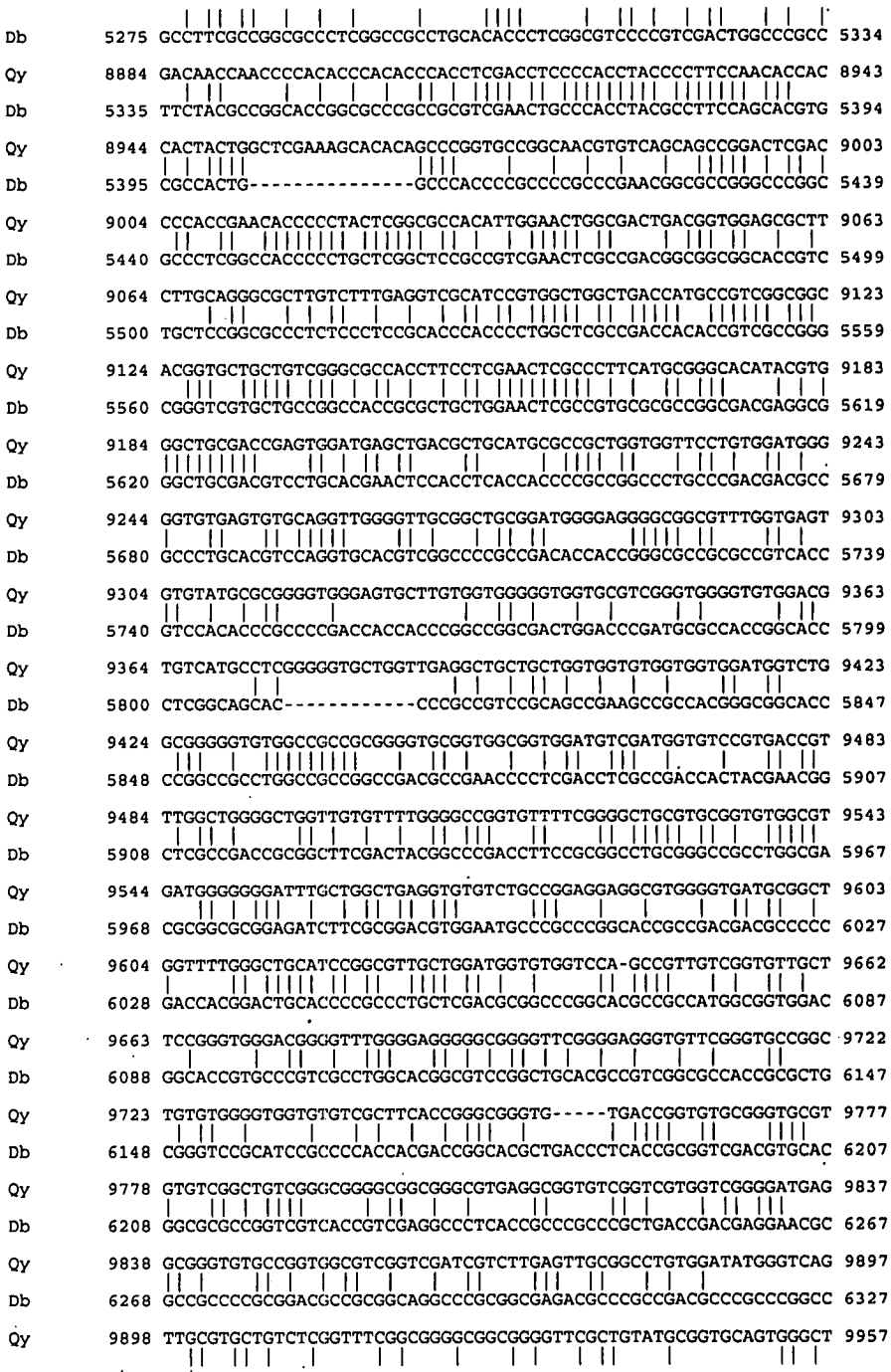





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RESULT 11
AX211705
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REFERENCE   1  (bases 1 to 65140)
  AUTHORS   Zotchev,S.B., Sekurova,O.N., Fjaervik,E., Brautaset,T.,
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  TITLE     Gene cluster encoding a nystatin polyketide synthase and its
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  JOURNAL   Patent: WO 0159126-A 1 16-AUG-2001;
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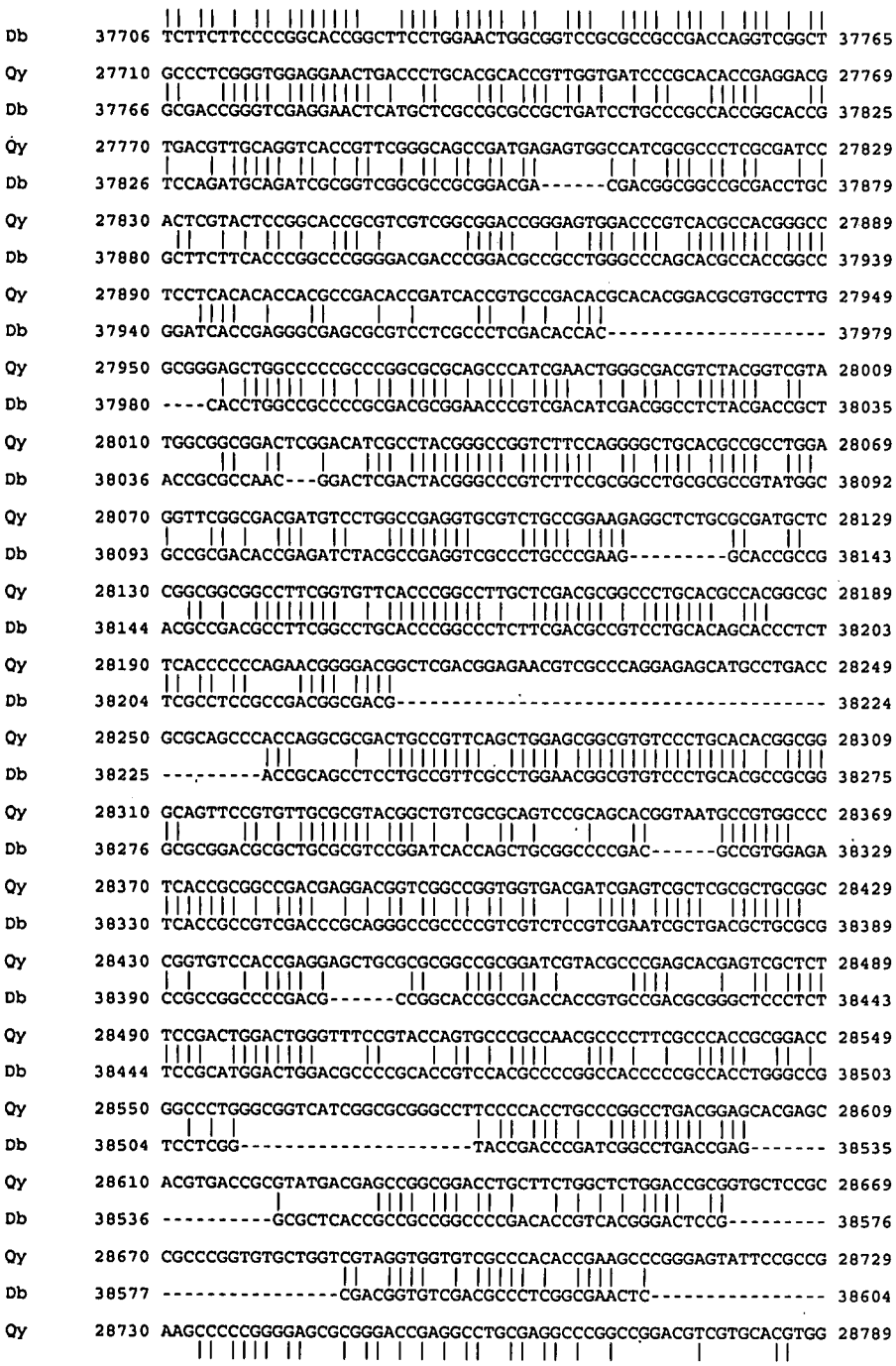
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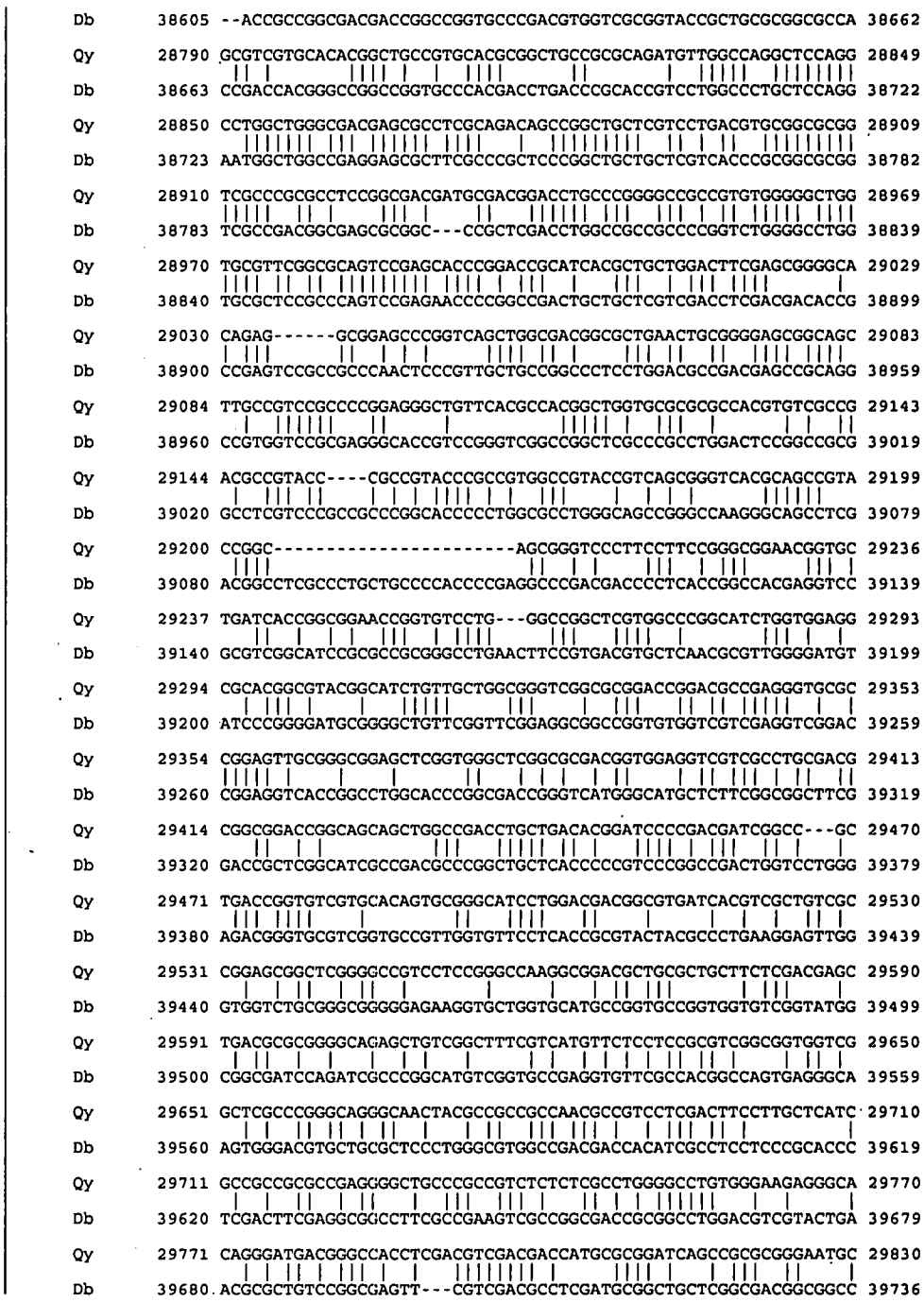
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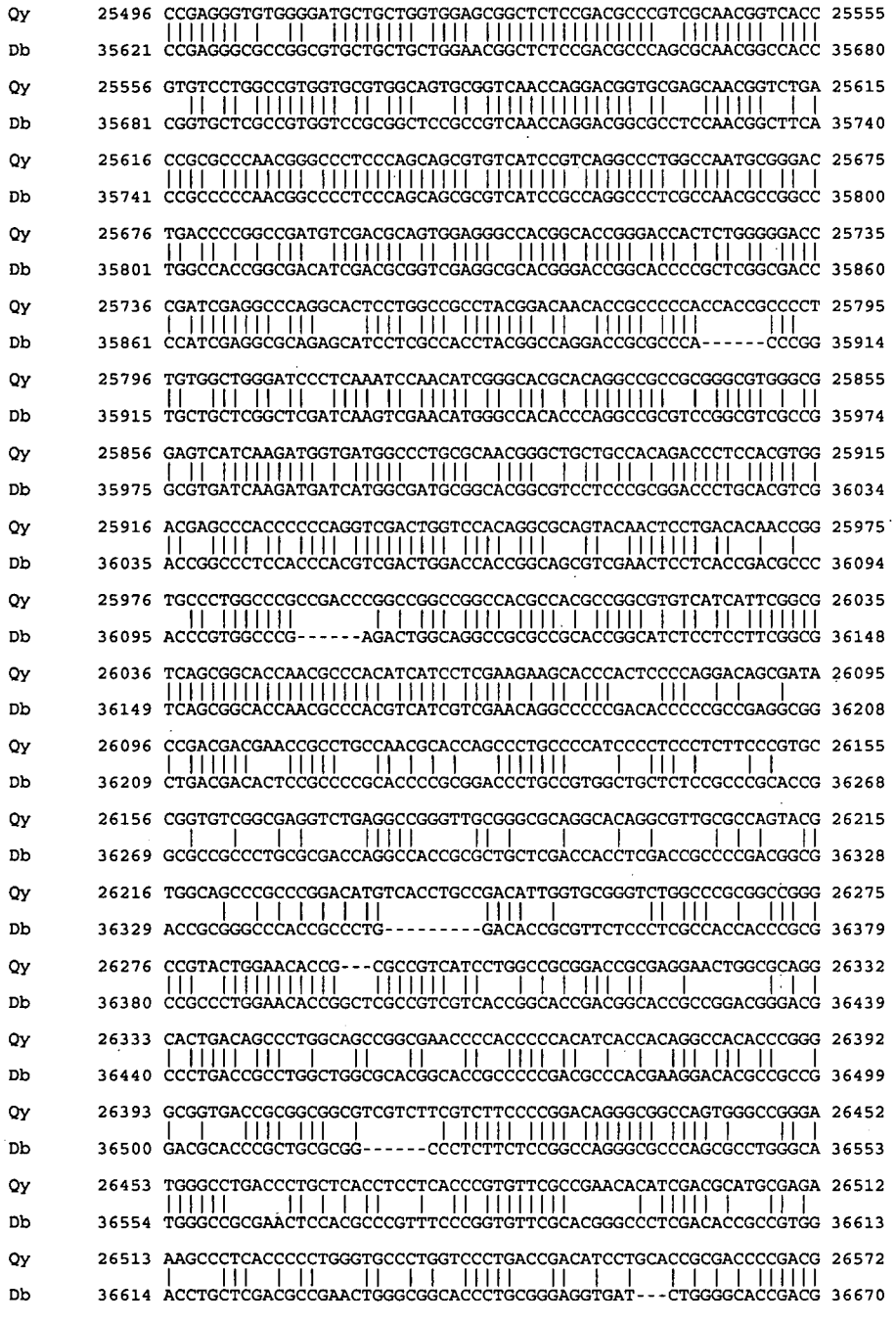
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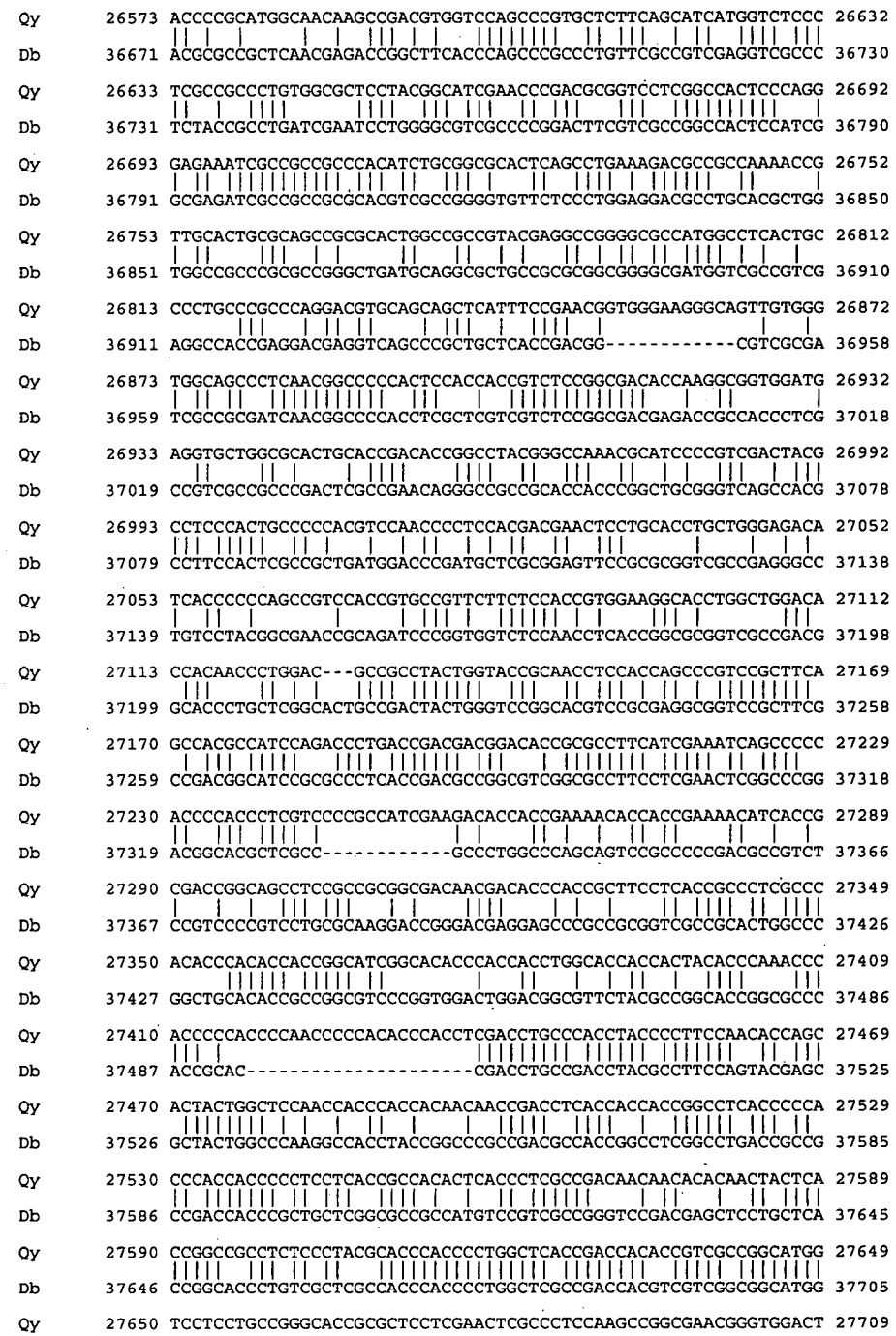
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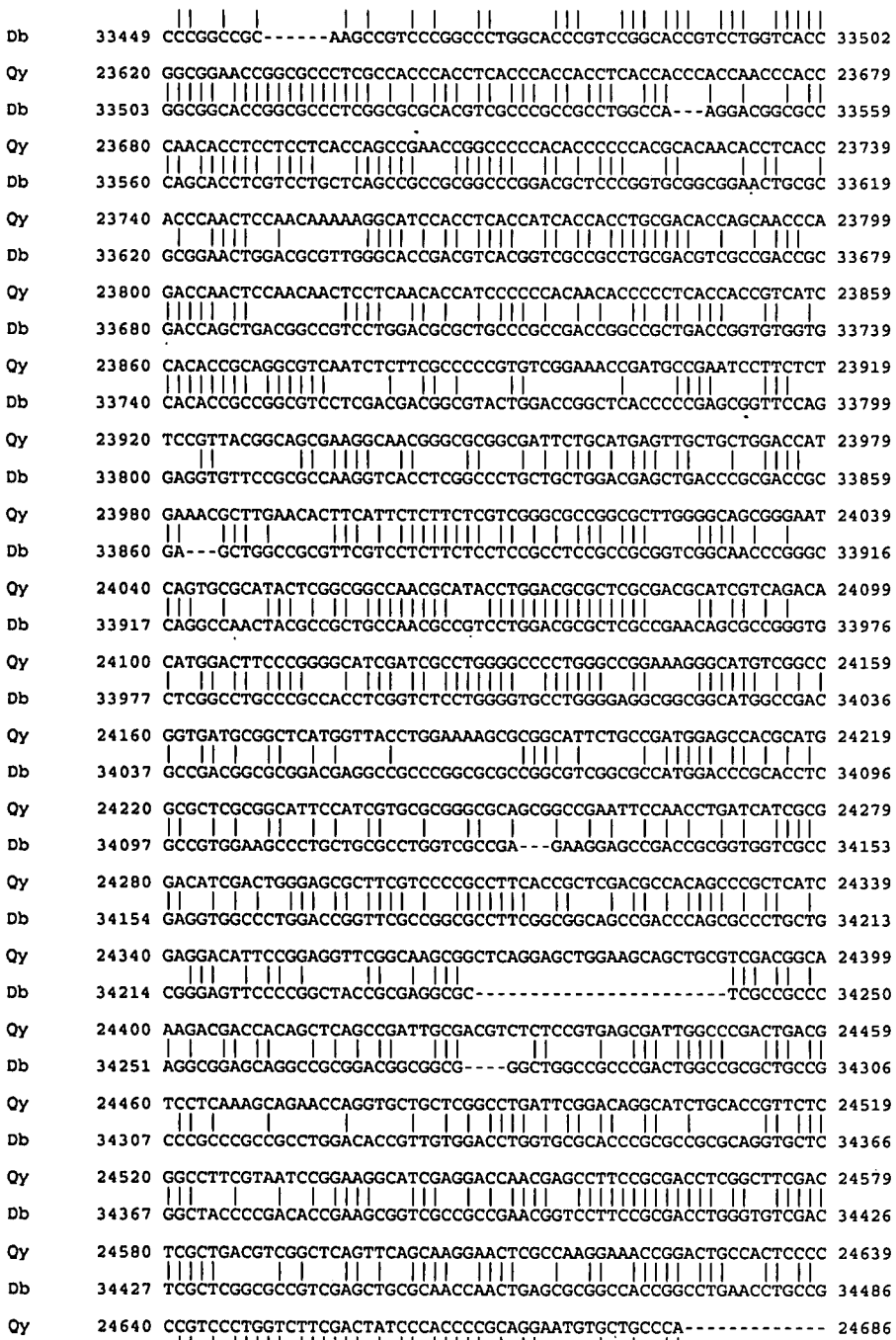
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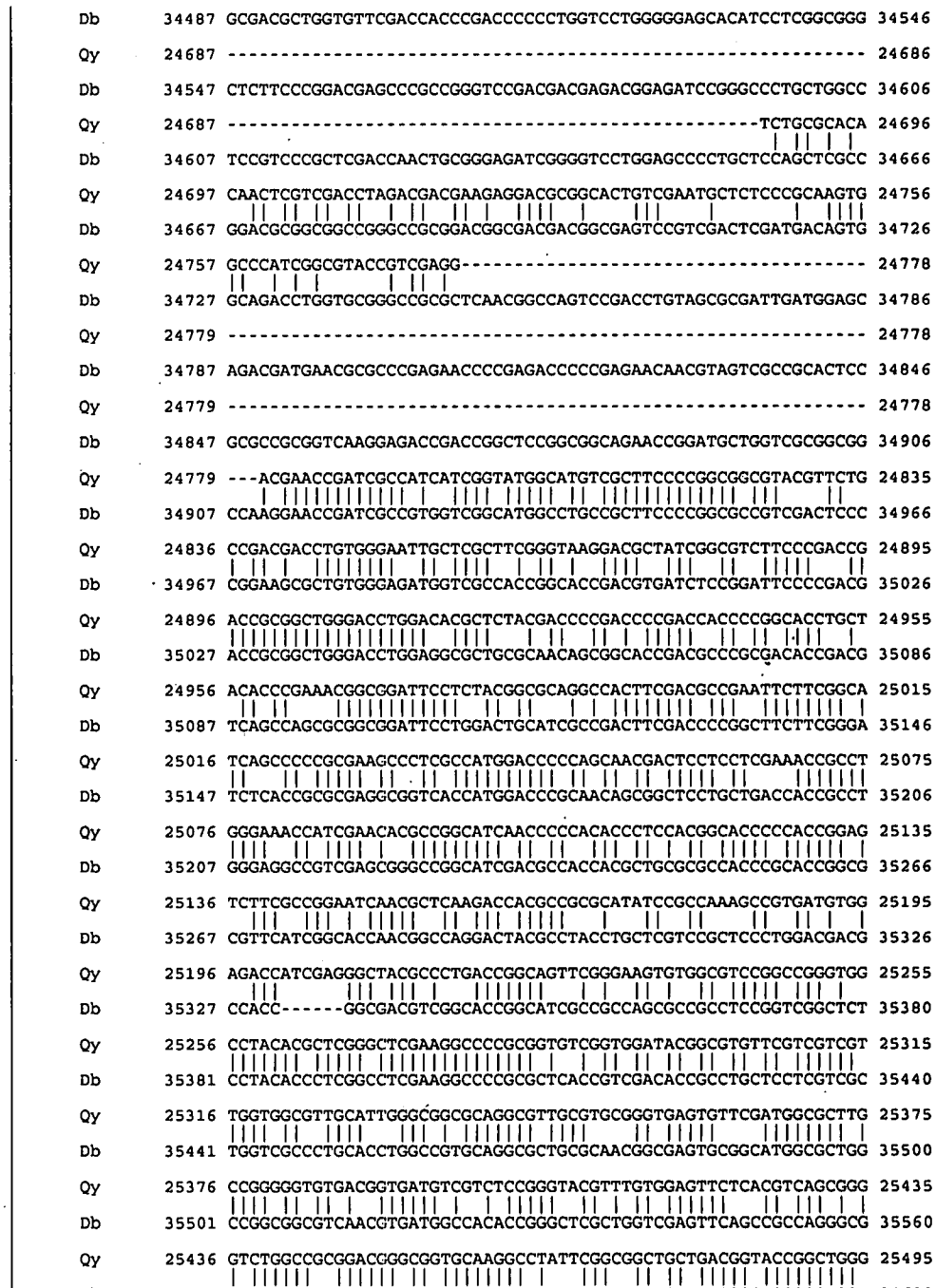


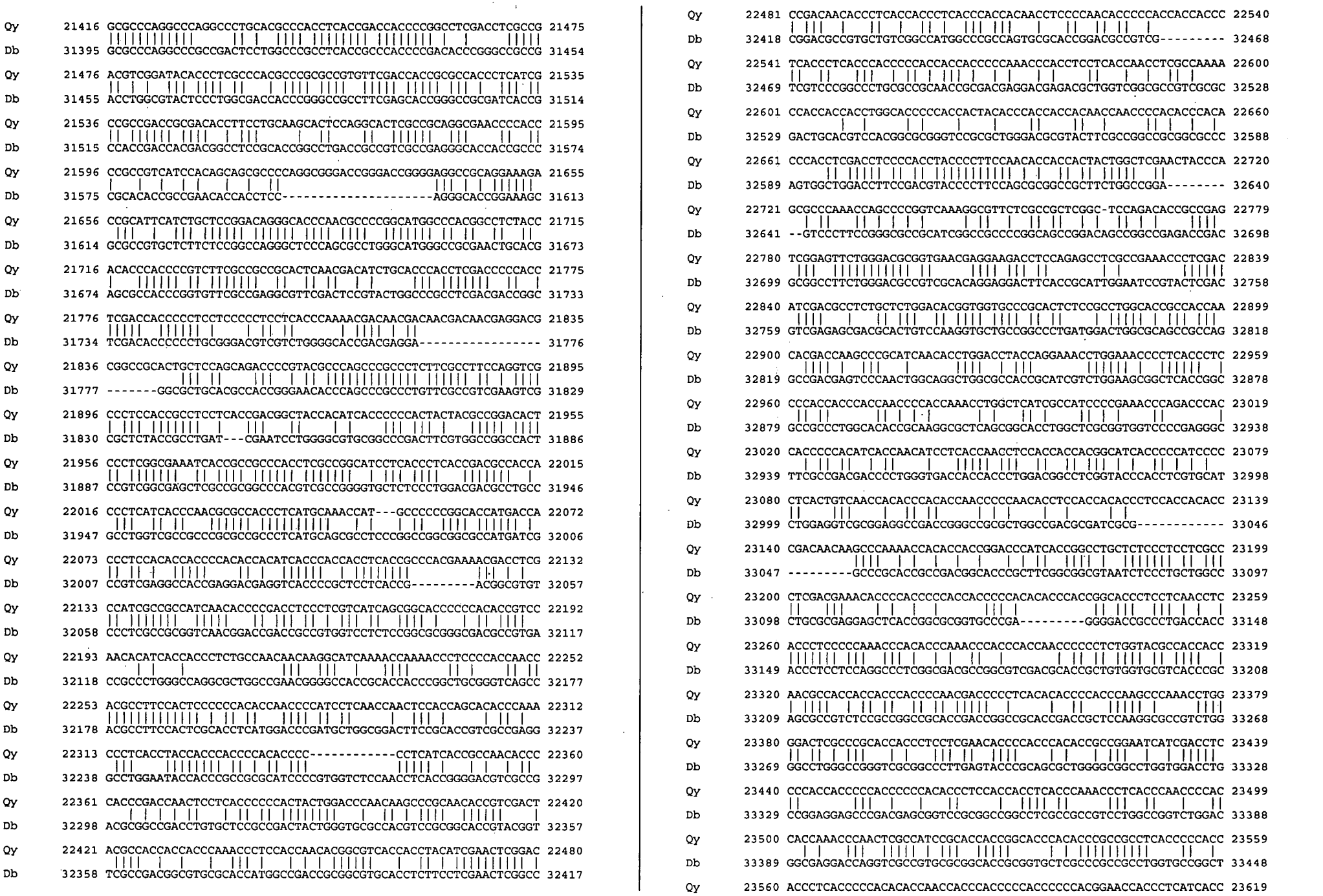


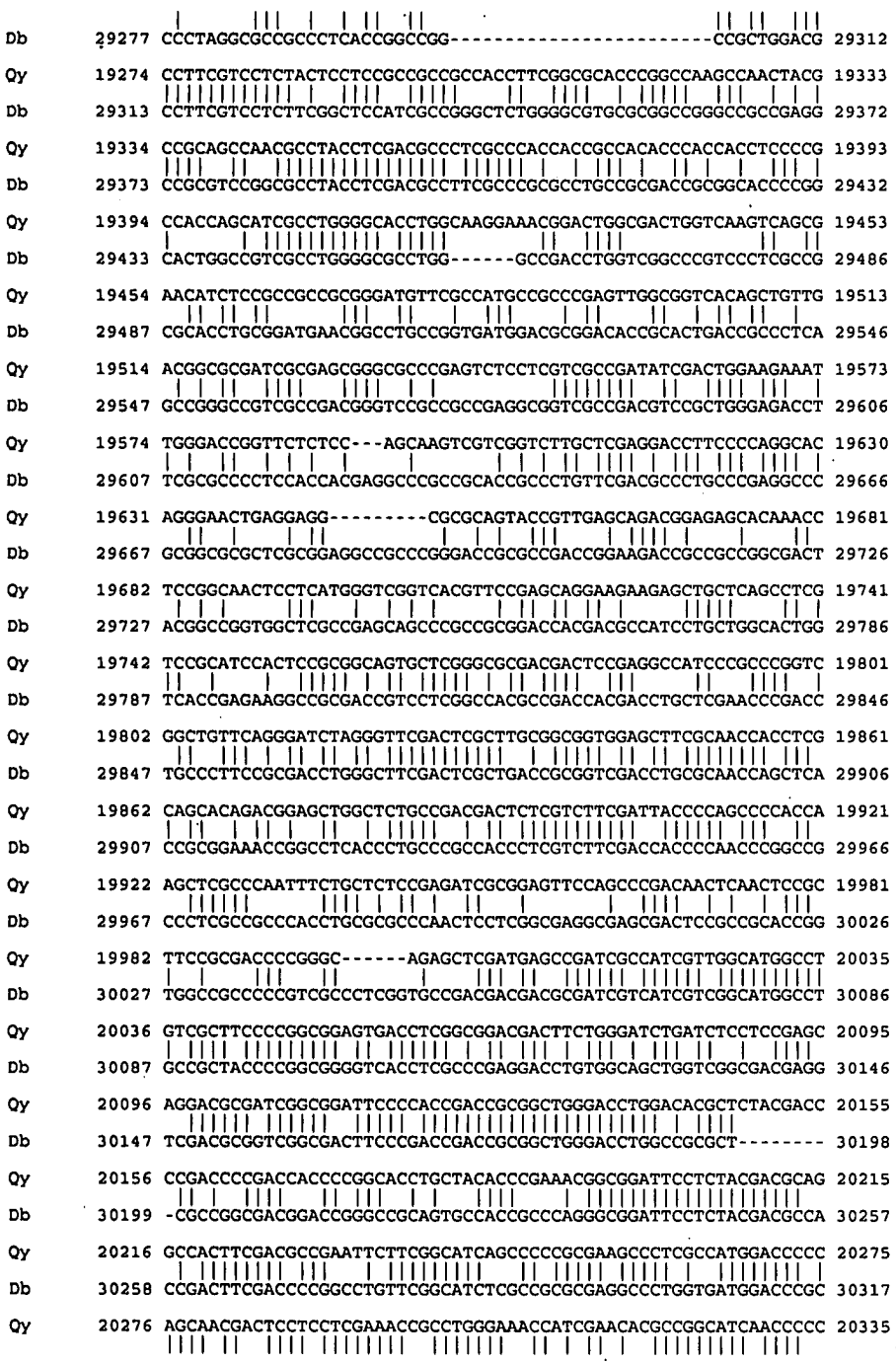


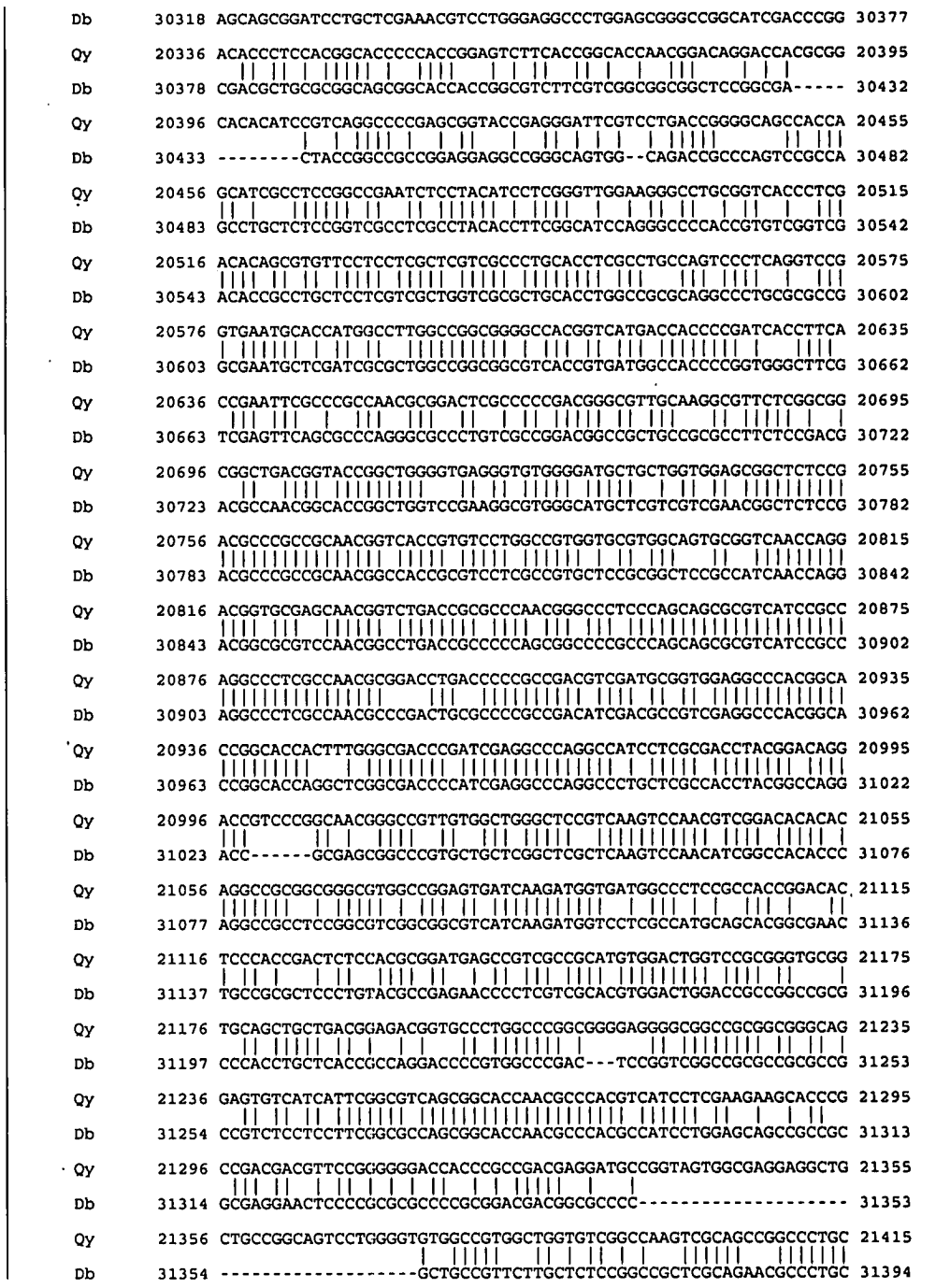


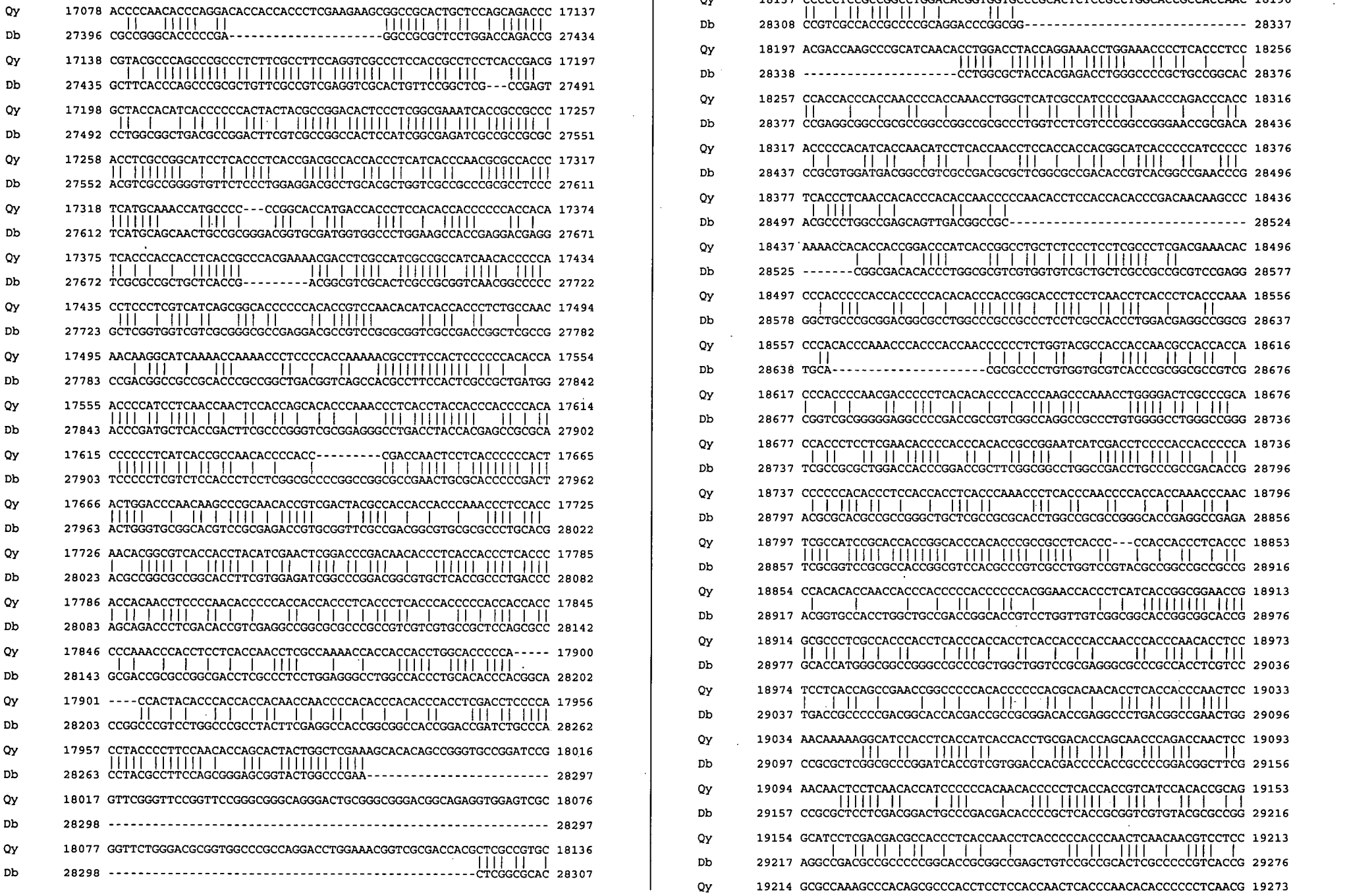


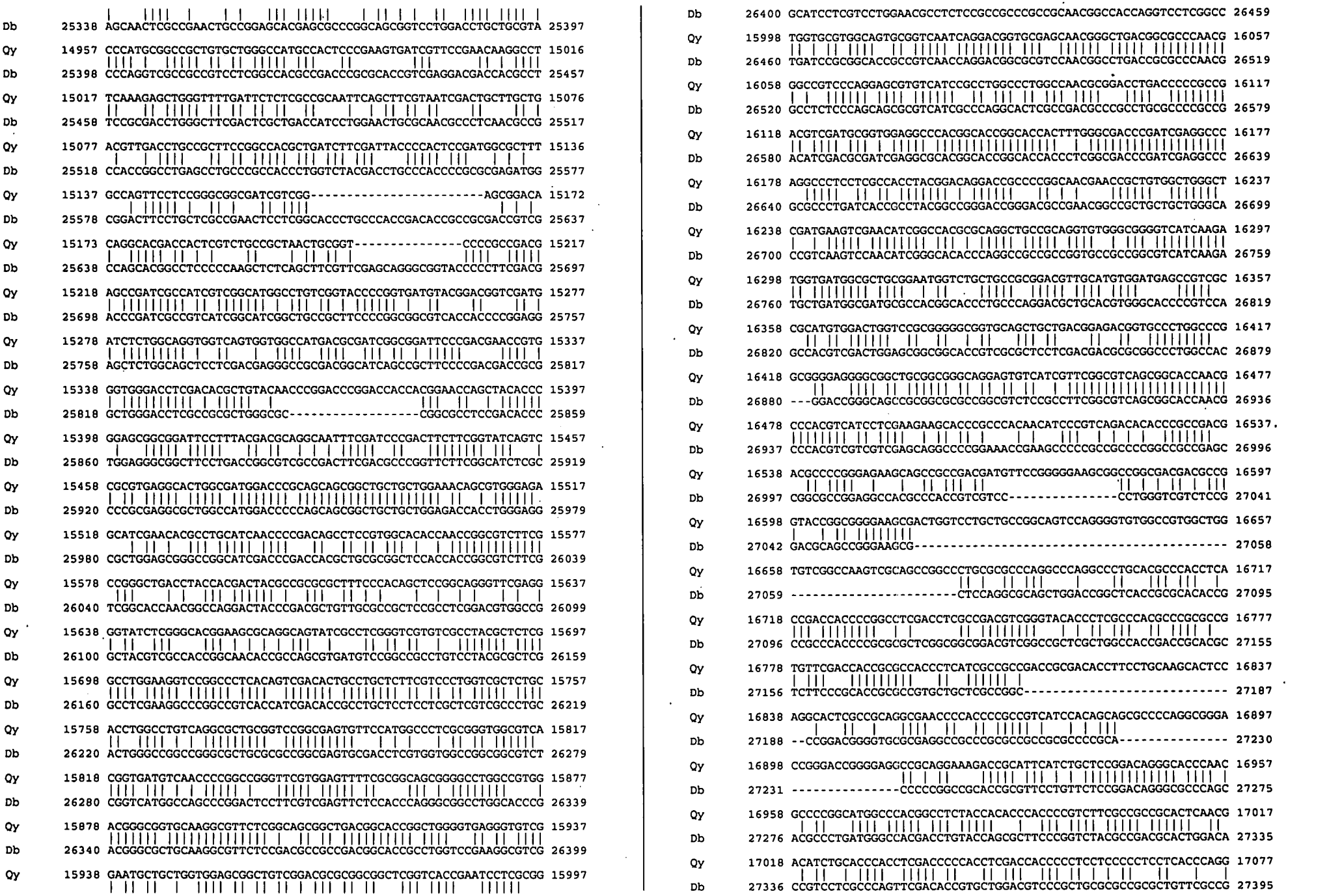


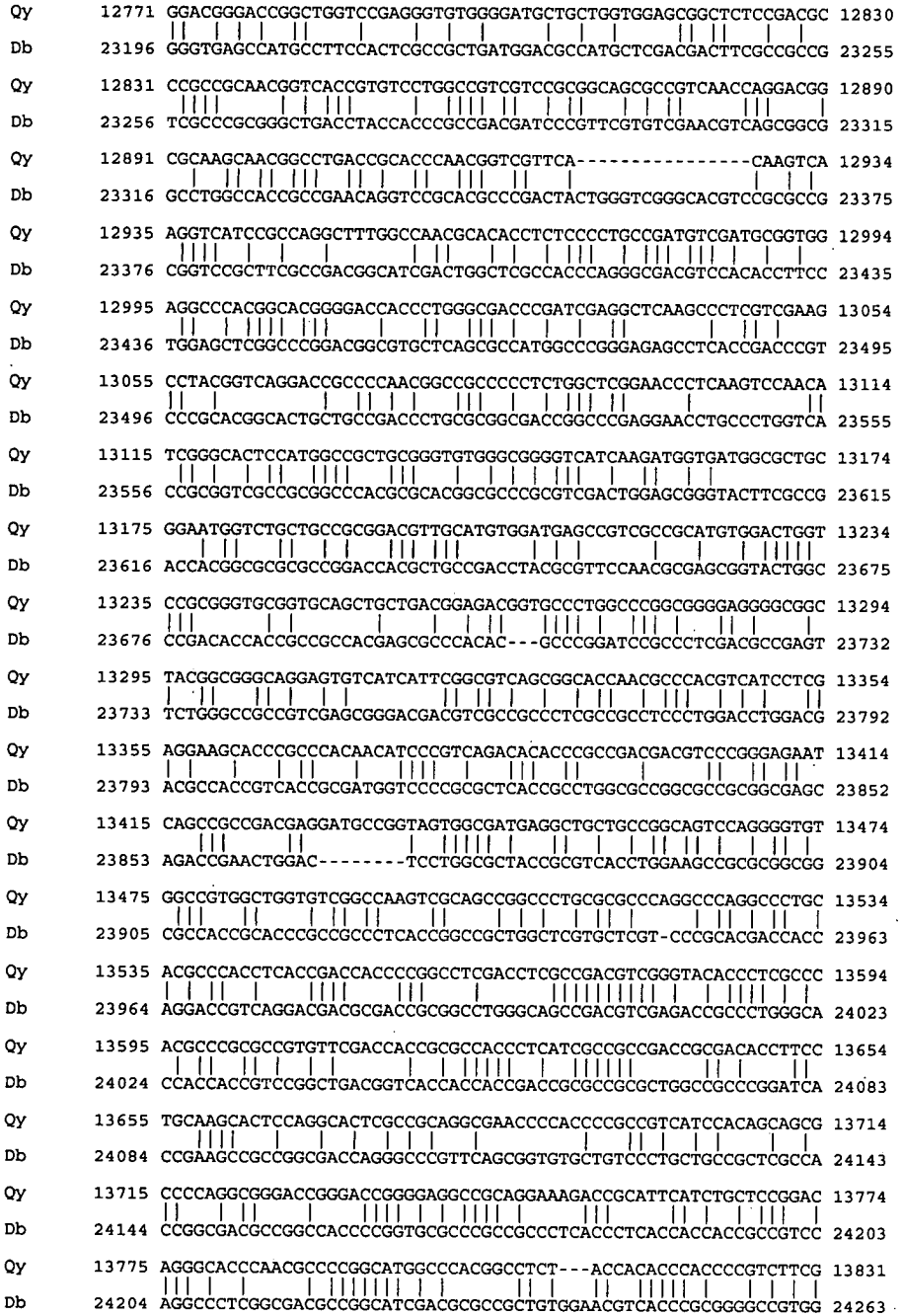


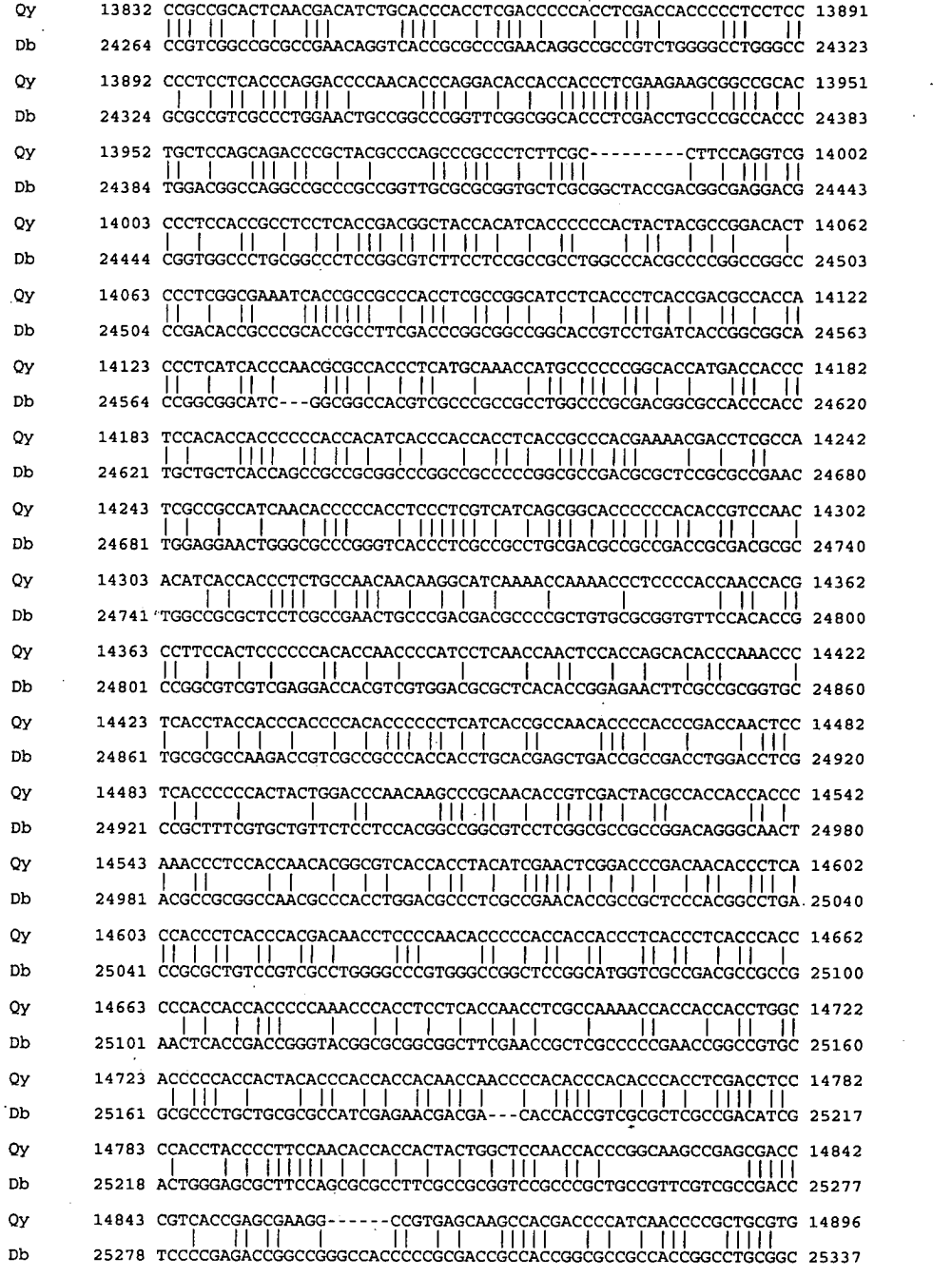

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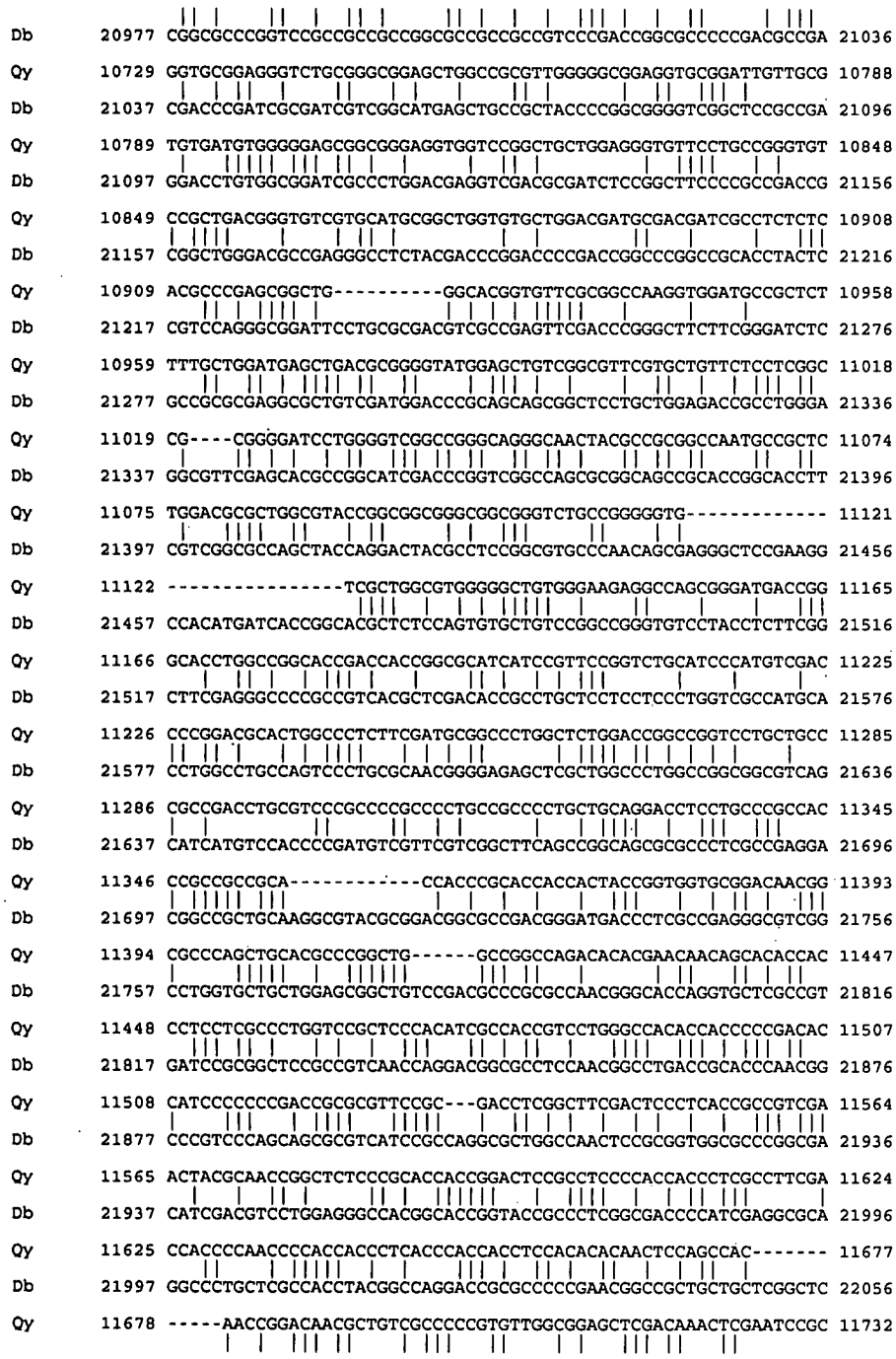

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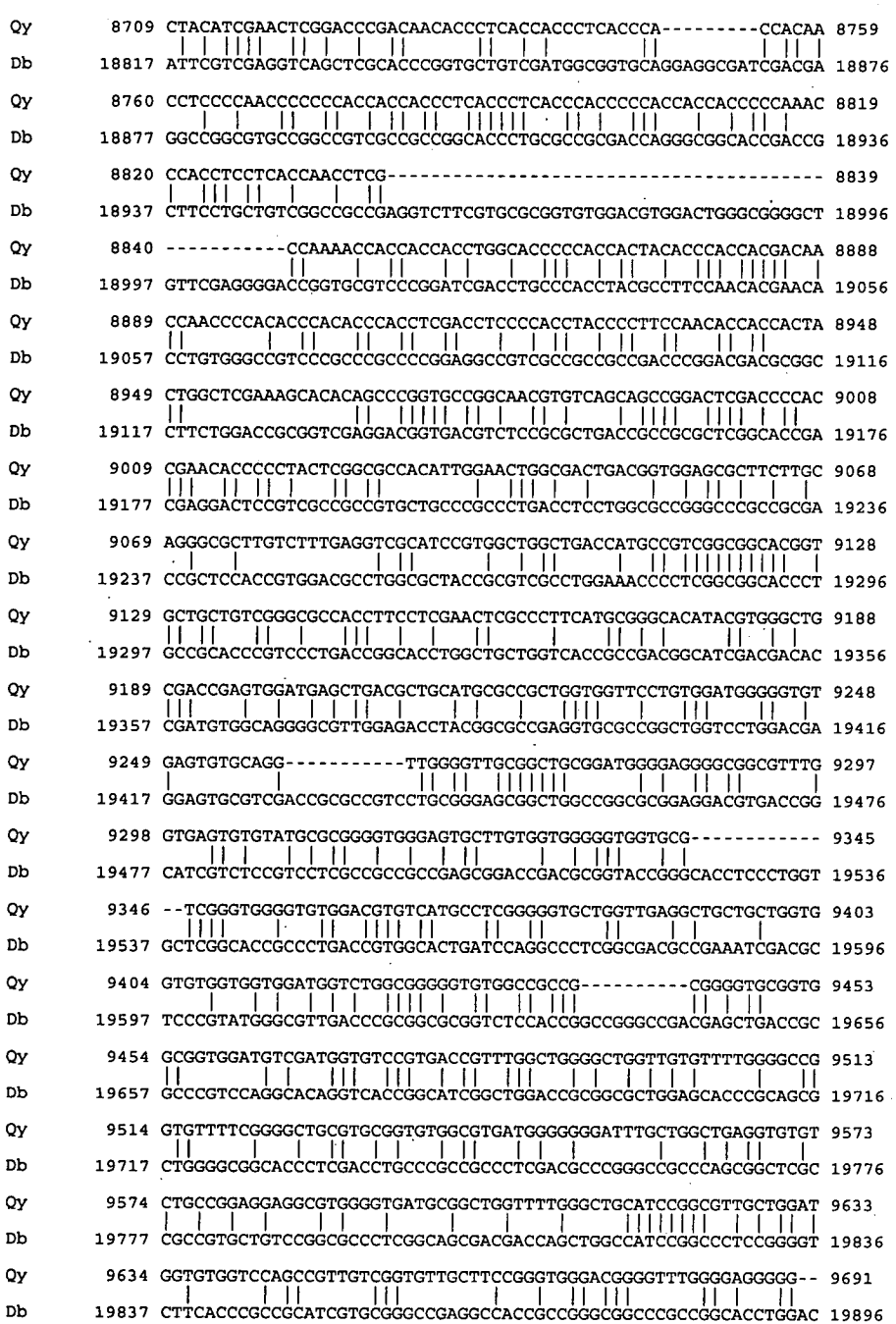


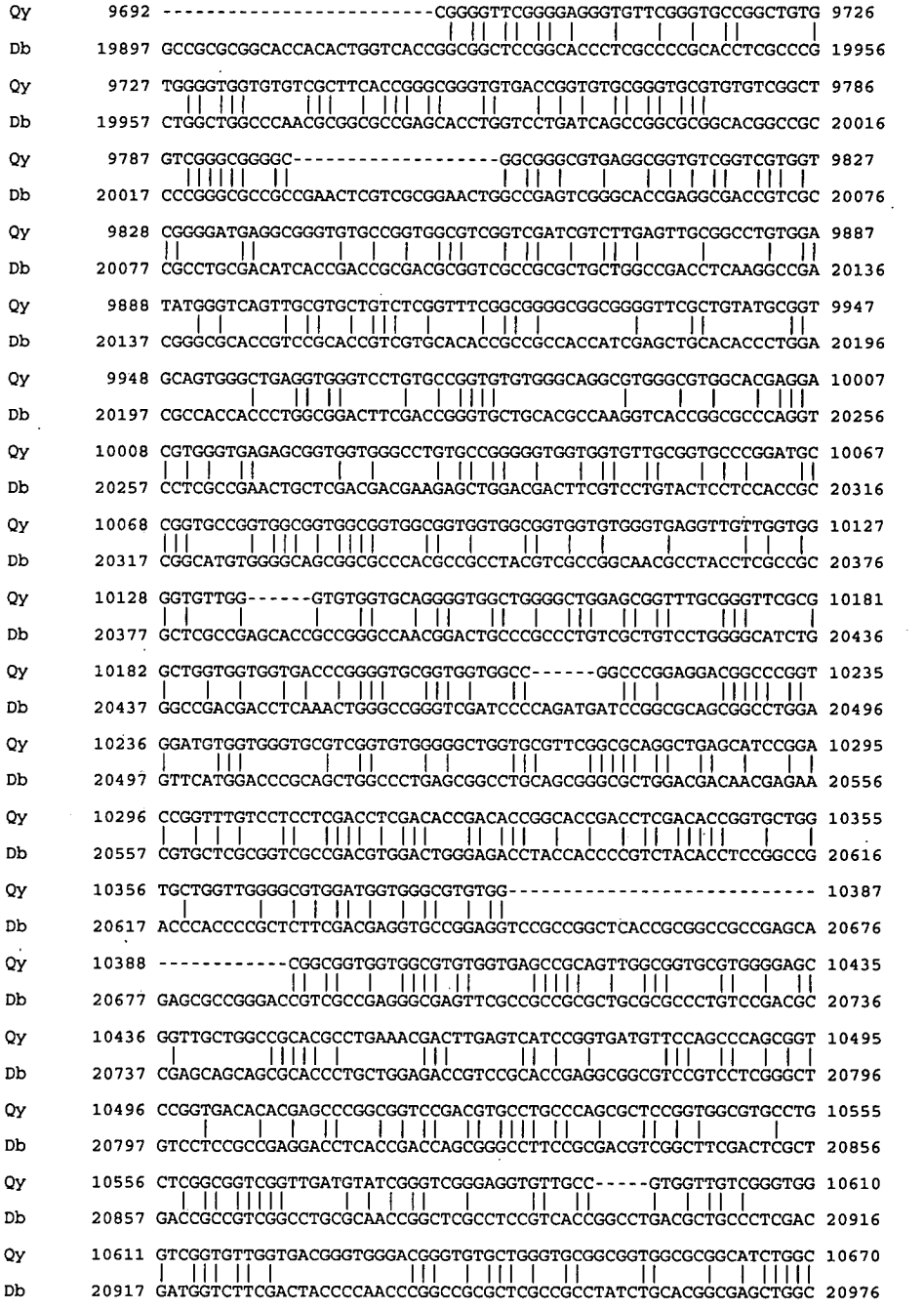


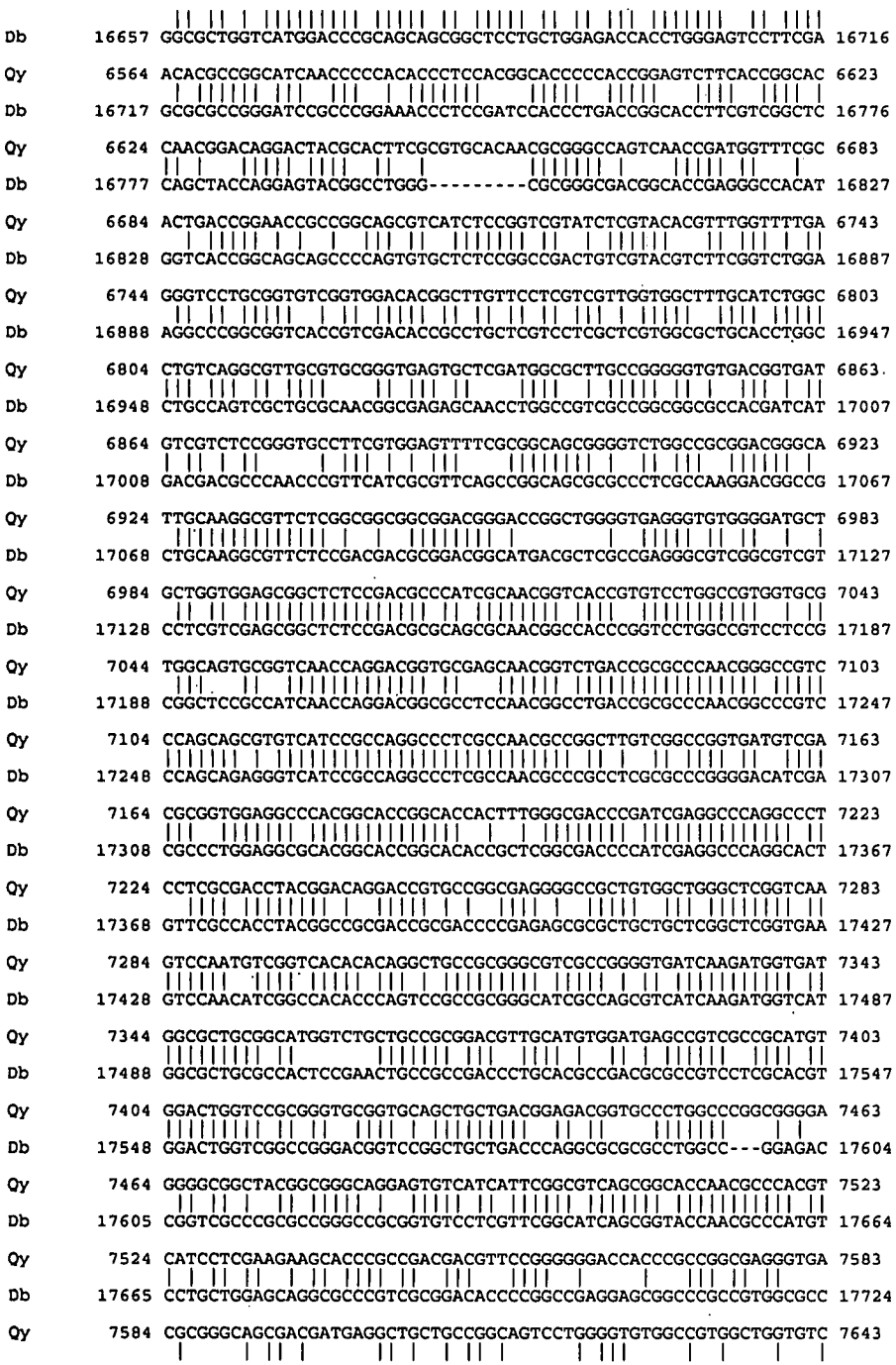


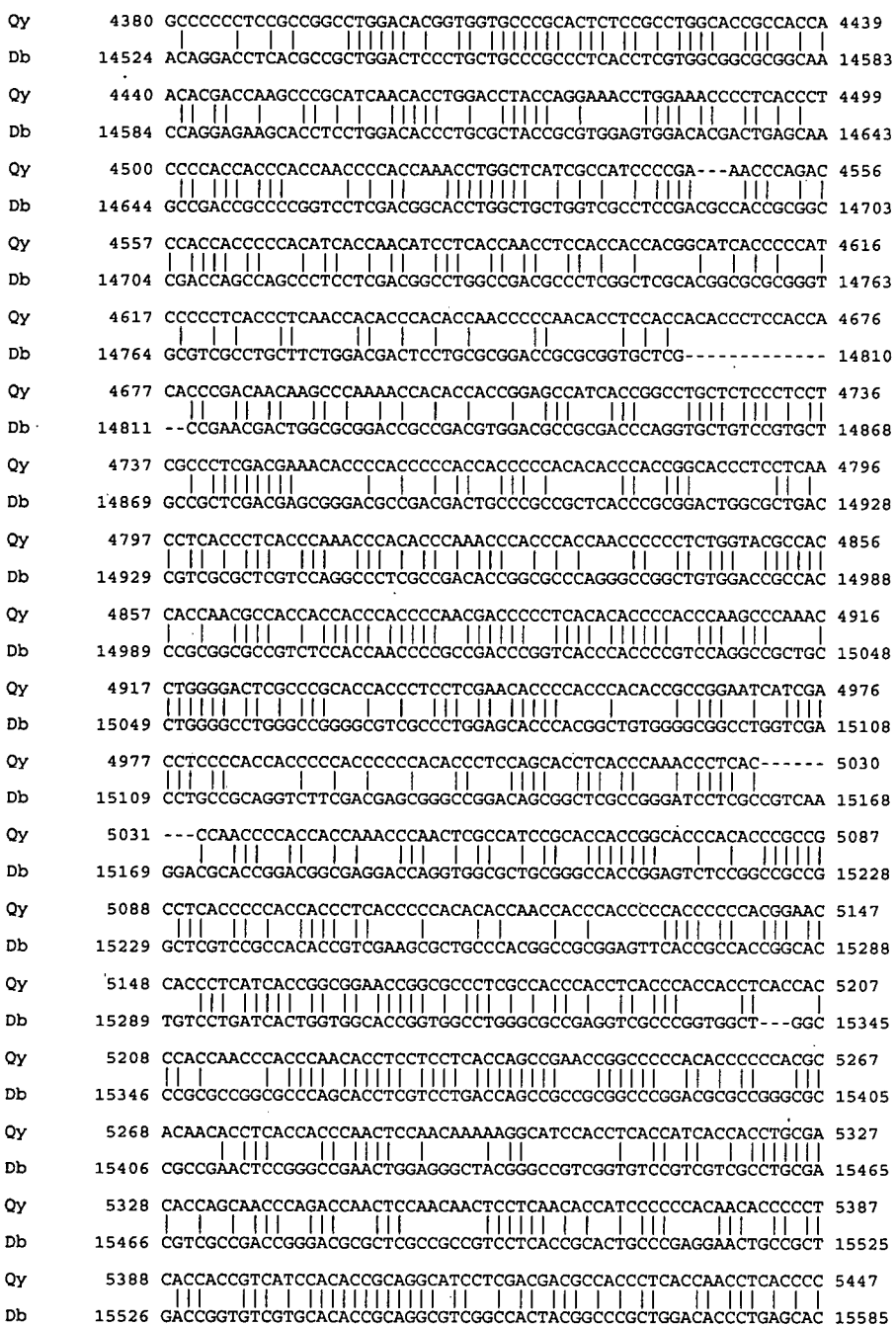


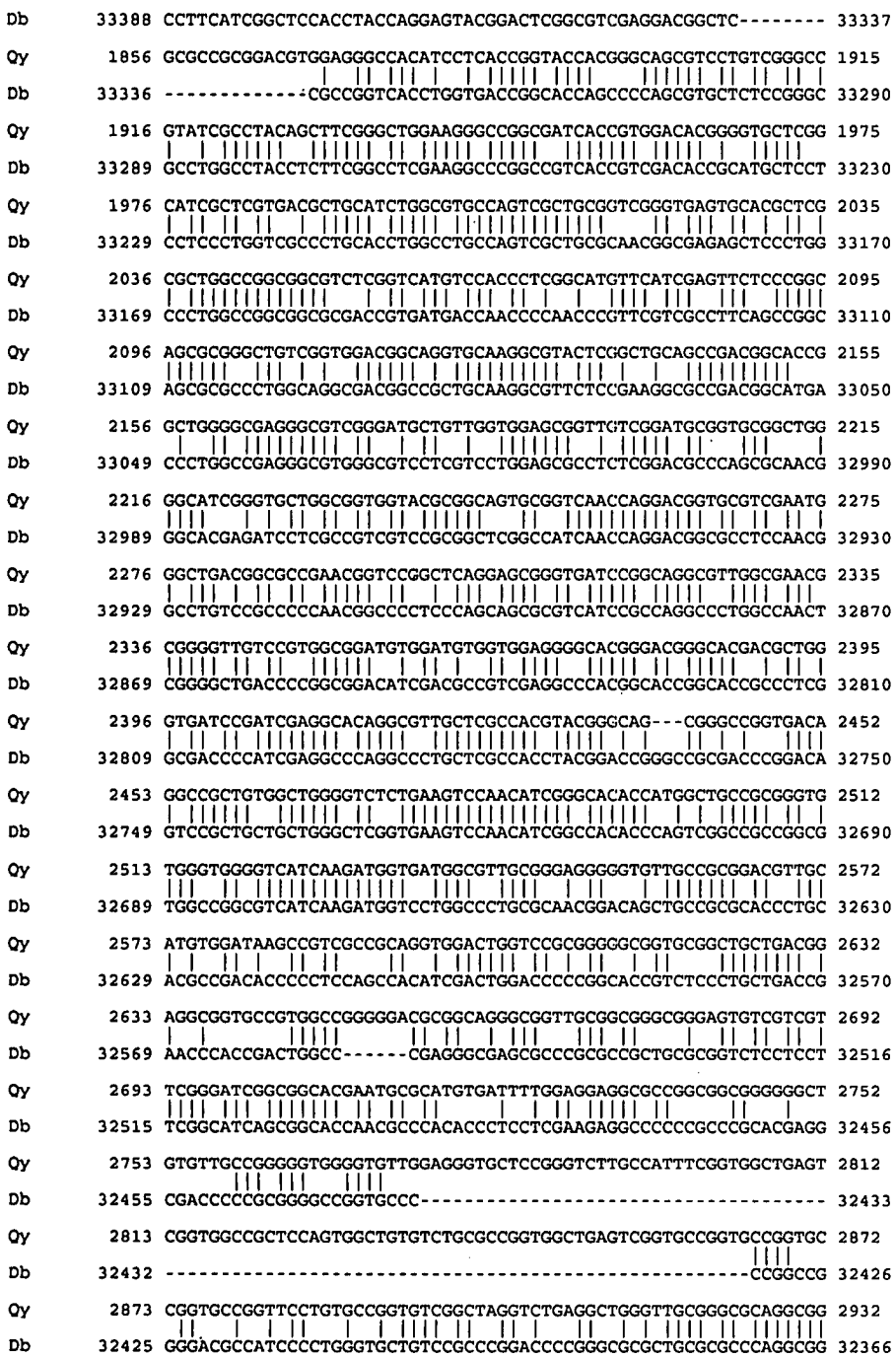

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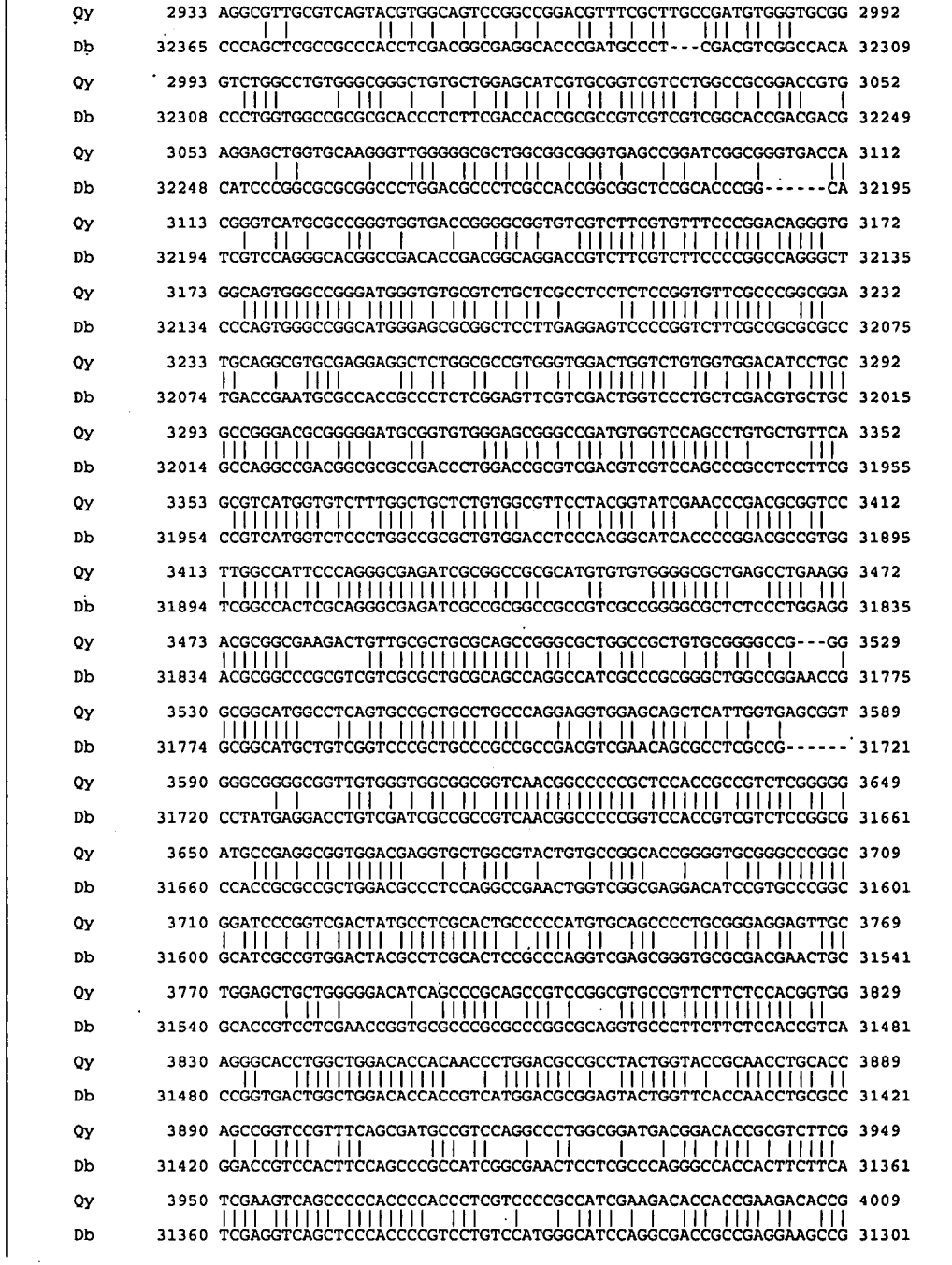

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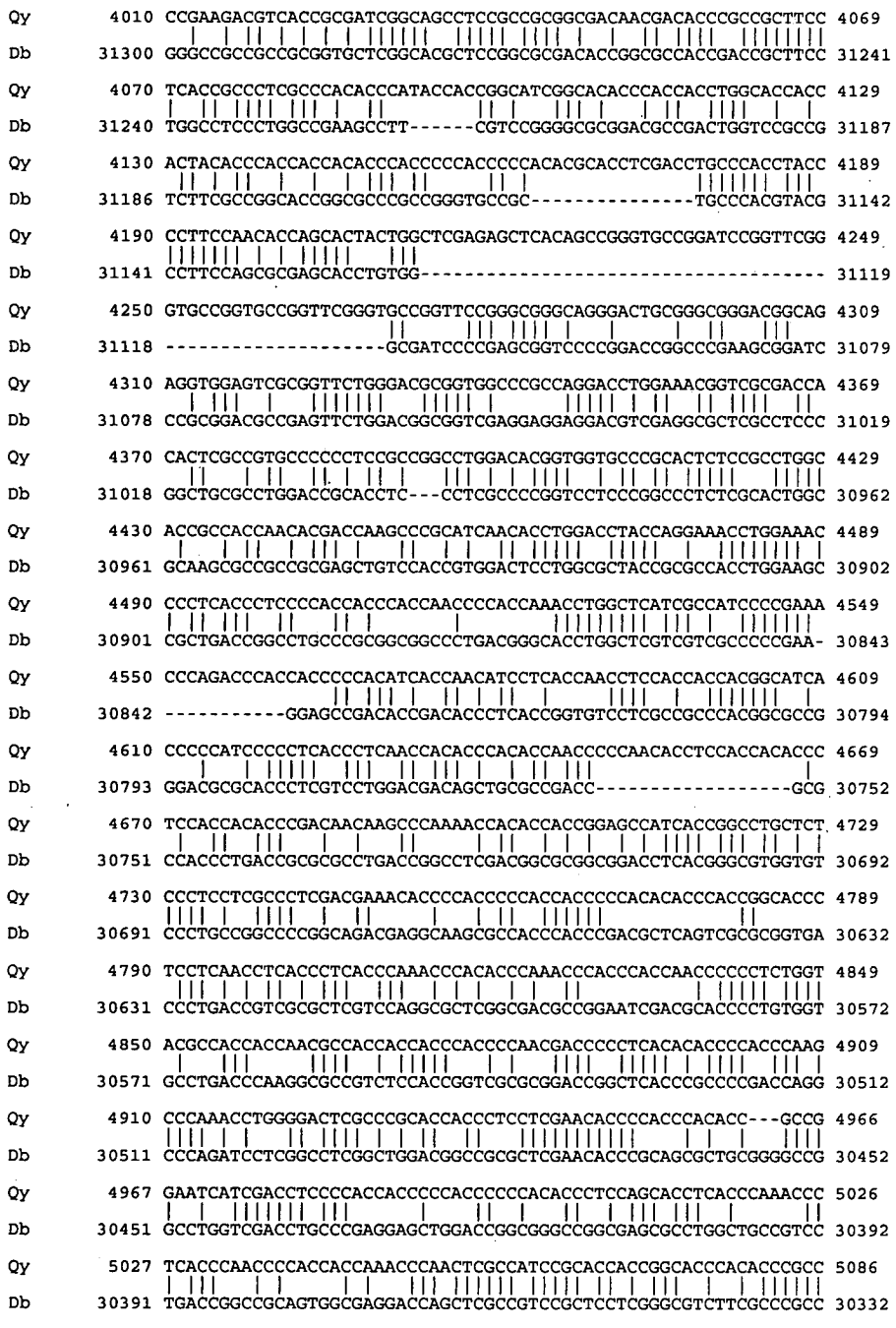

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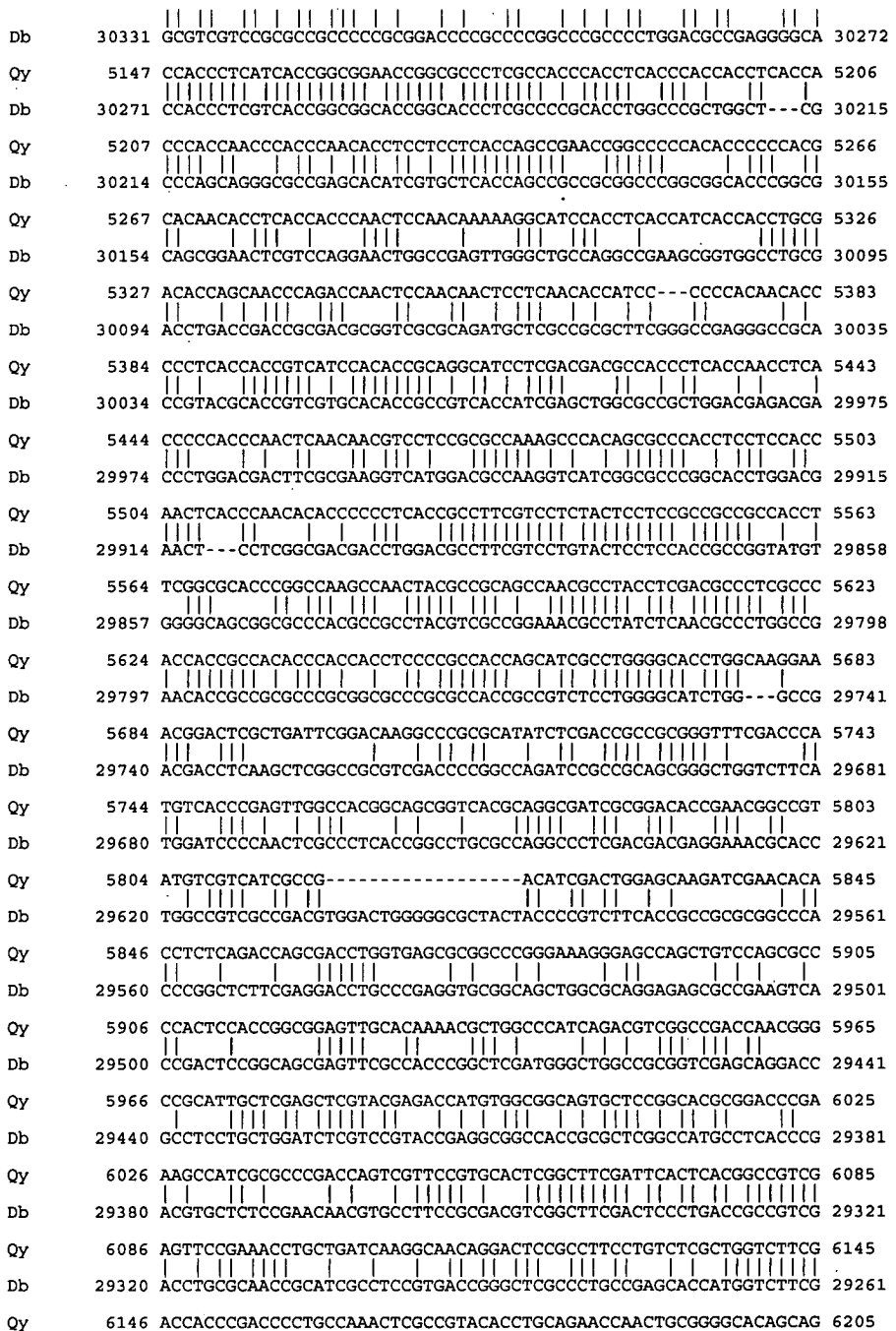

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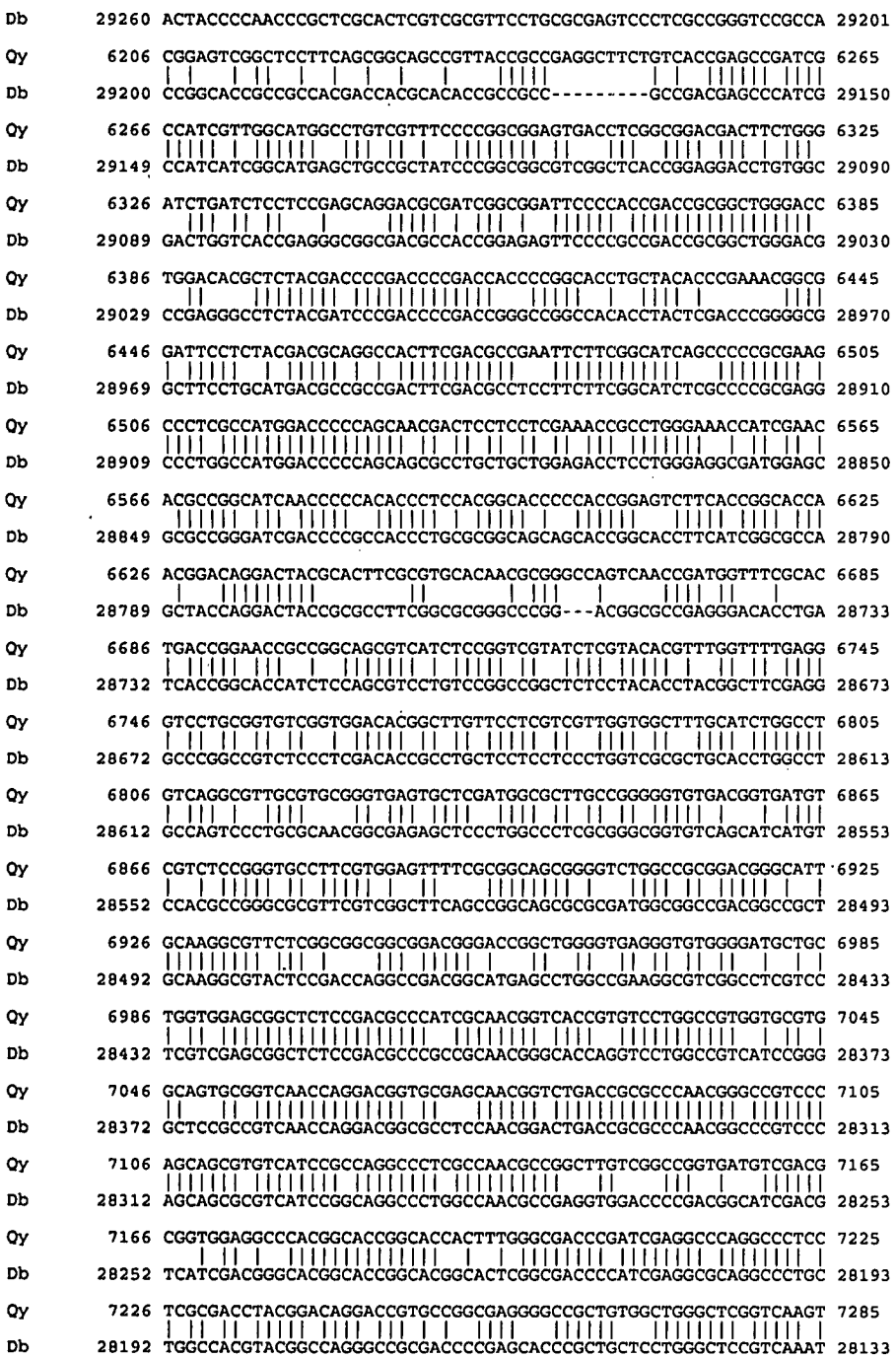

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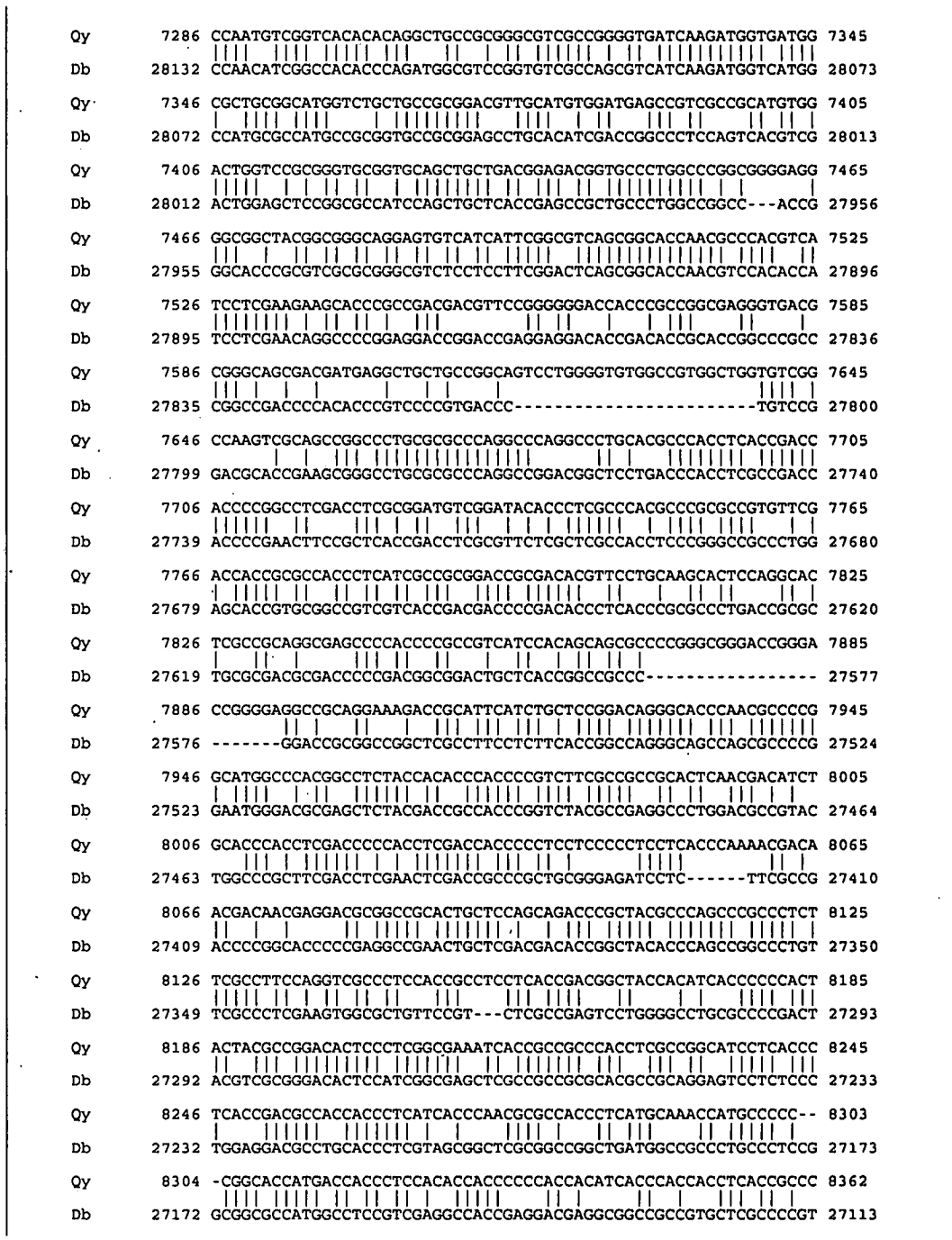

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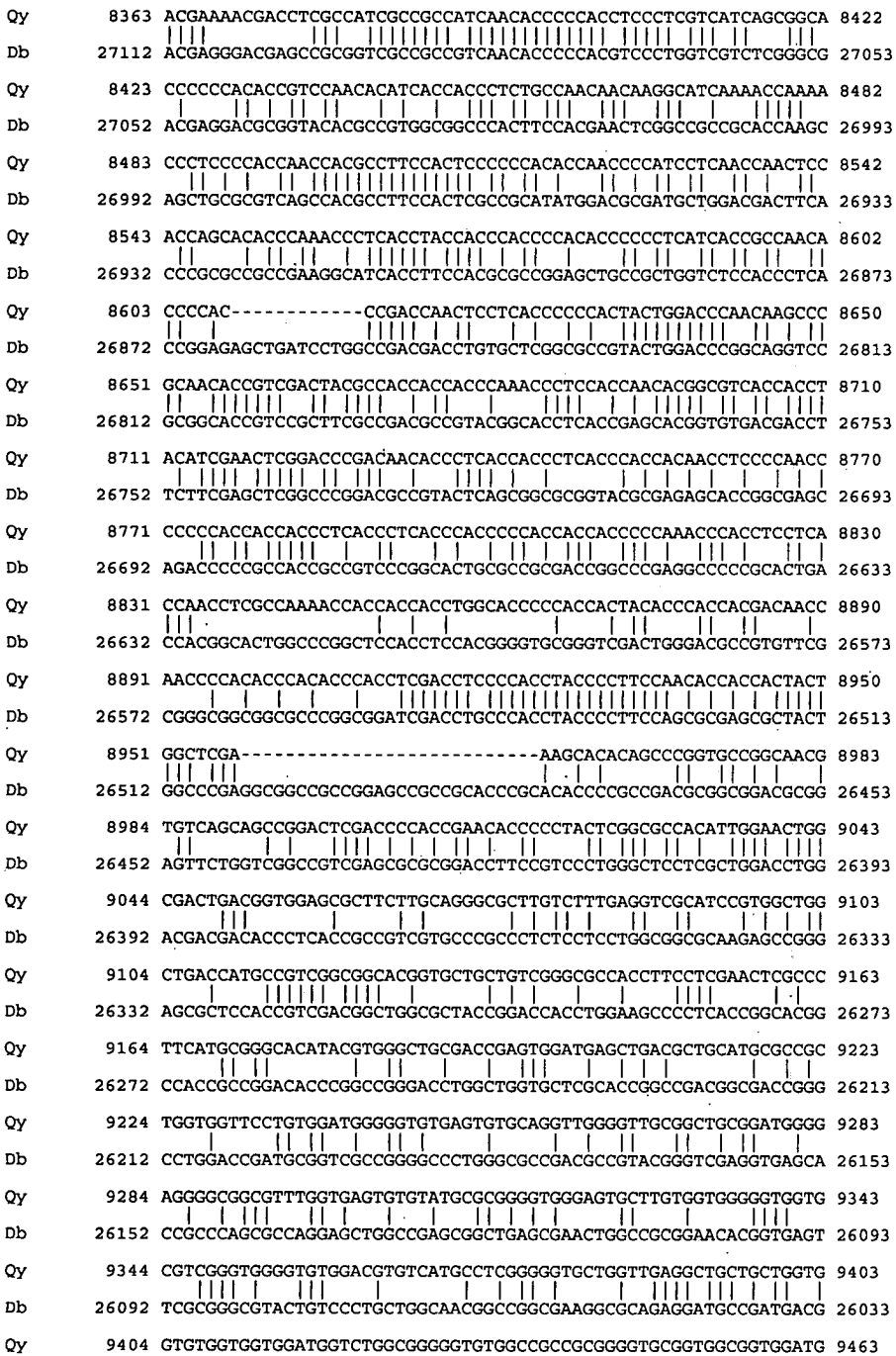

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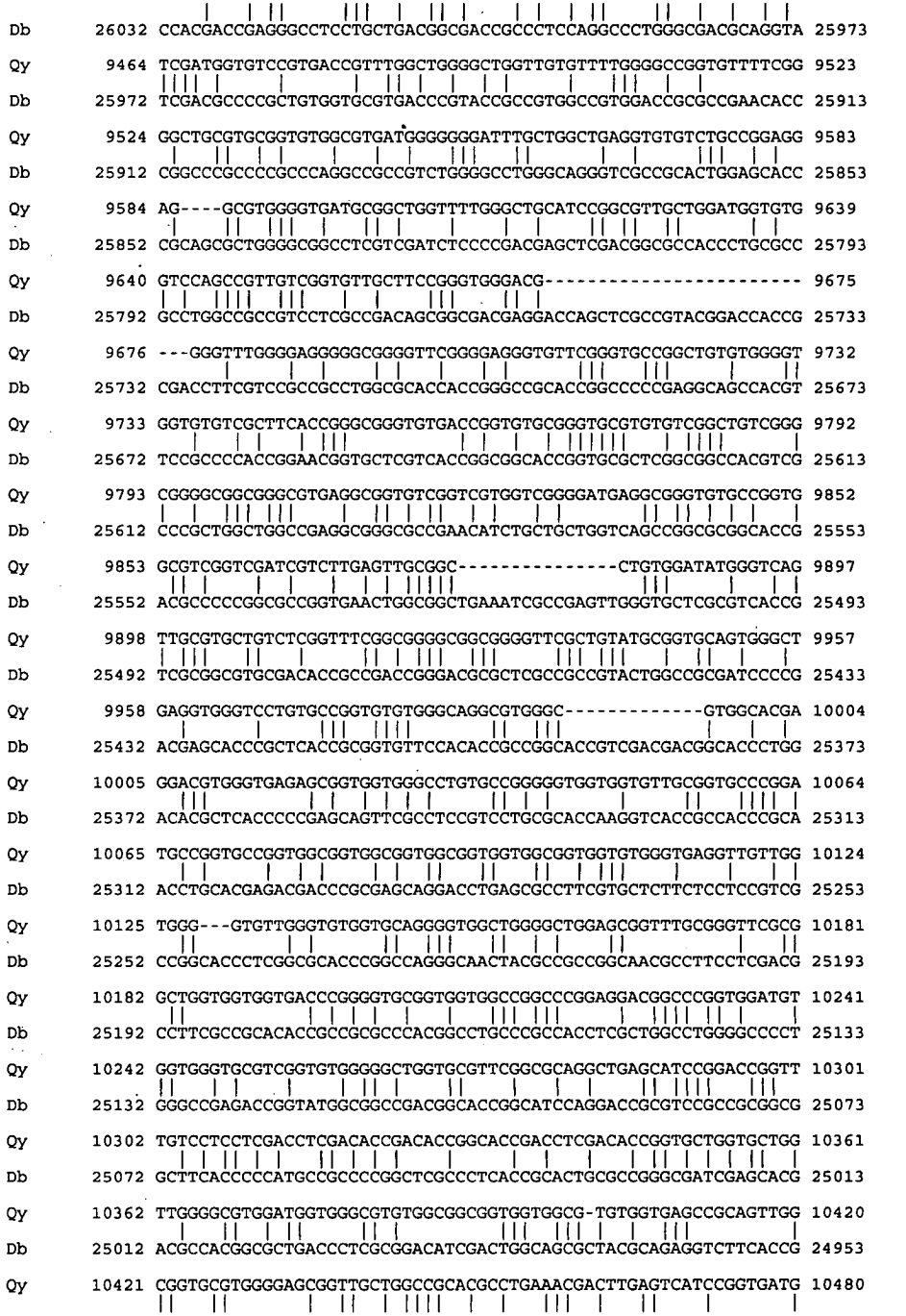


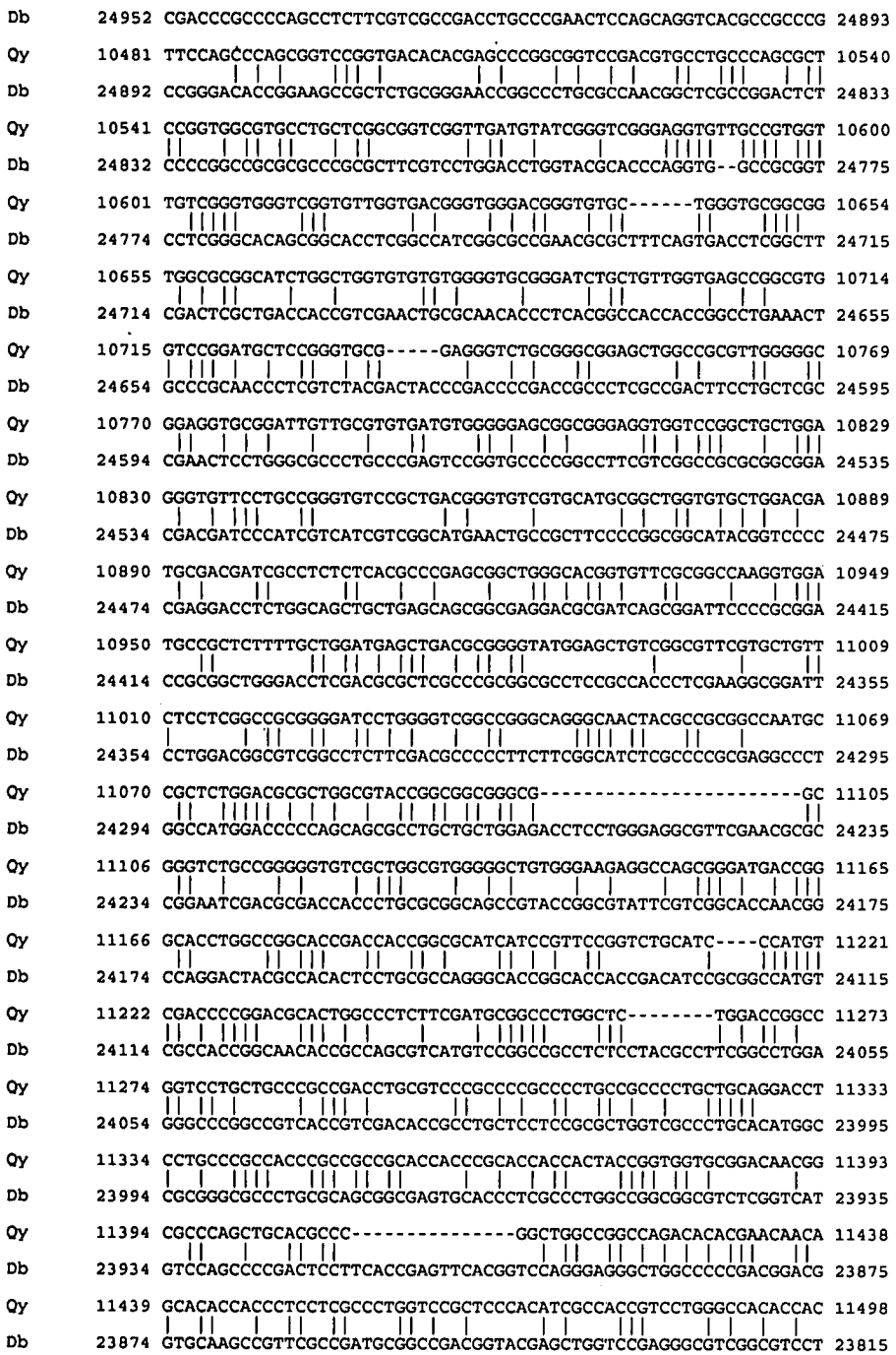


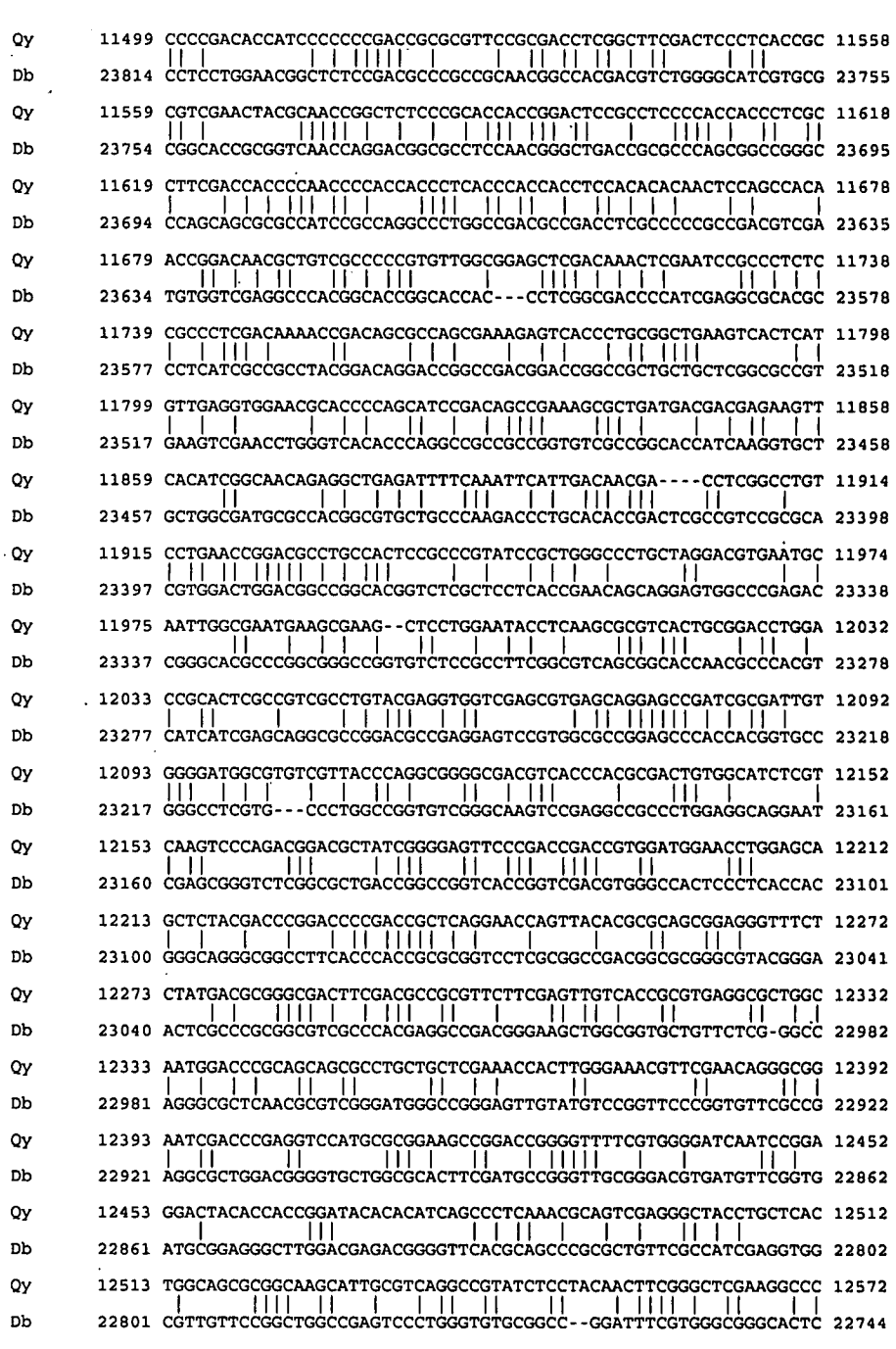

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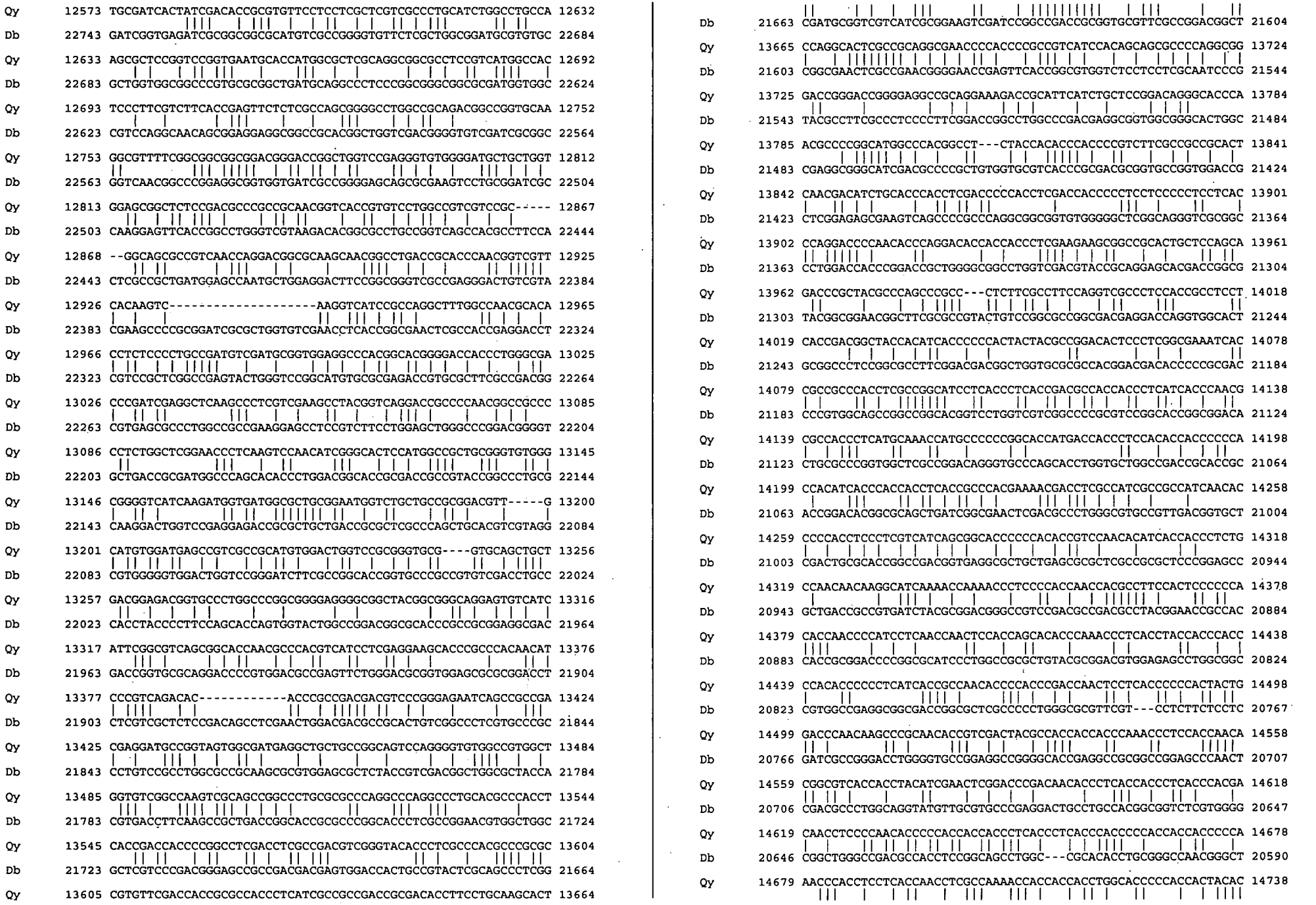

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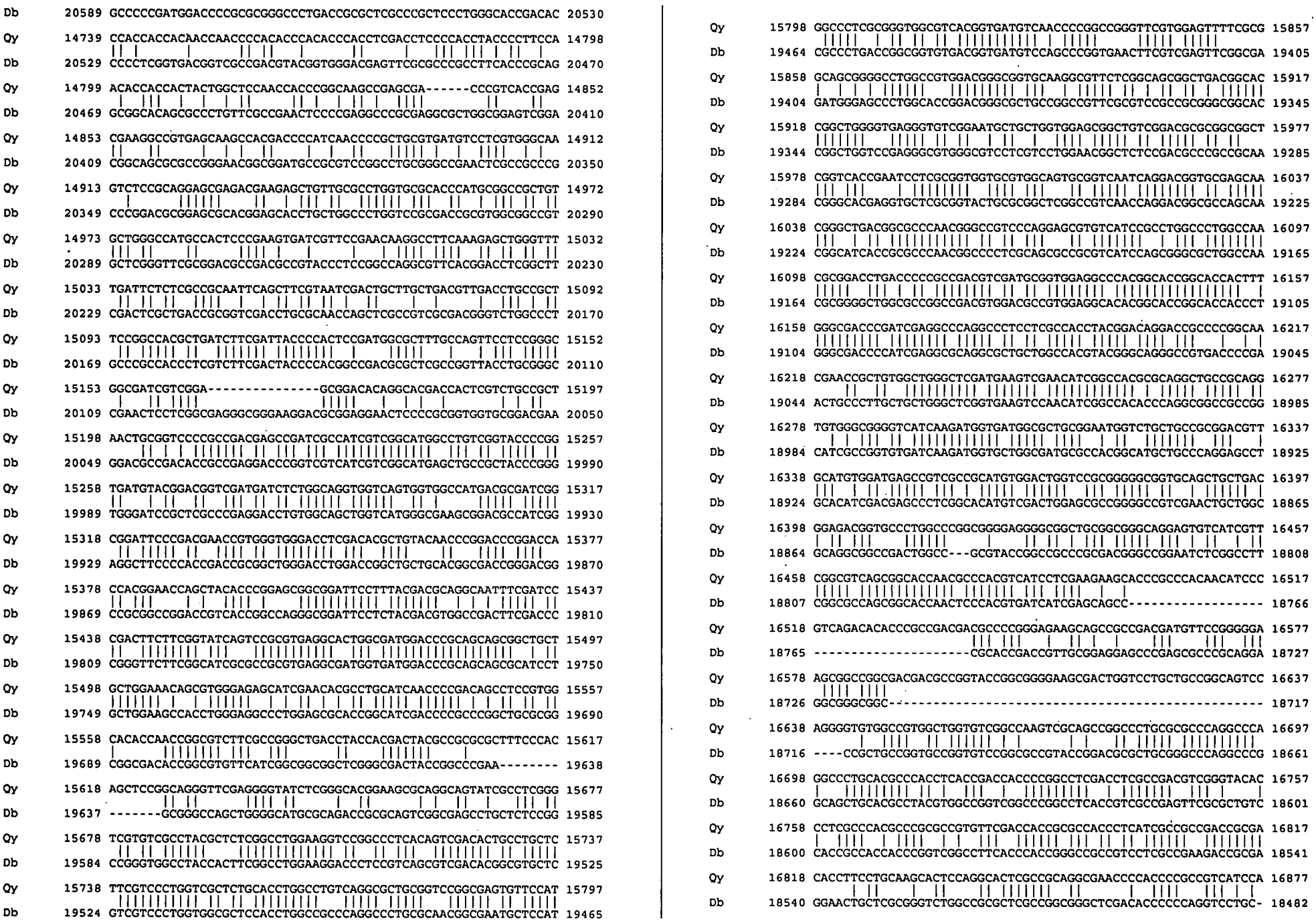


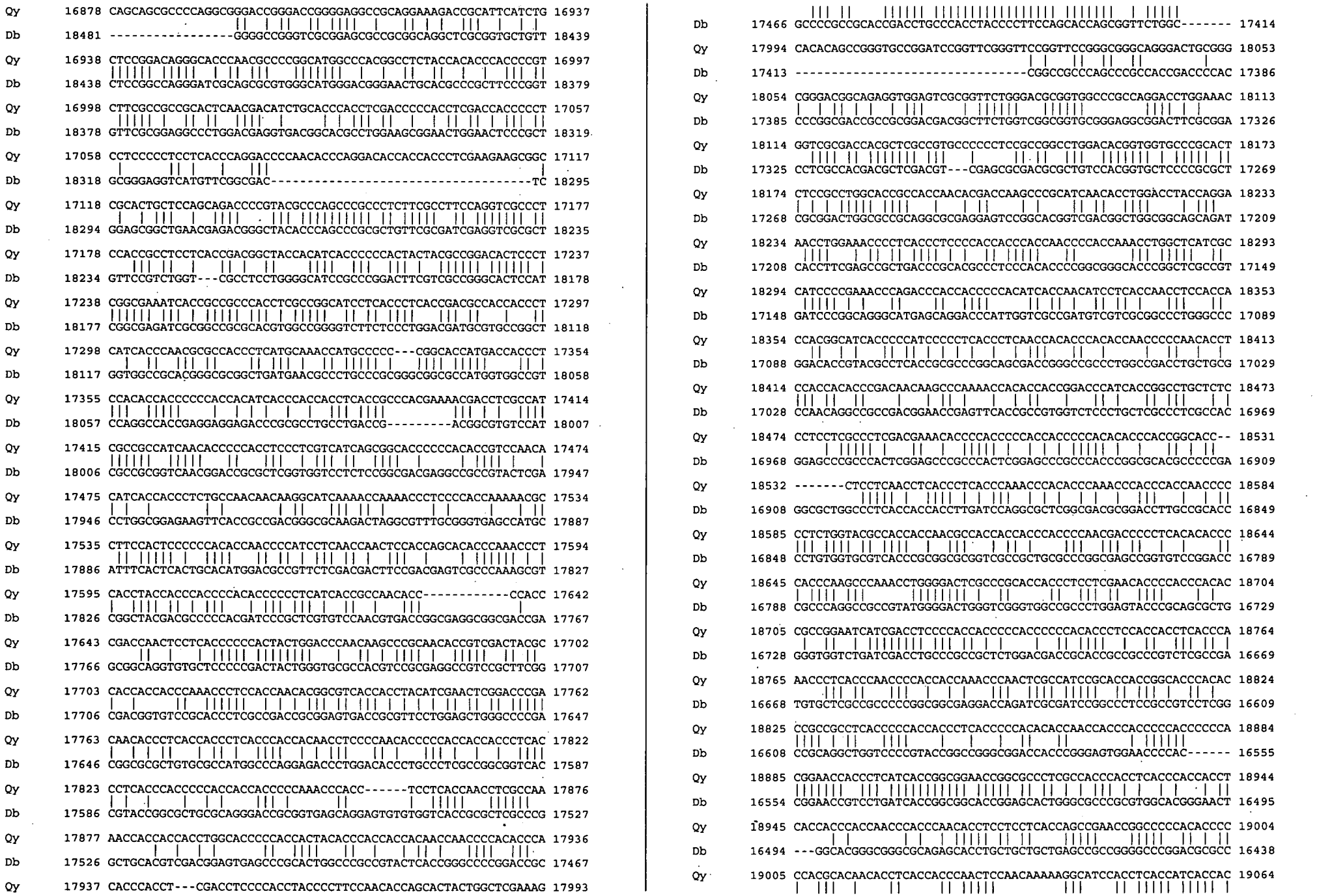


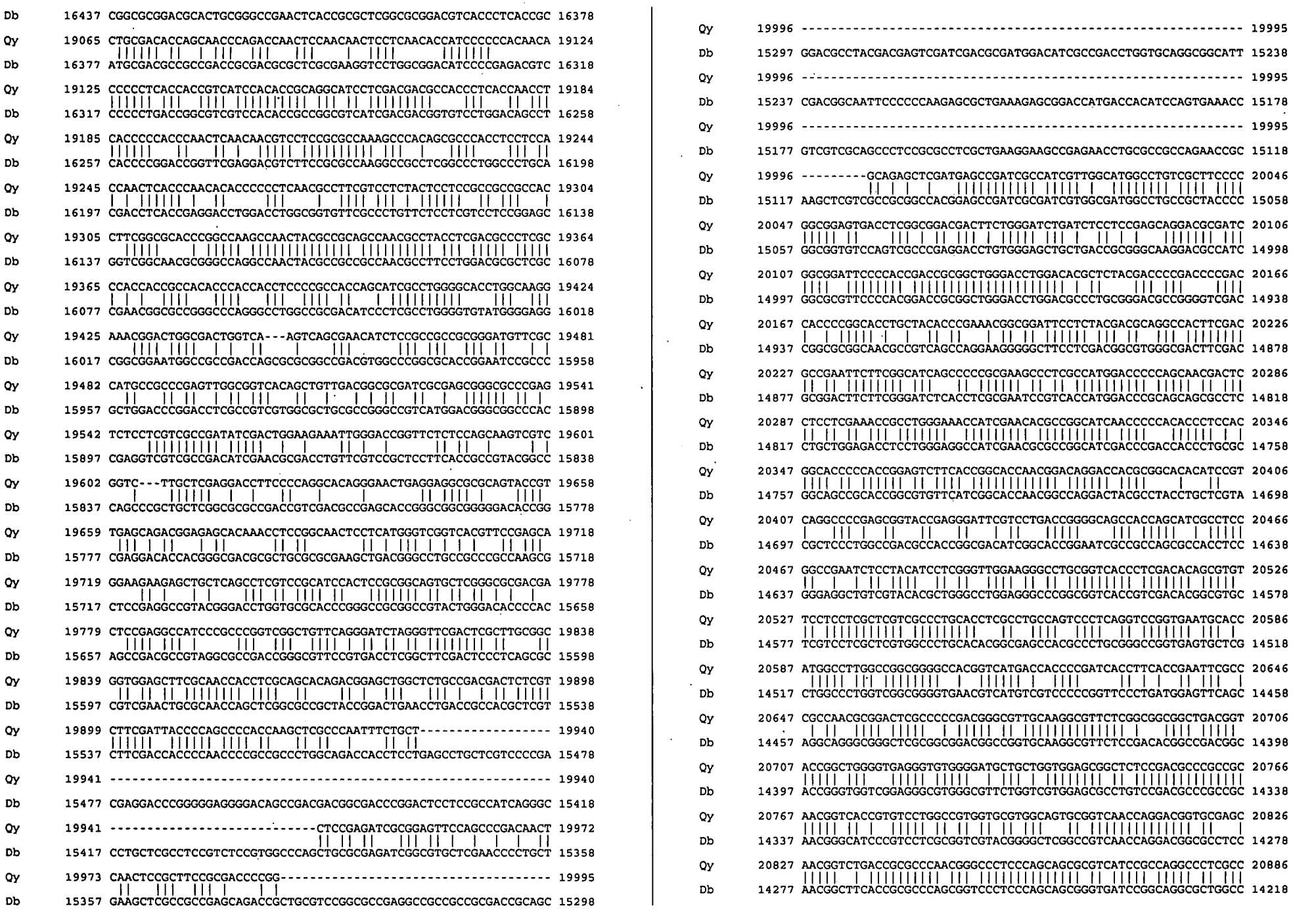

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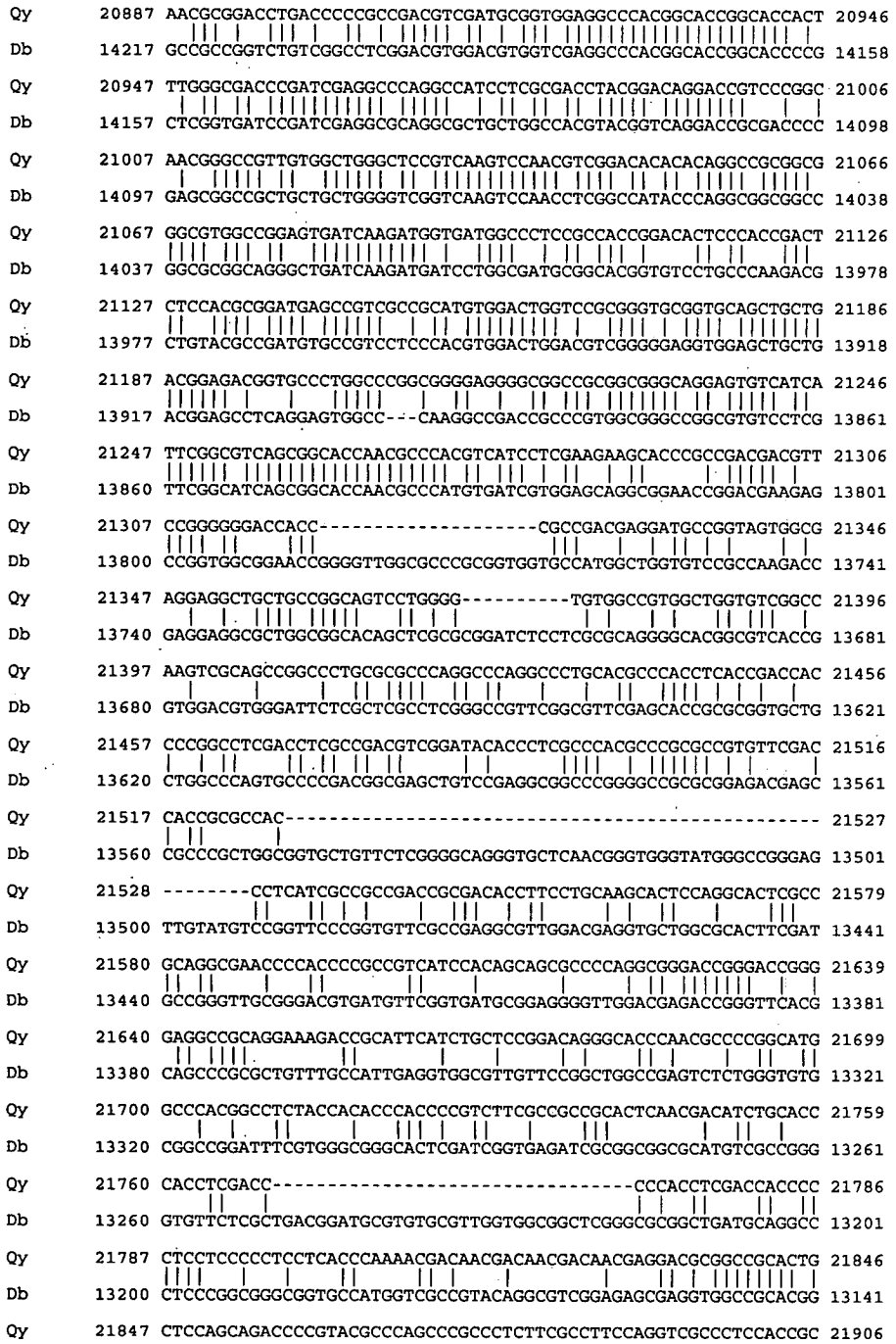

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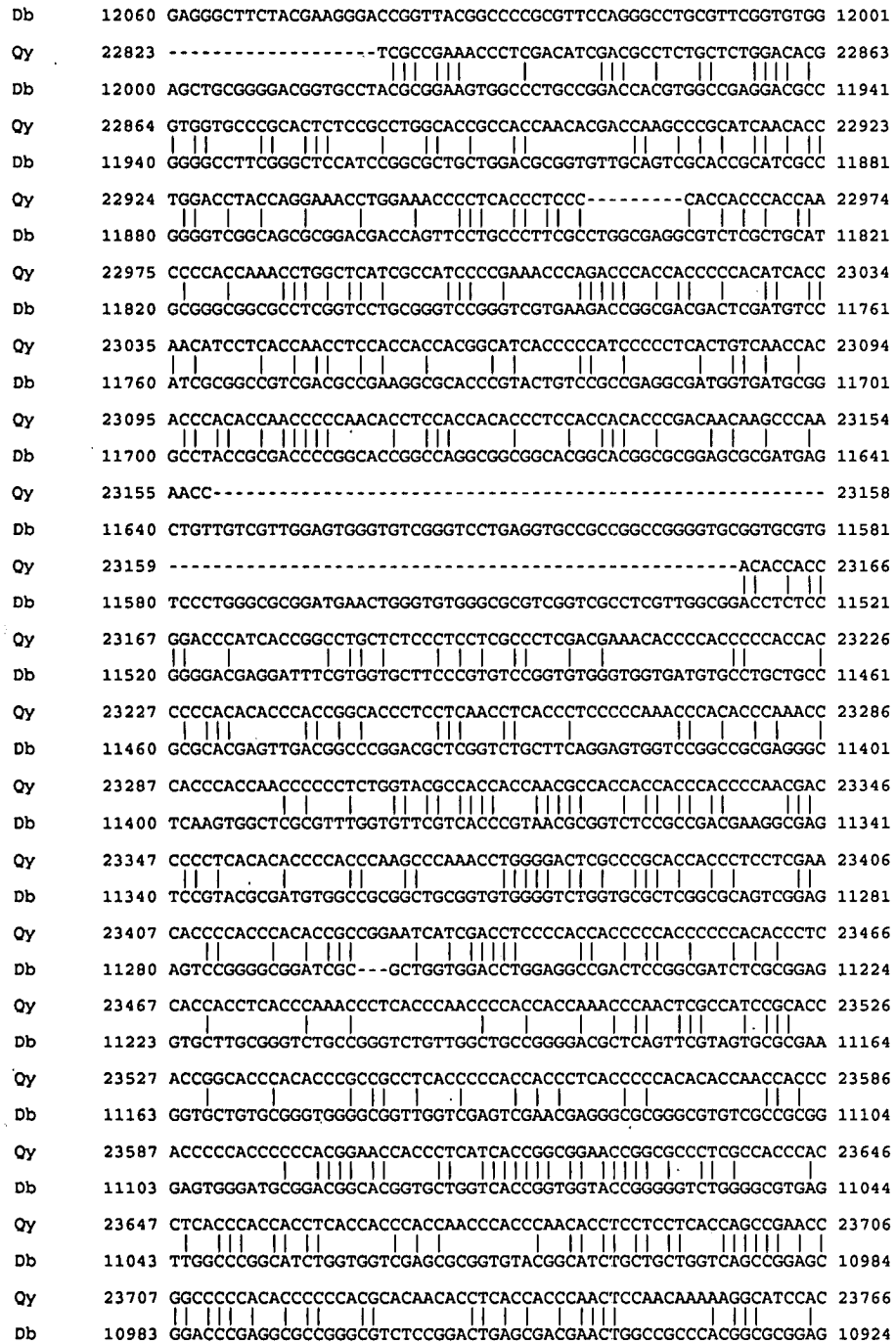


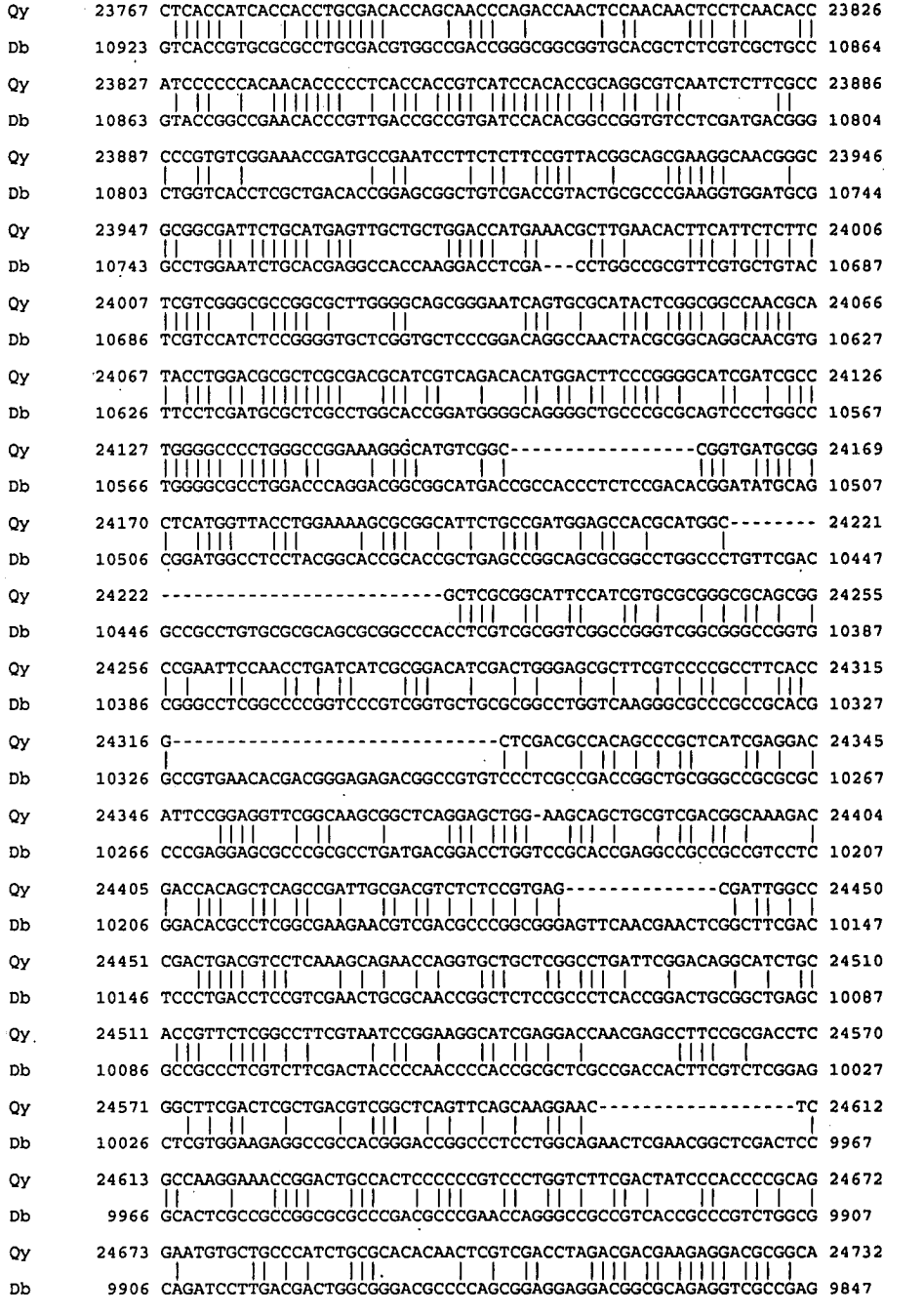


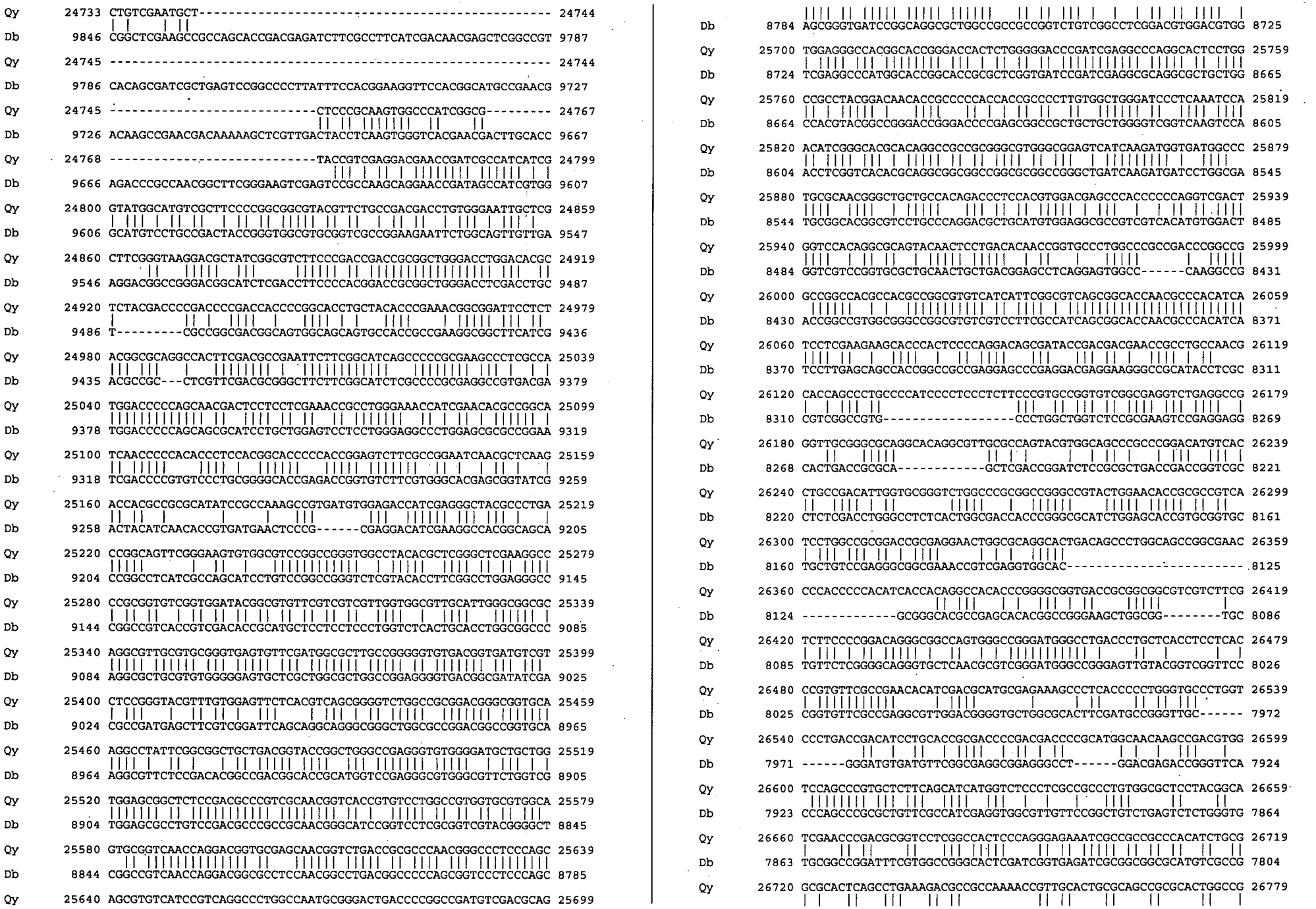


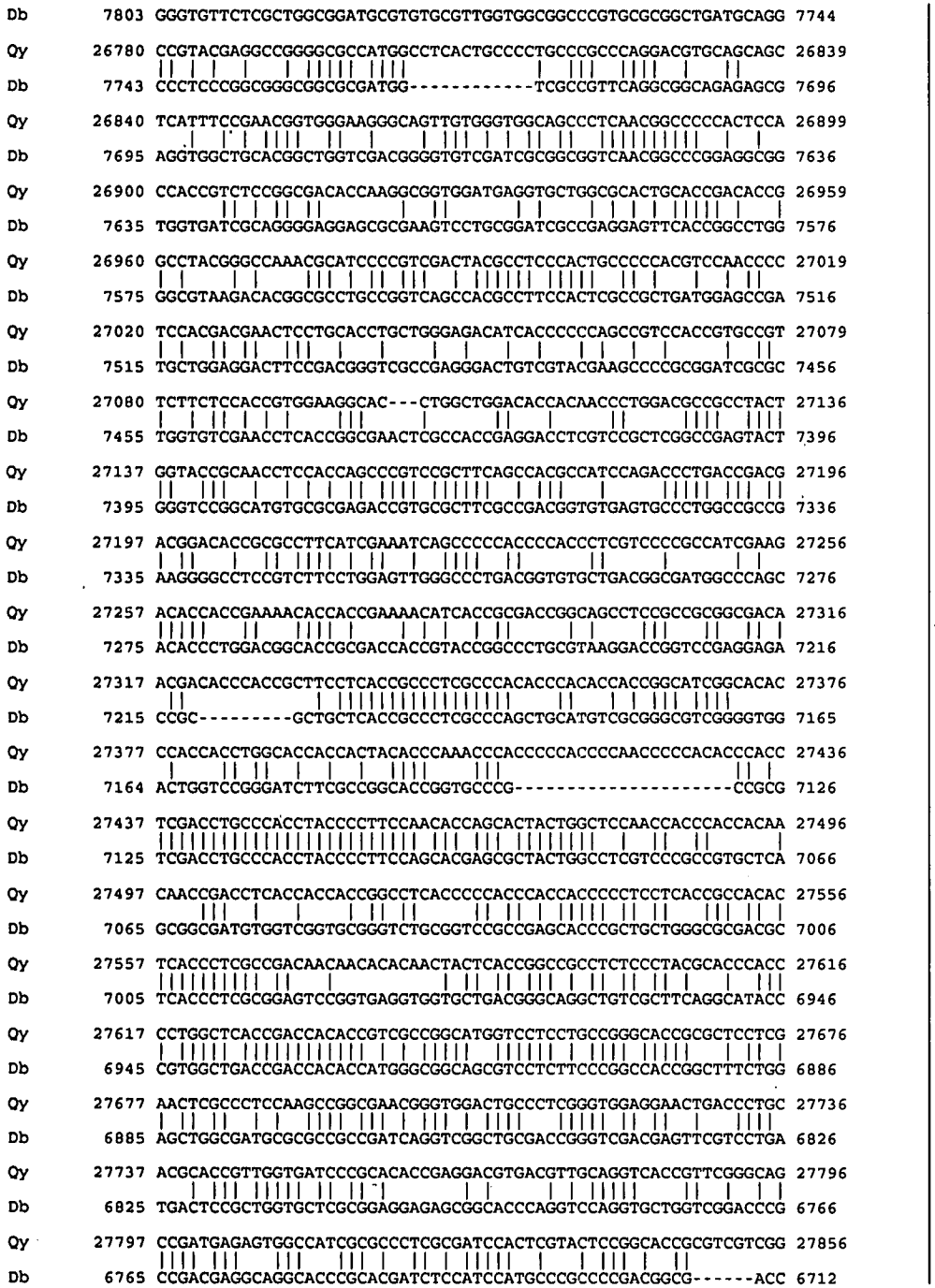



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  AUTHORS   Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C.,
            Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osonoe,T.,
            Kikuchi,H., Shiba,T., Sakaki,Y. and Hattori,M.
  TITLE     Genome sequence of an industrial microorganism Streptomyces
            avermitilis: deducing the ability of producing secondary
            metabolites
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
  MEDLINE   21477403
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  AUTHORS   Ikeda,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-2001) Haruo Ikeda, Kitasato University, Dept. of
            Microbial Chemistry, School of Pharmaceutical Sciences; 5-9-1
            Shirokane, Minato-ku, Tokyo 108-8641, Japan
            (E-mail:ikeda@mc.pharm.kitasato-u.ac.jp, Tel:+81-3-5791-6242,
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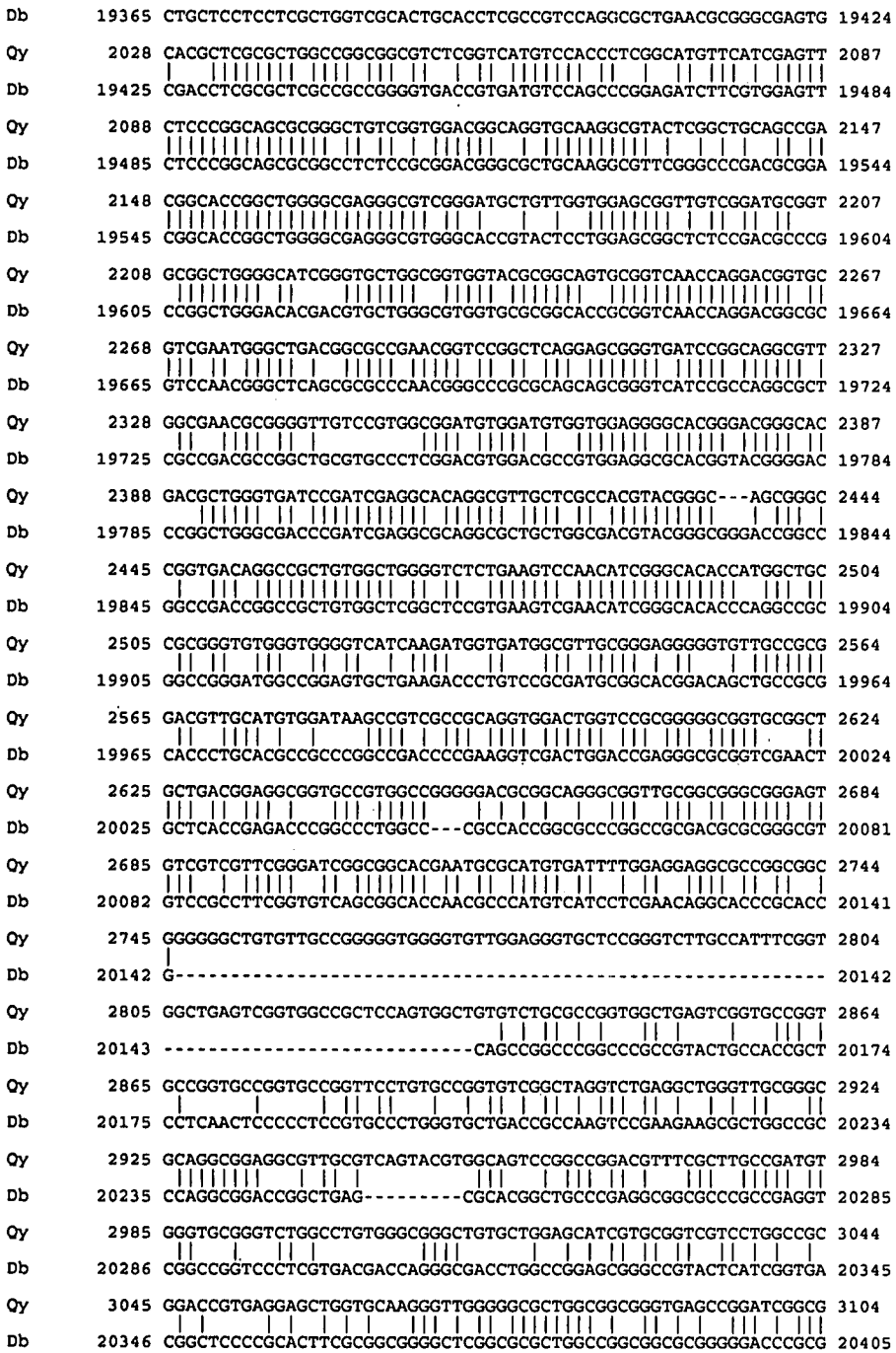
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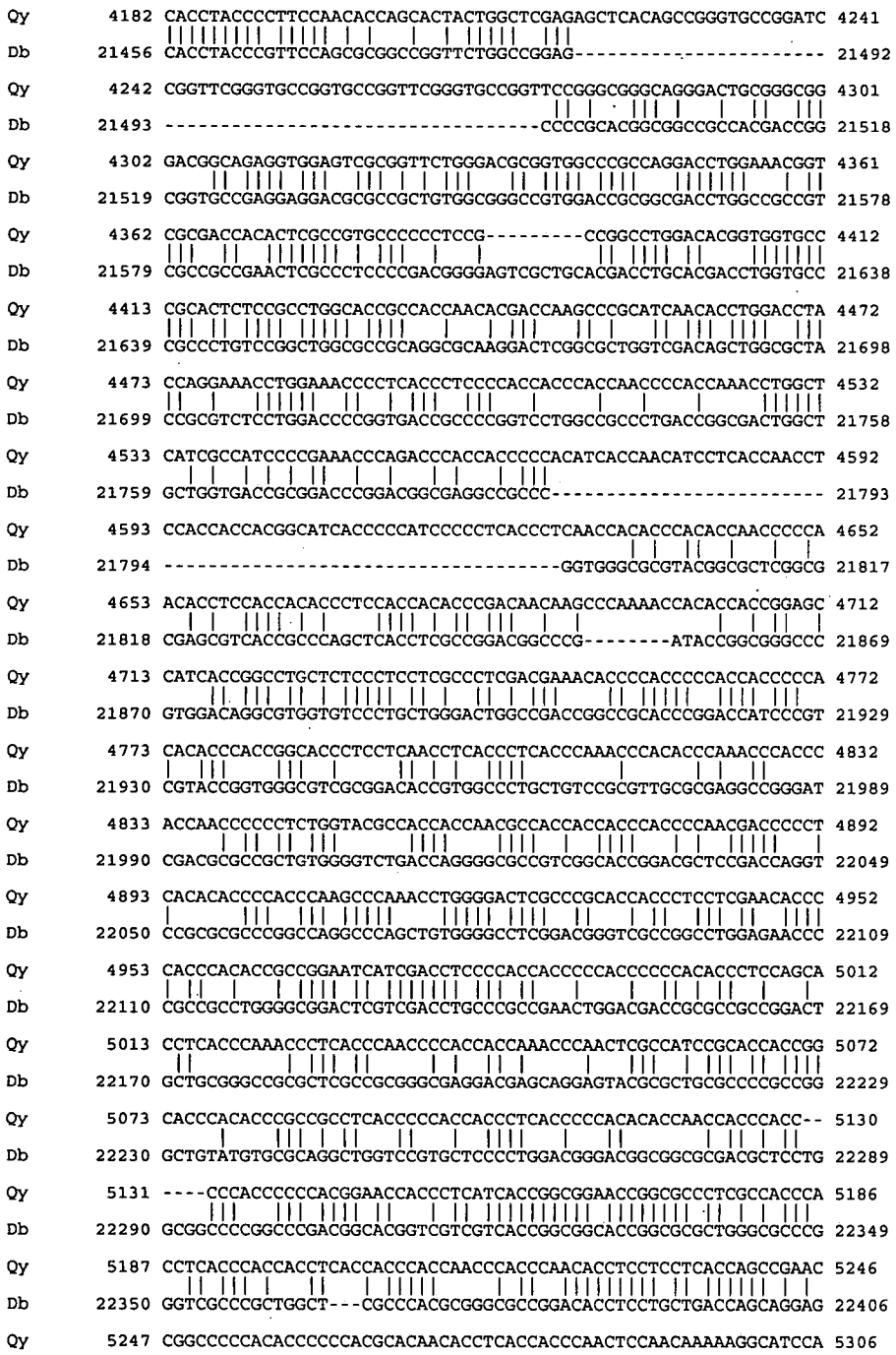
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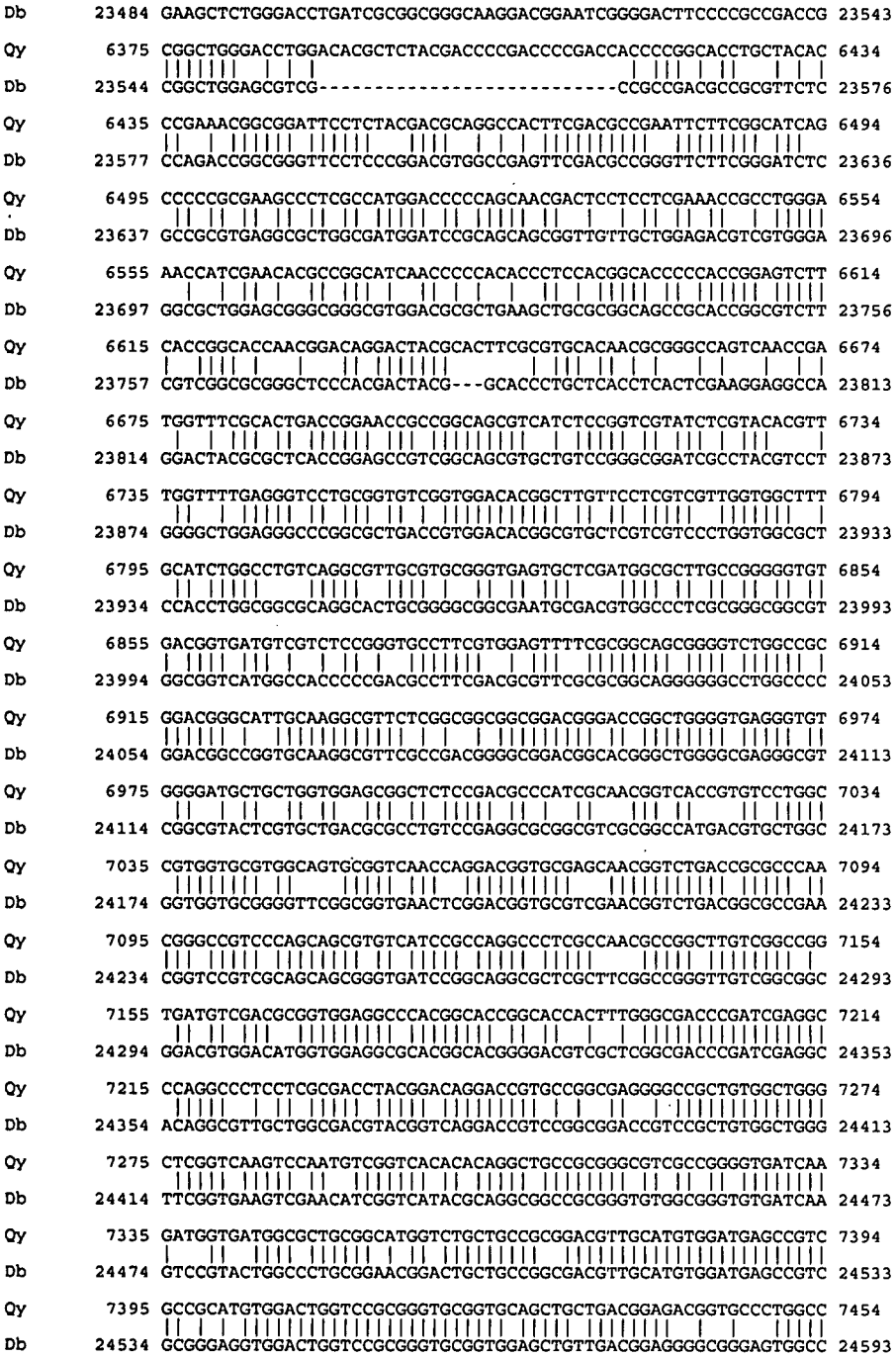
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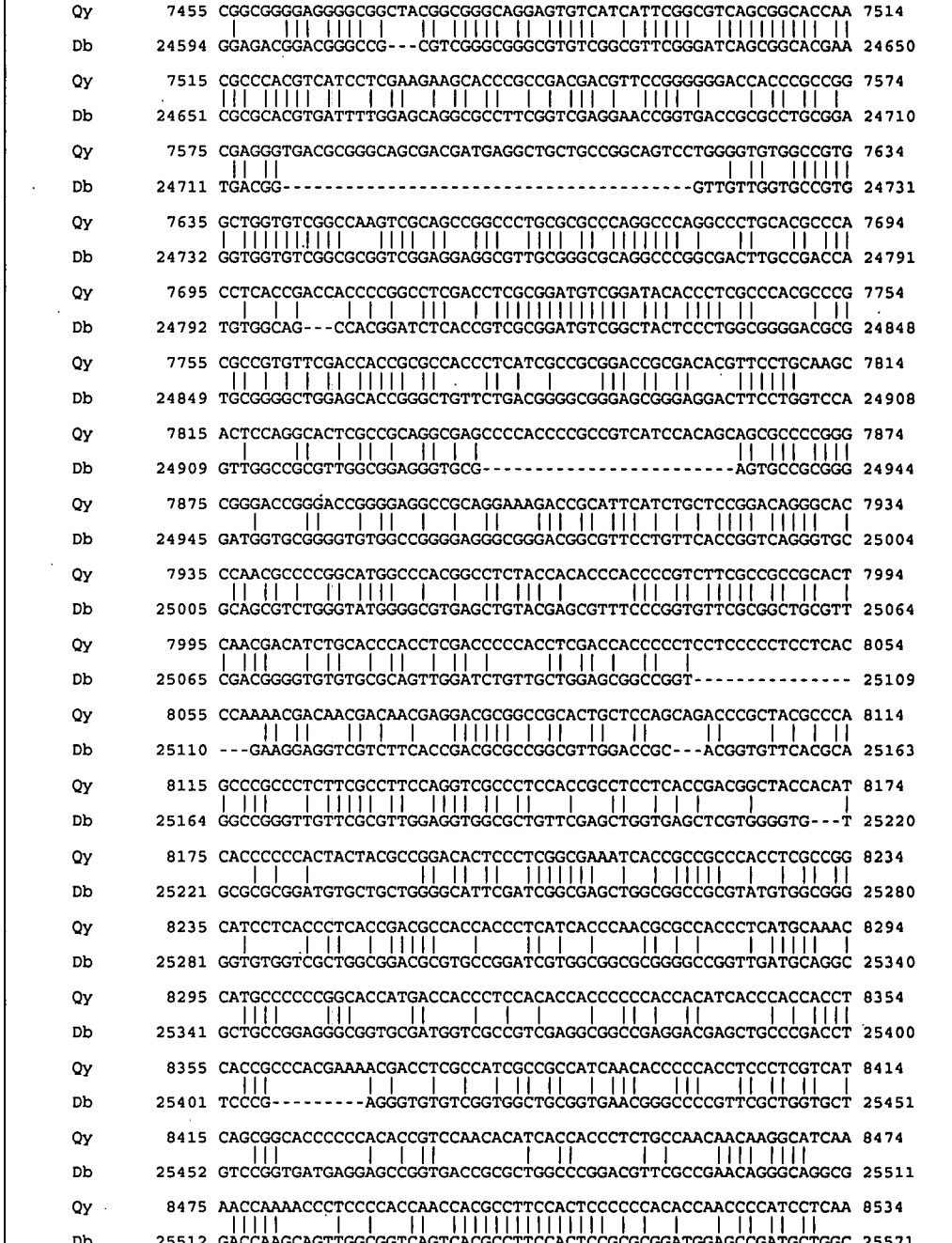
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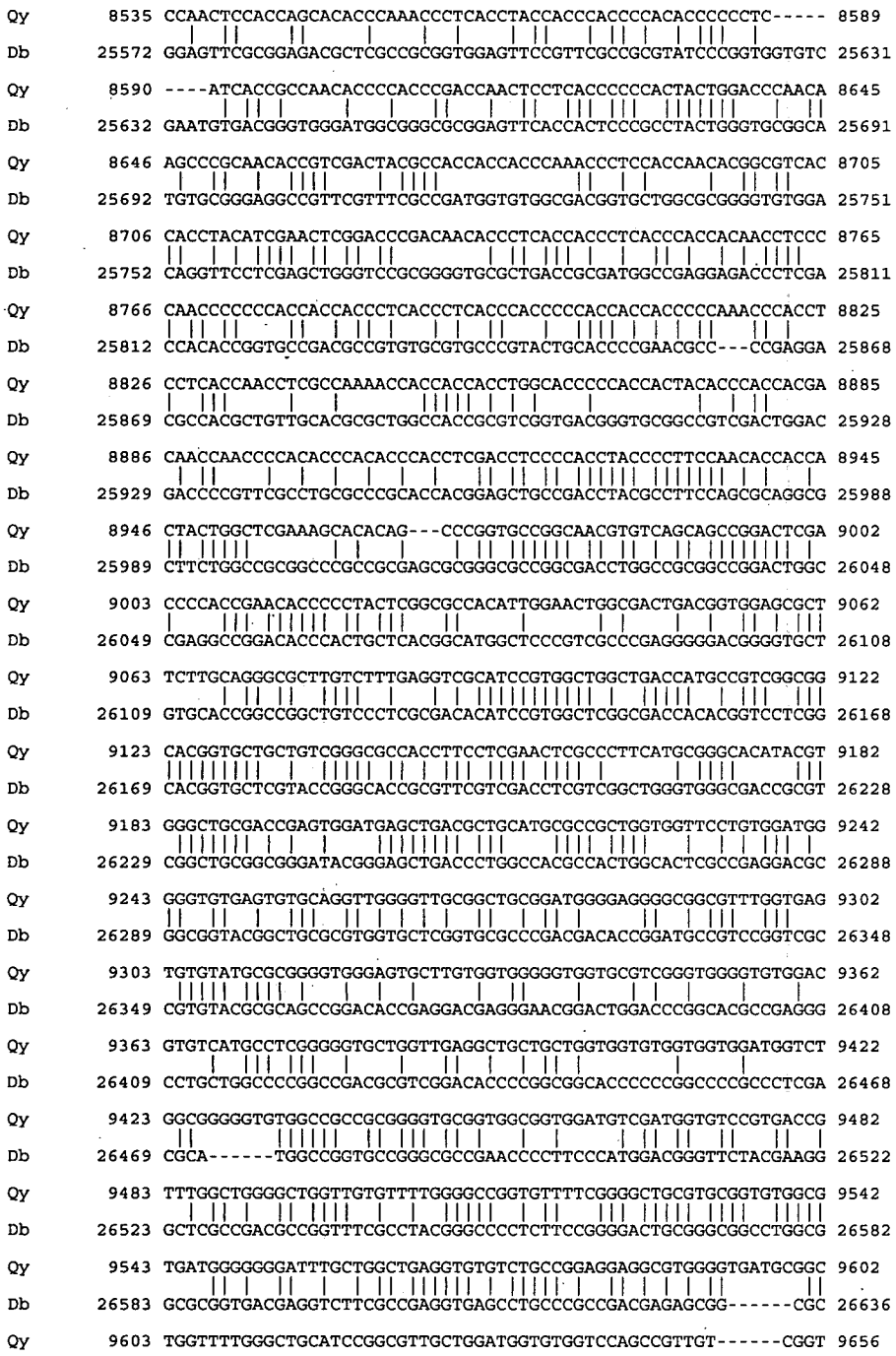
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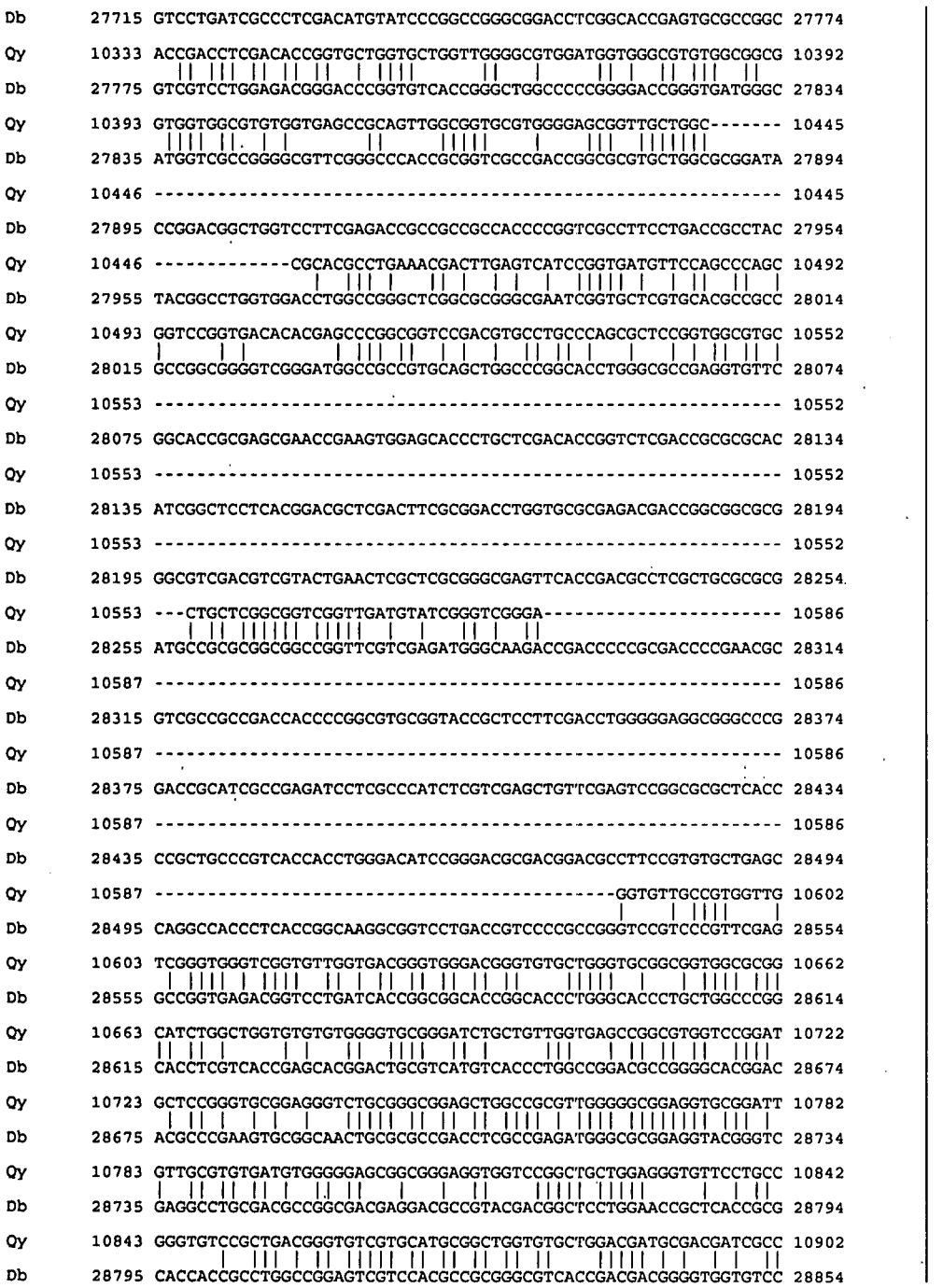

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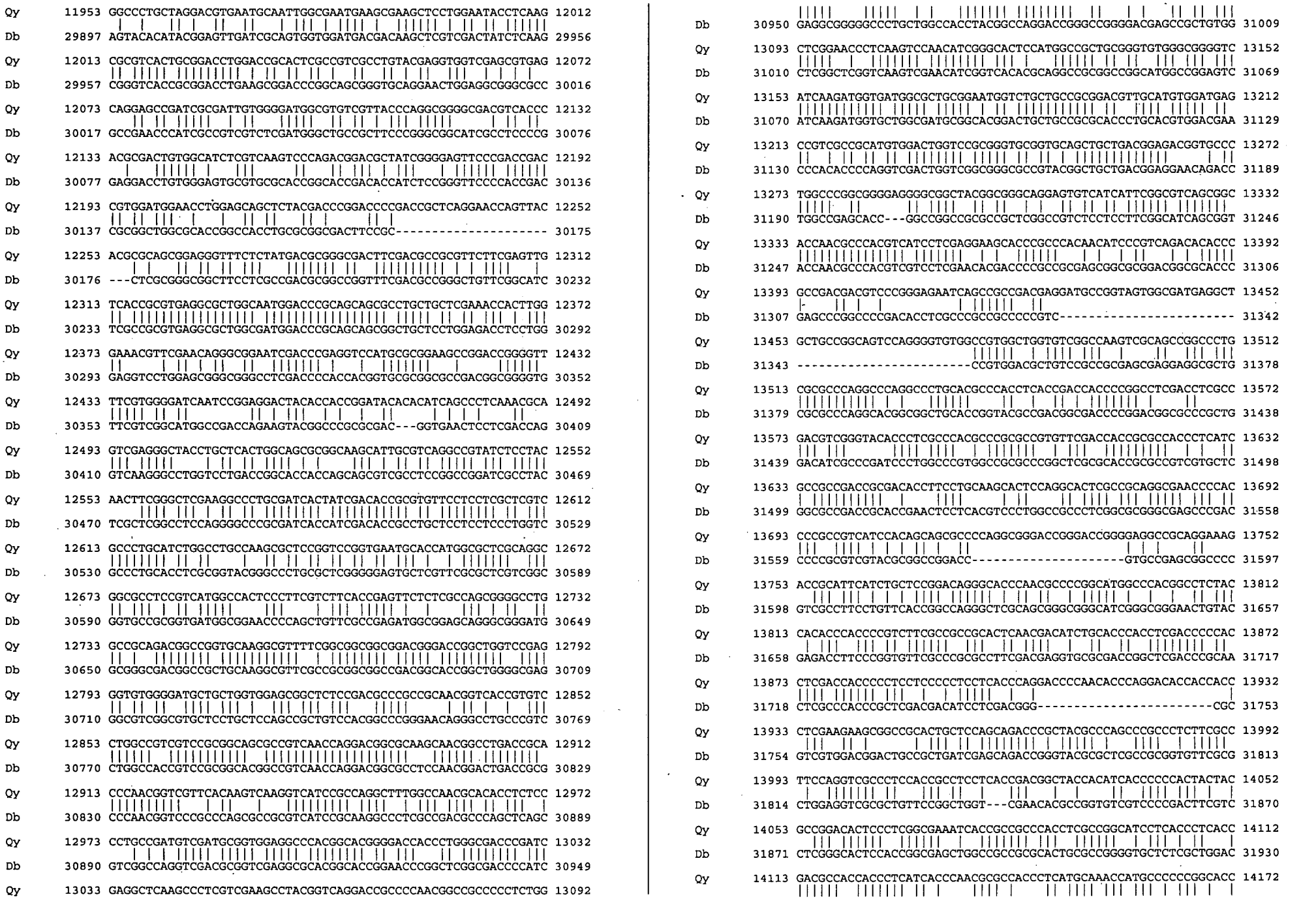


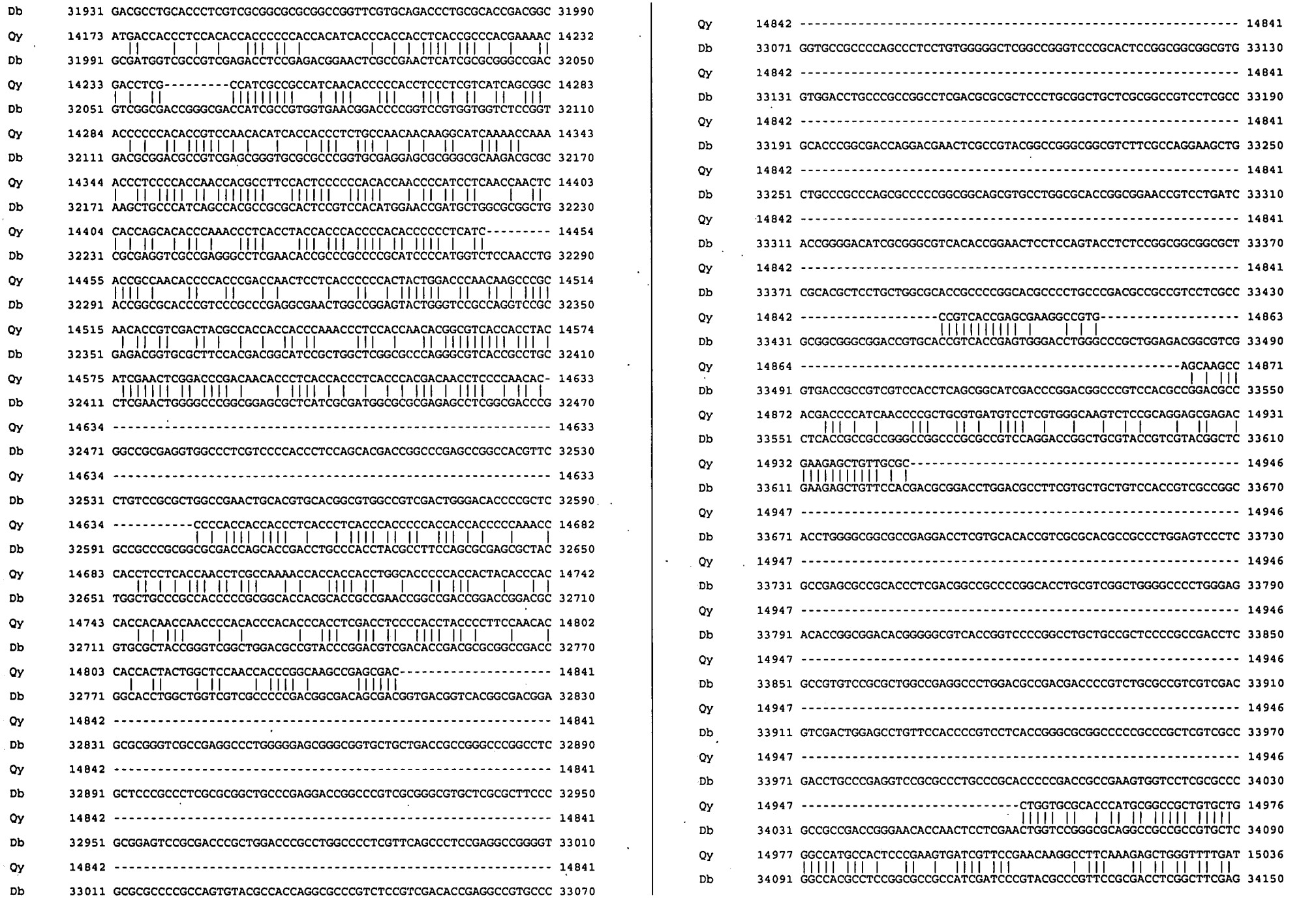


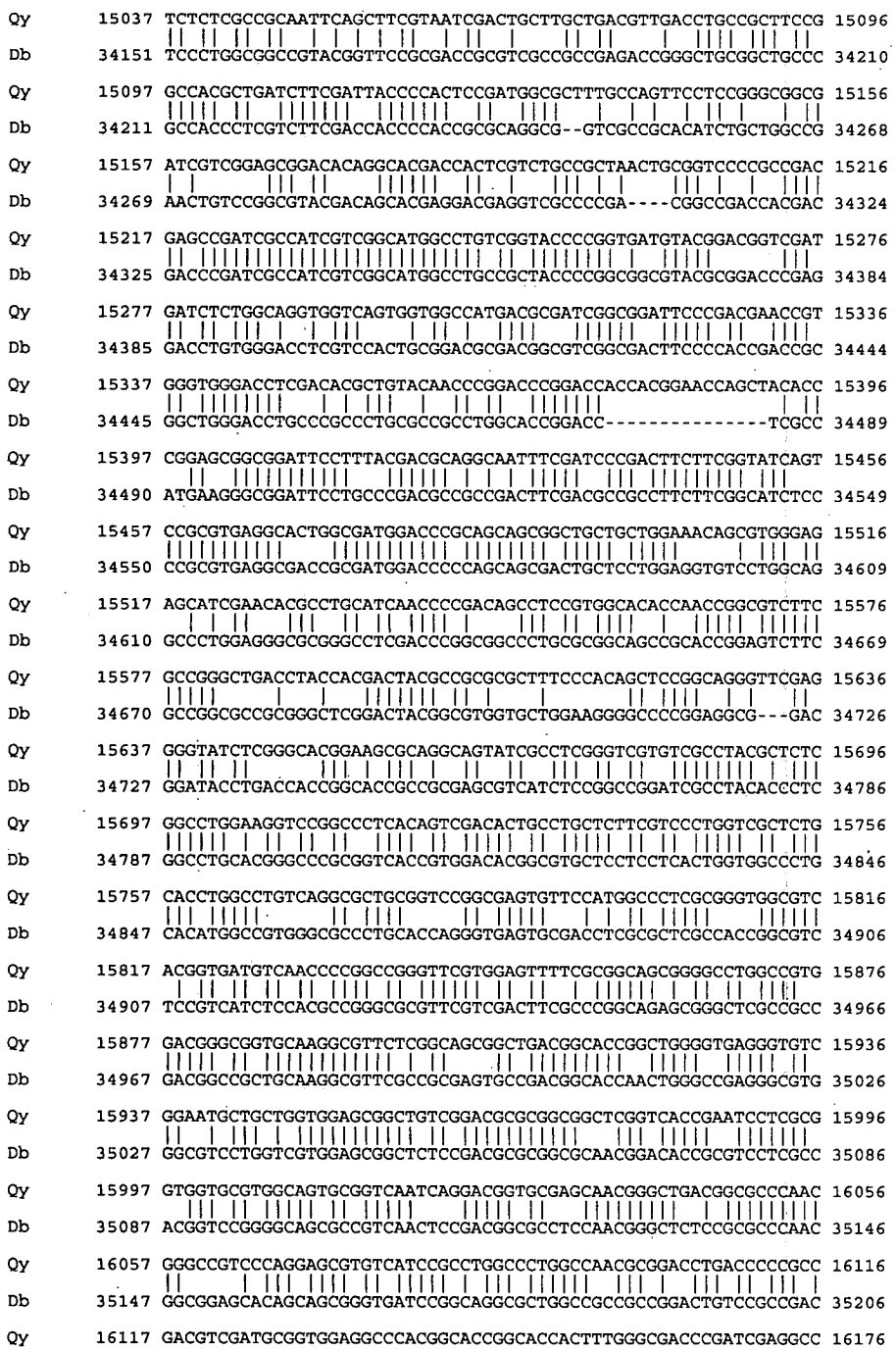


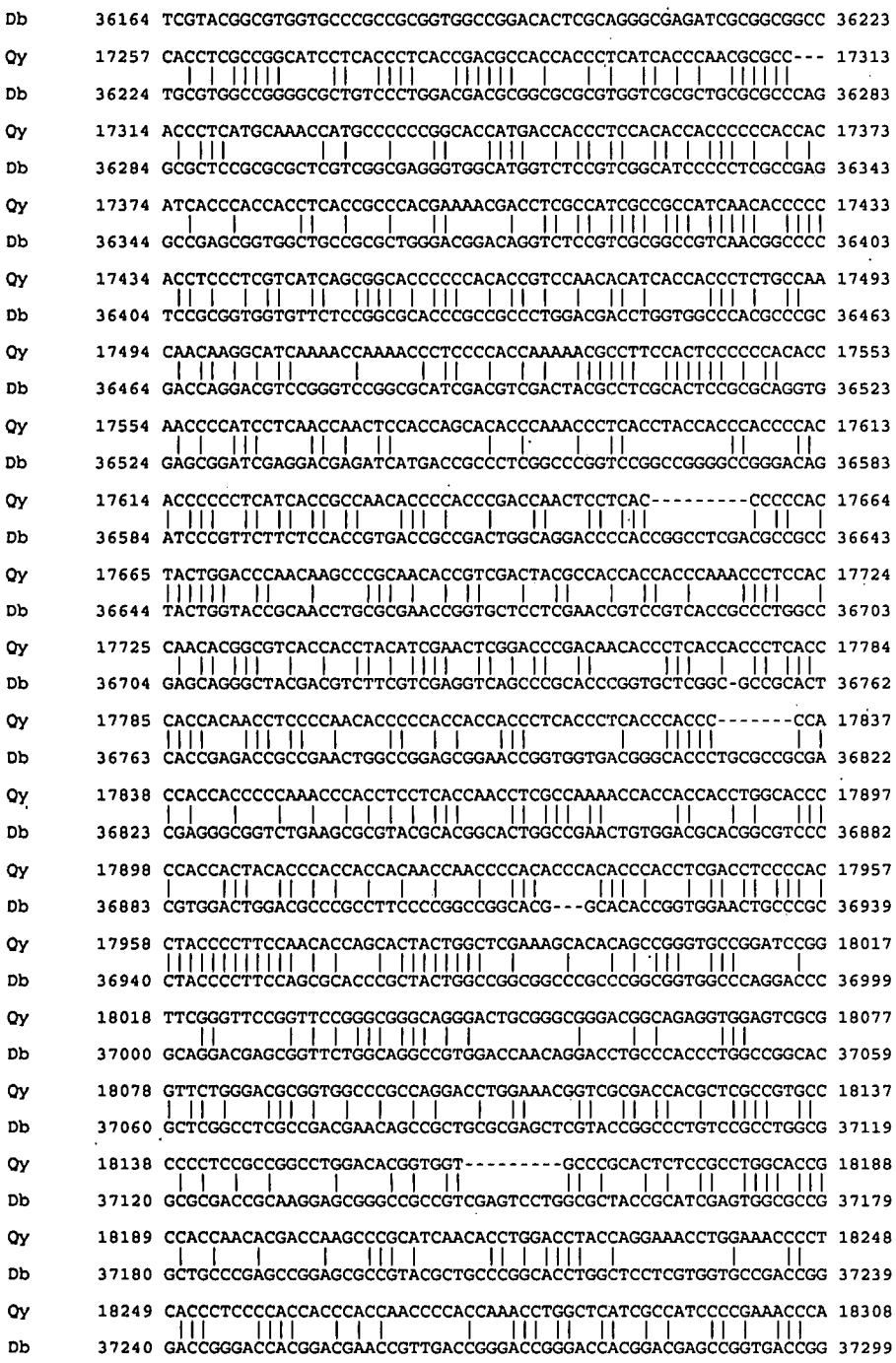

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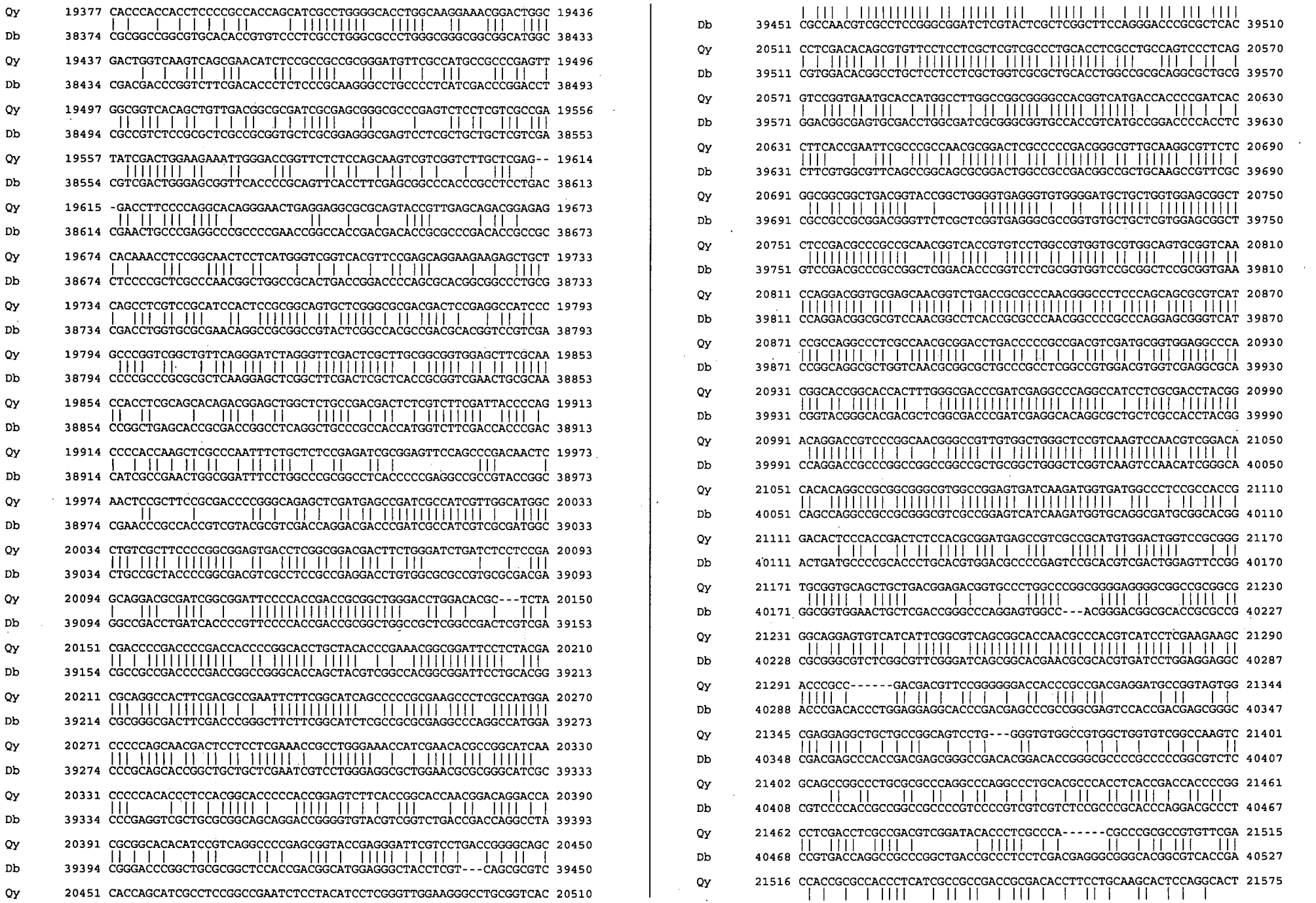

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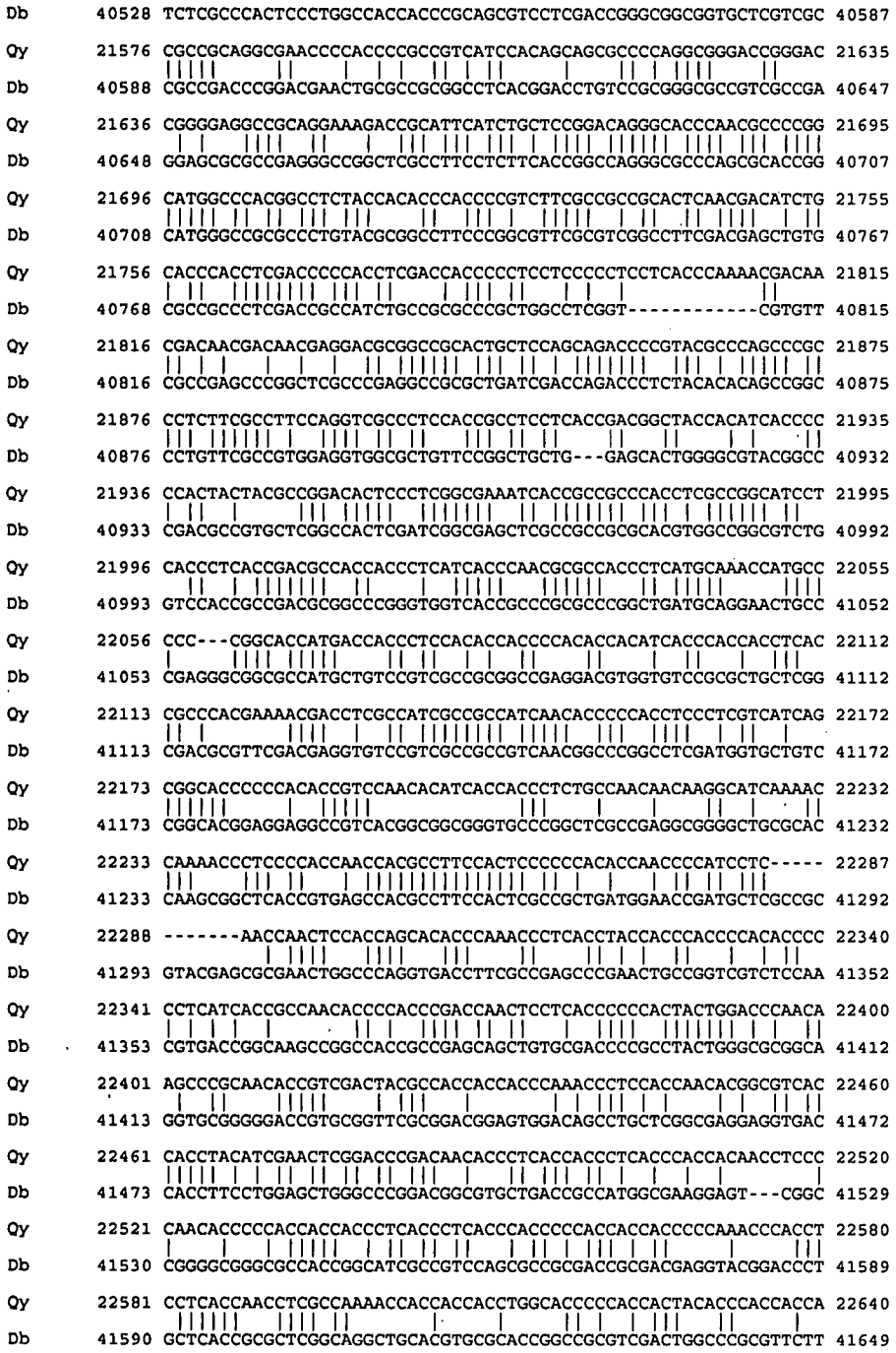


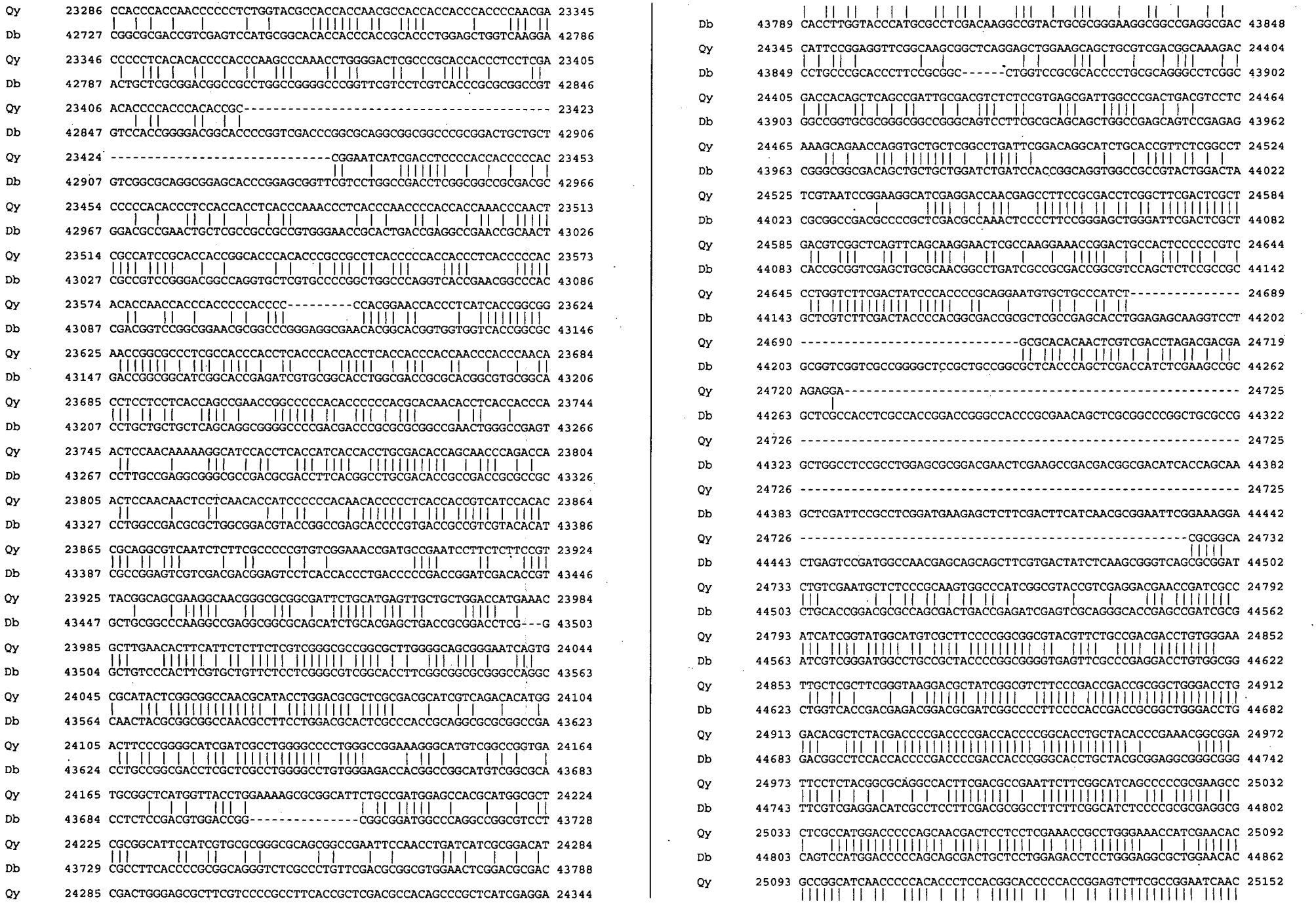


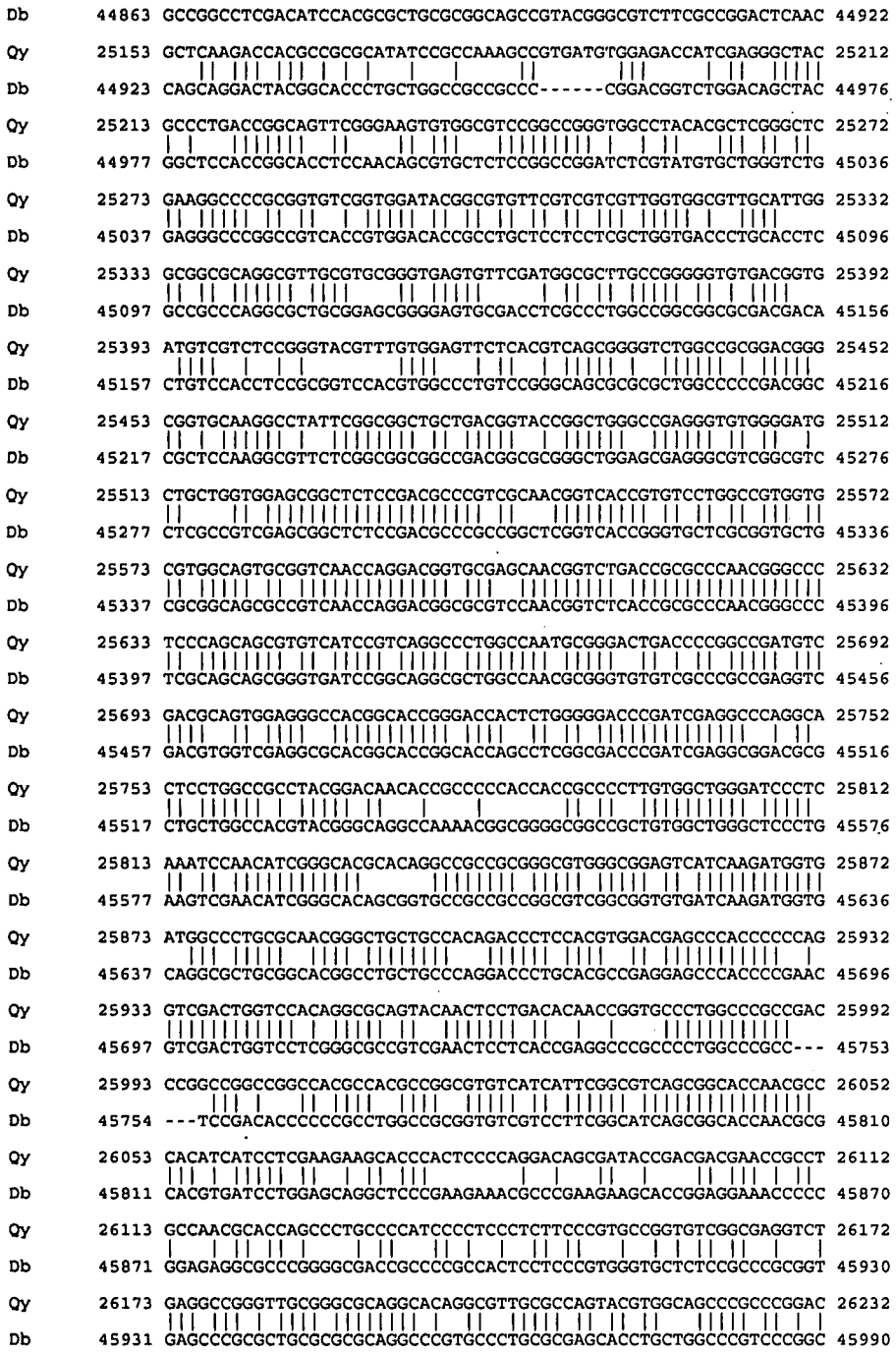

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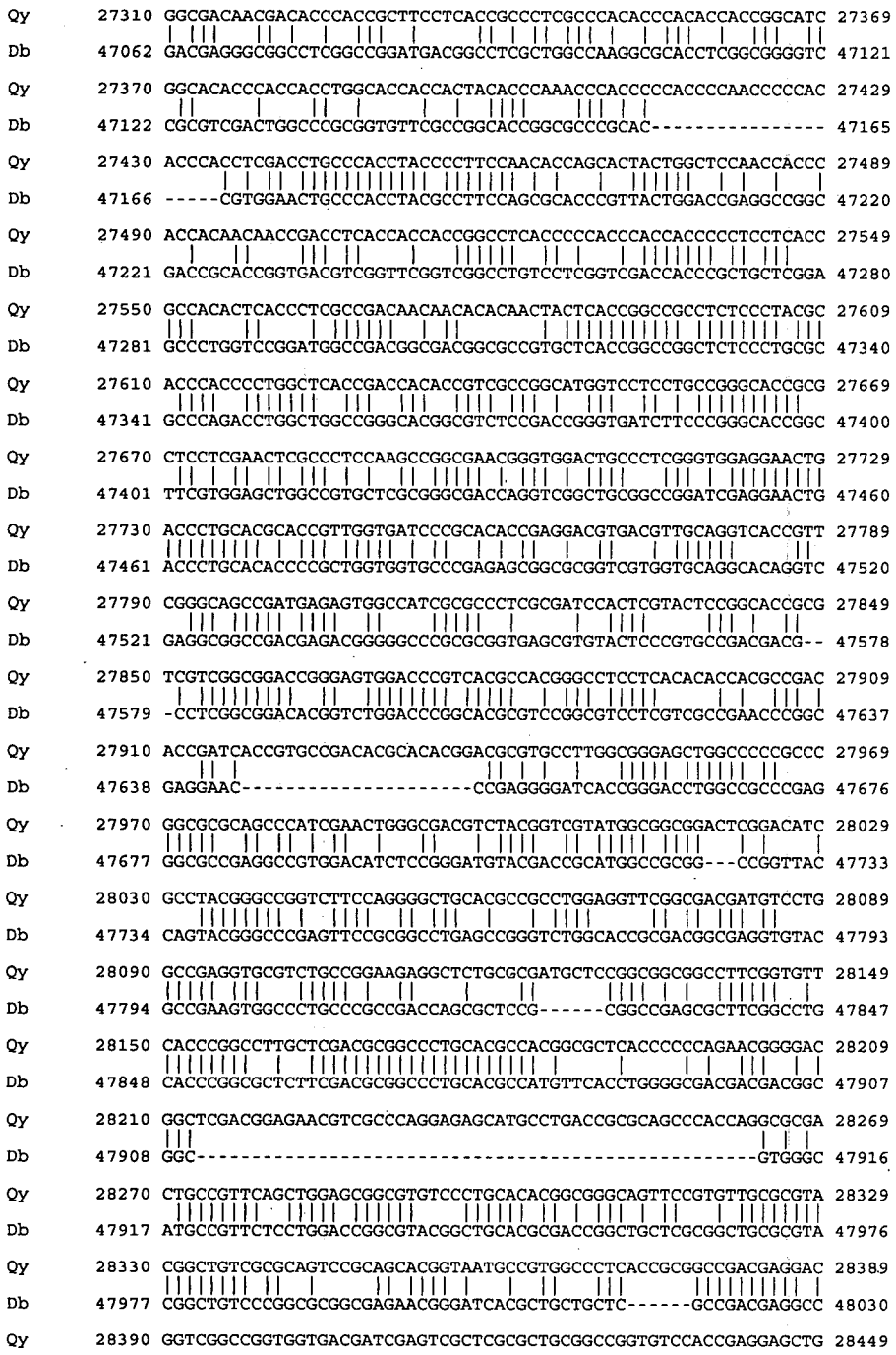

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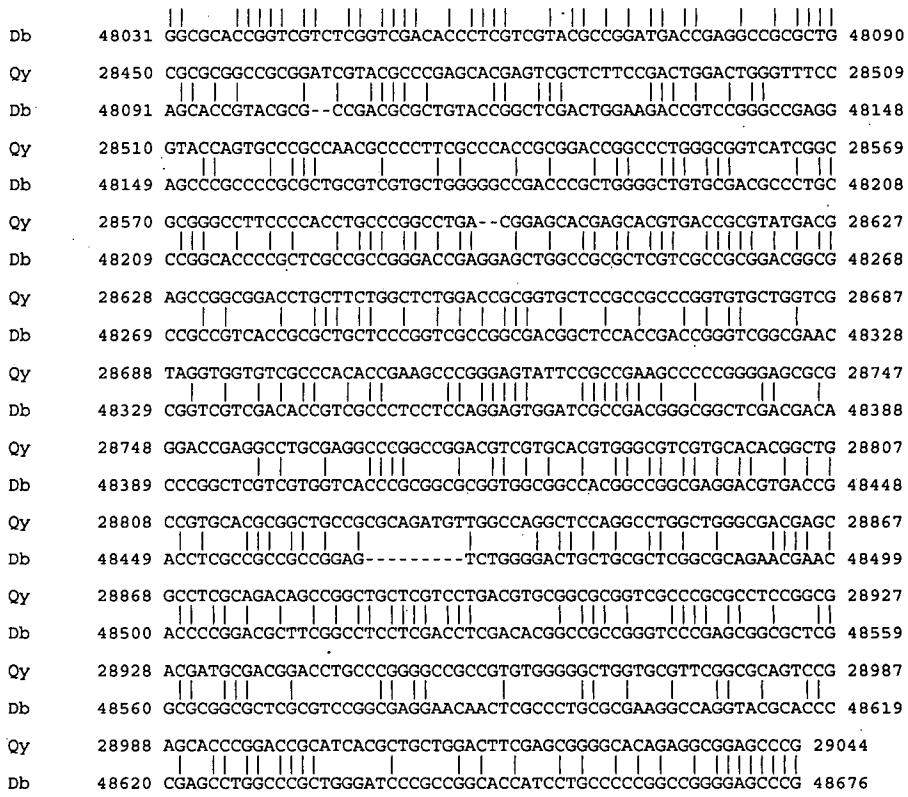



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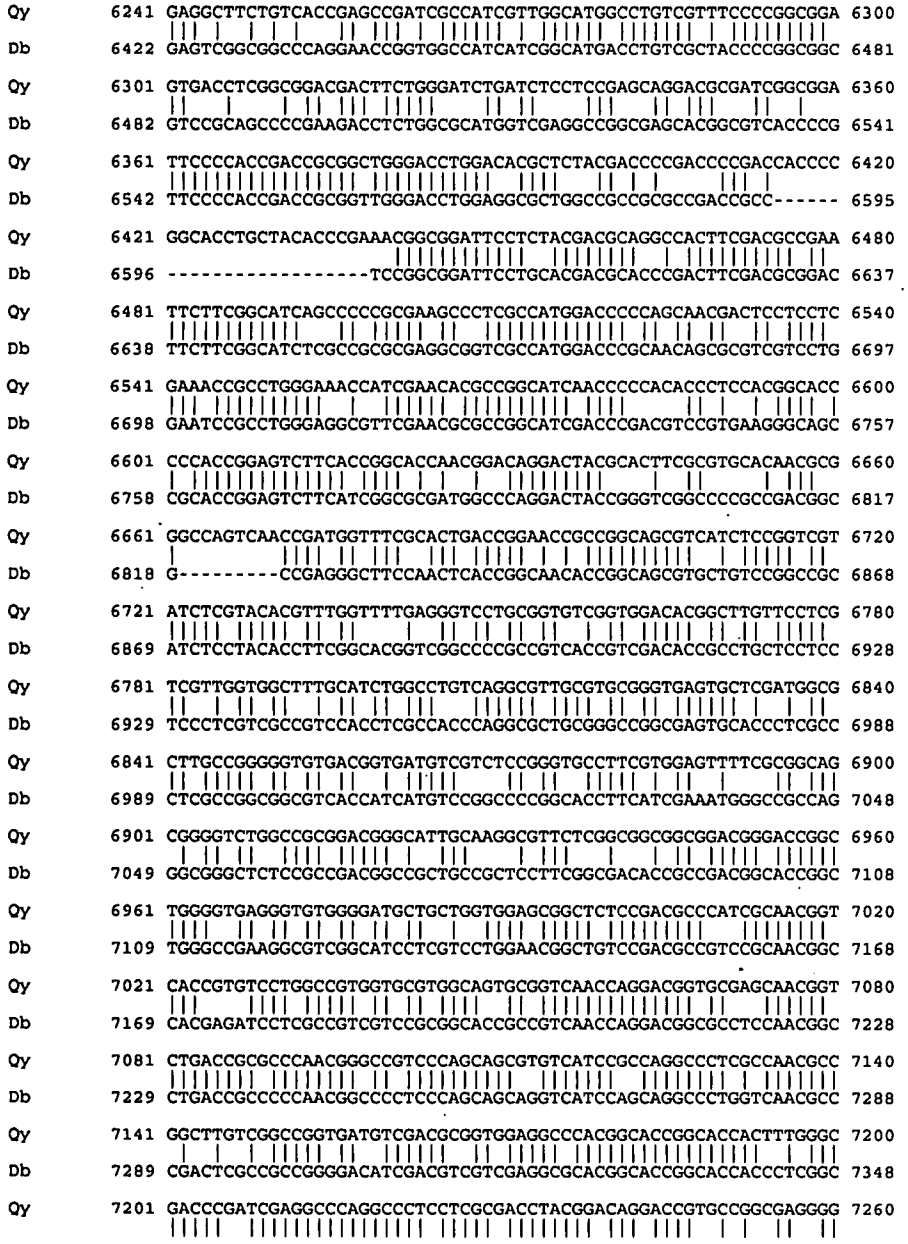


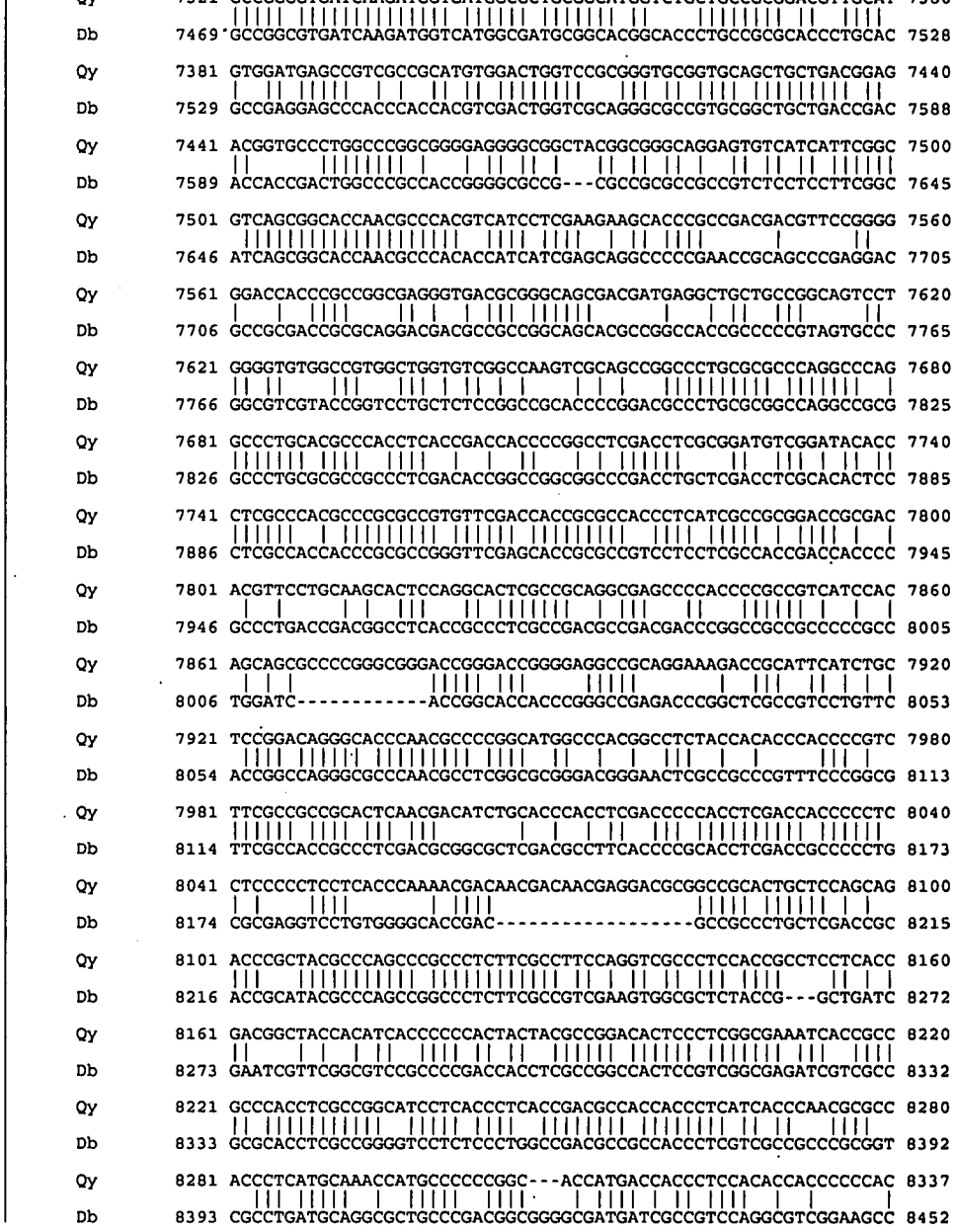


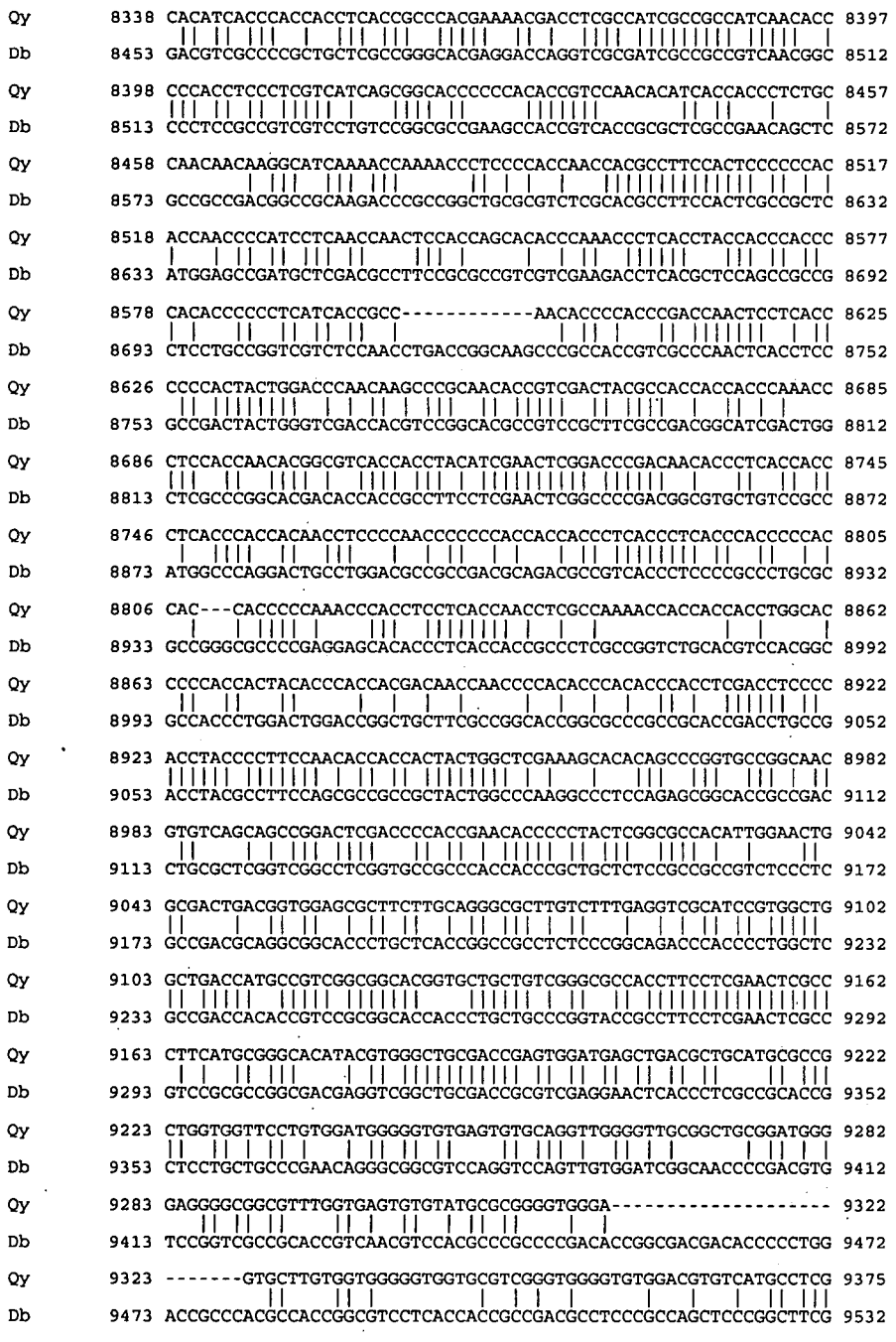
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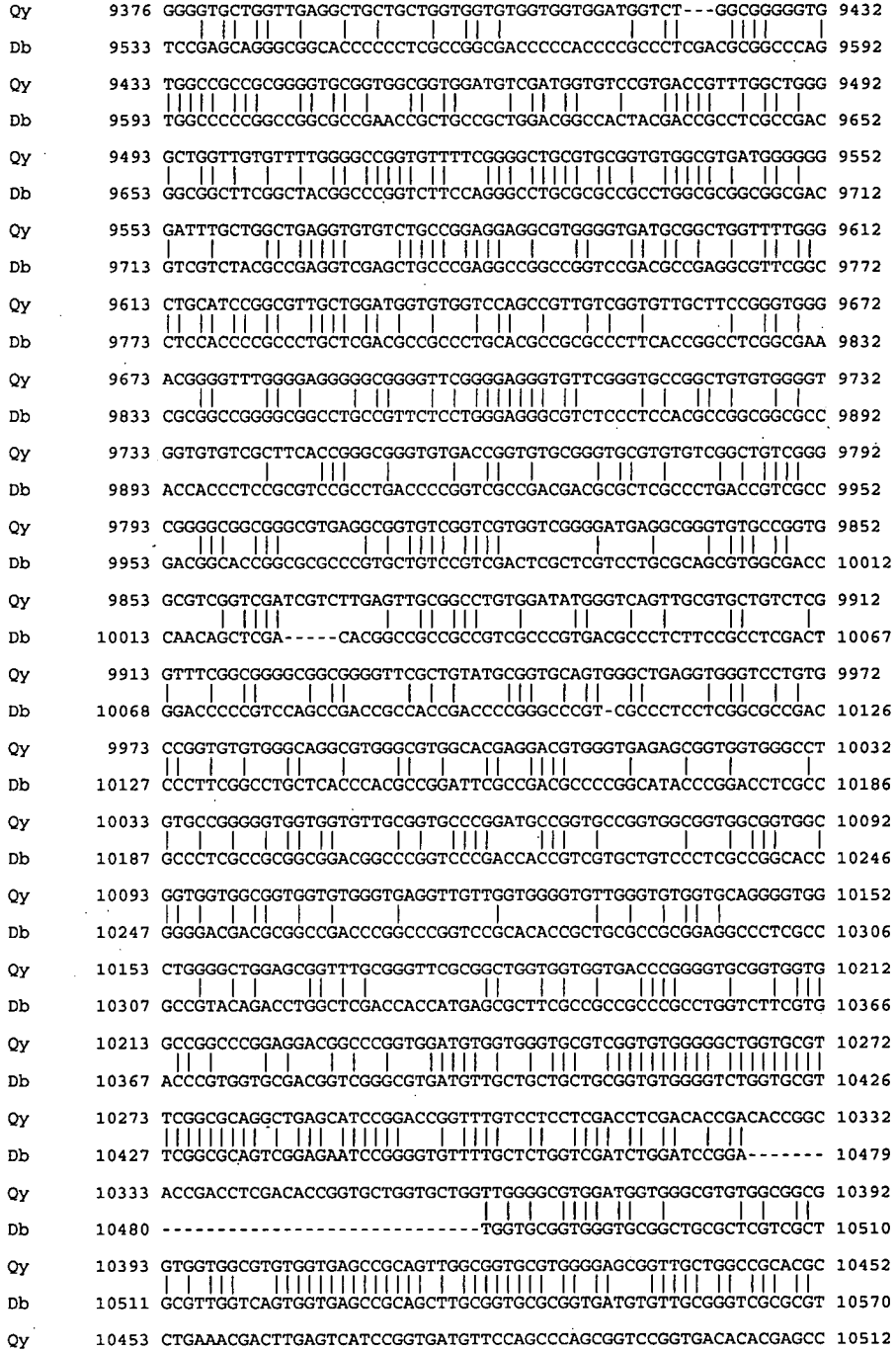
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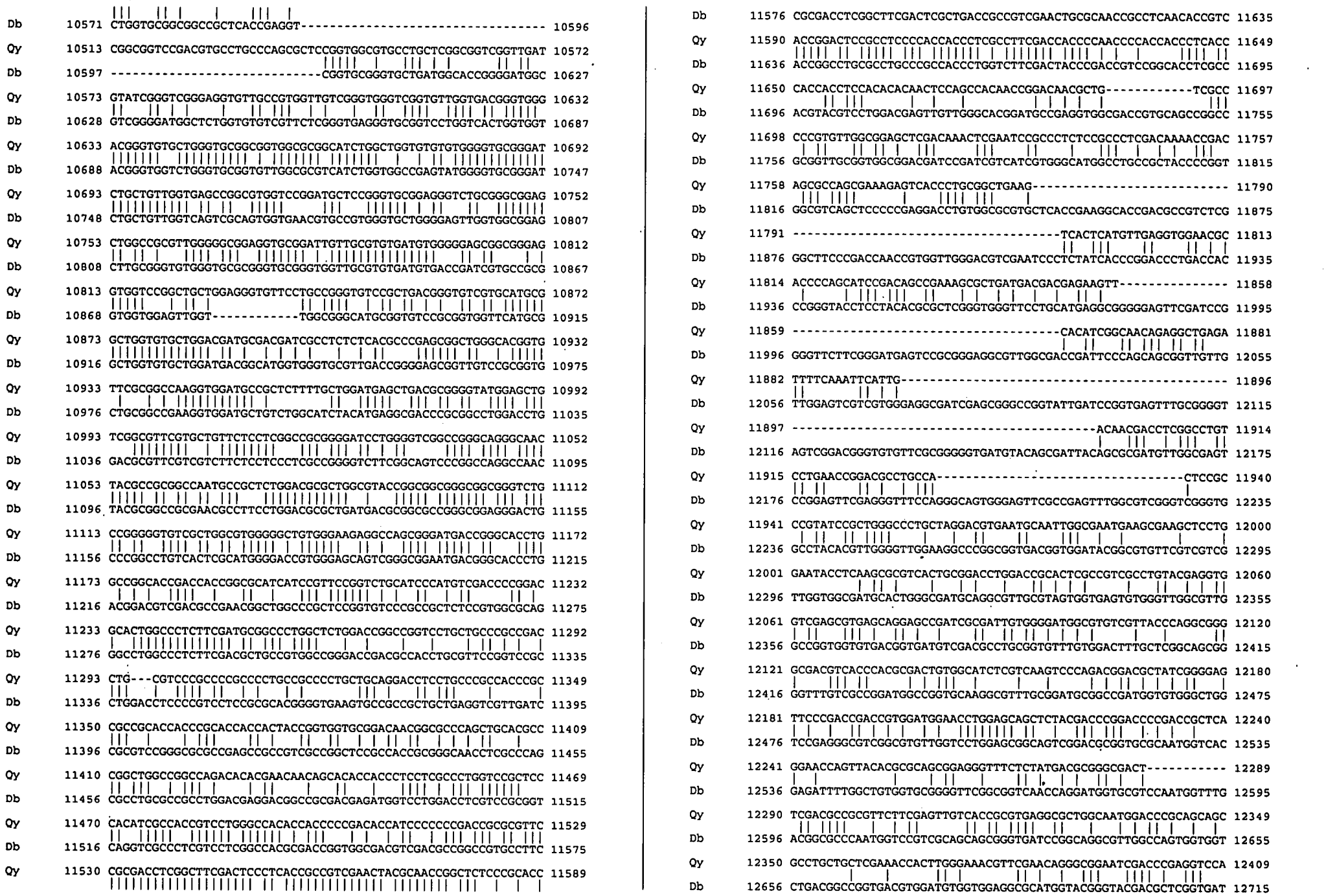
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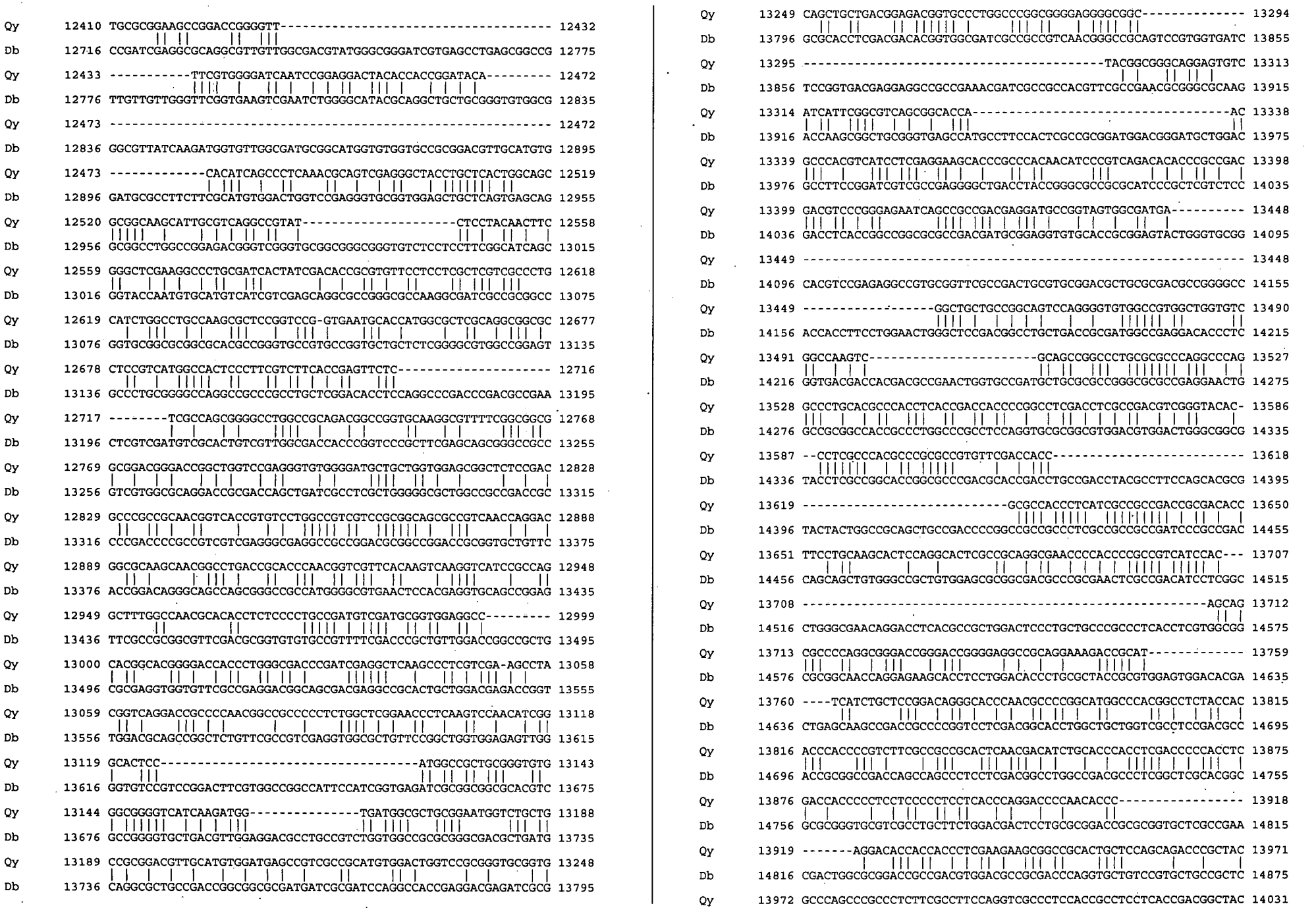


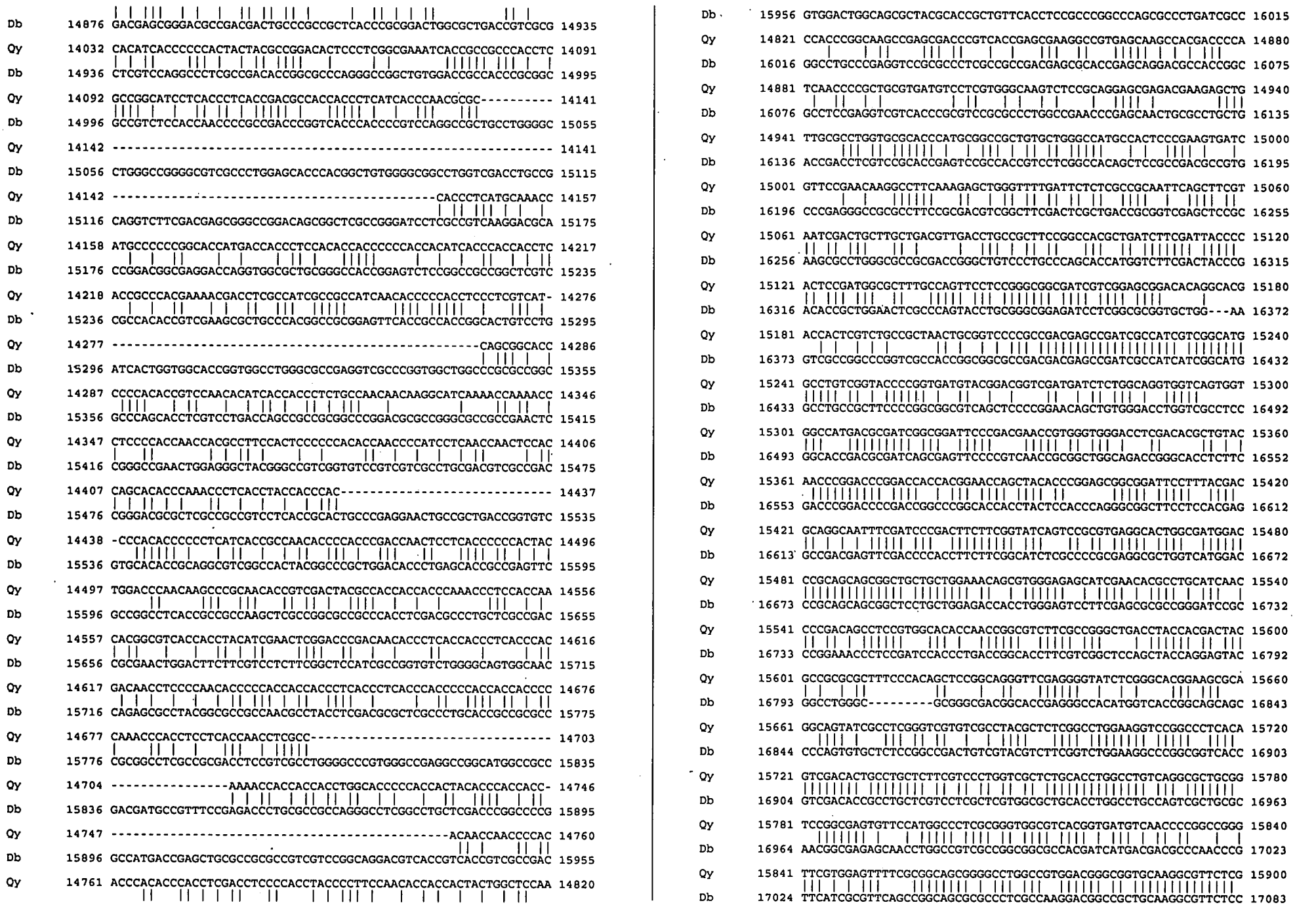


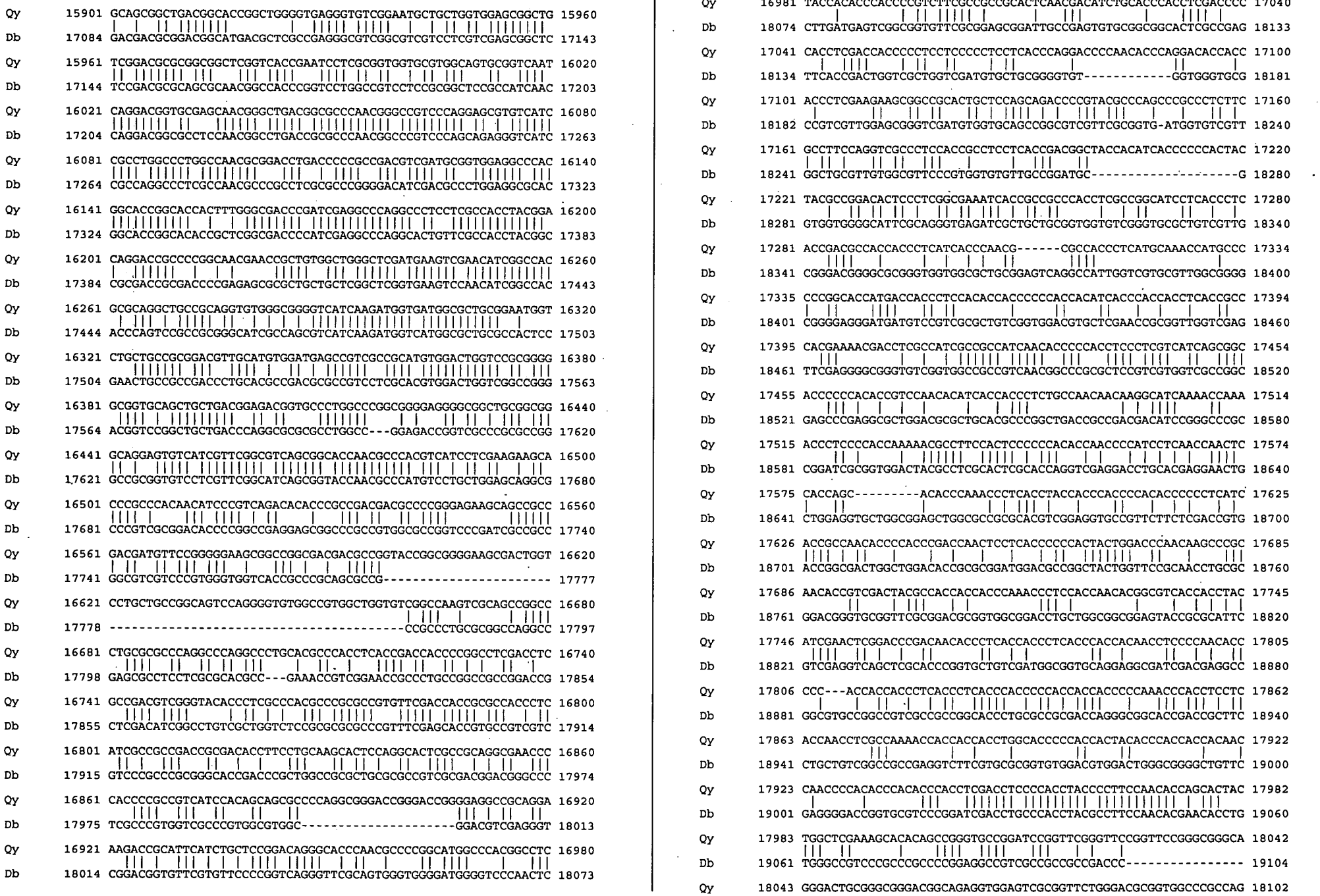


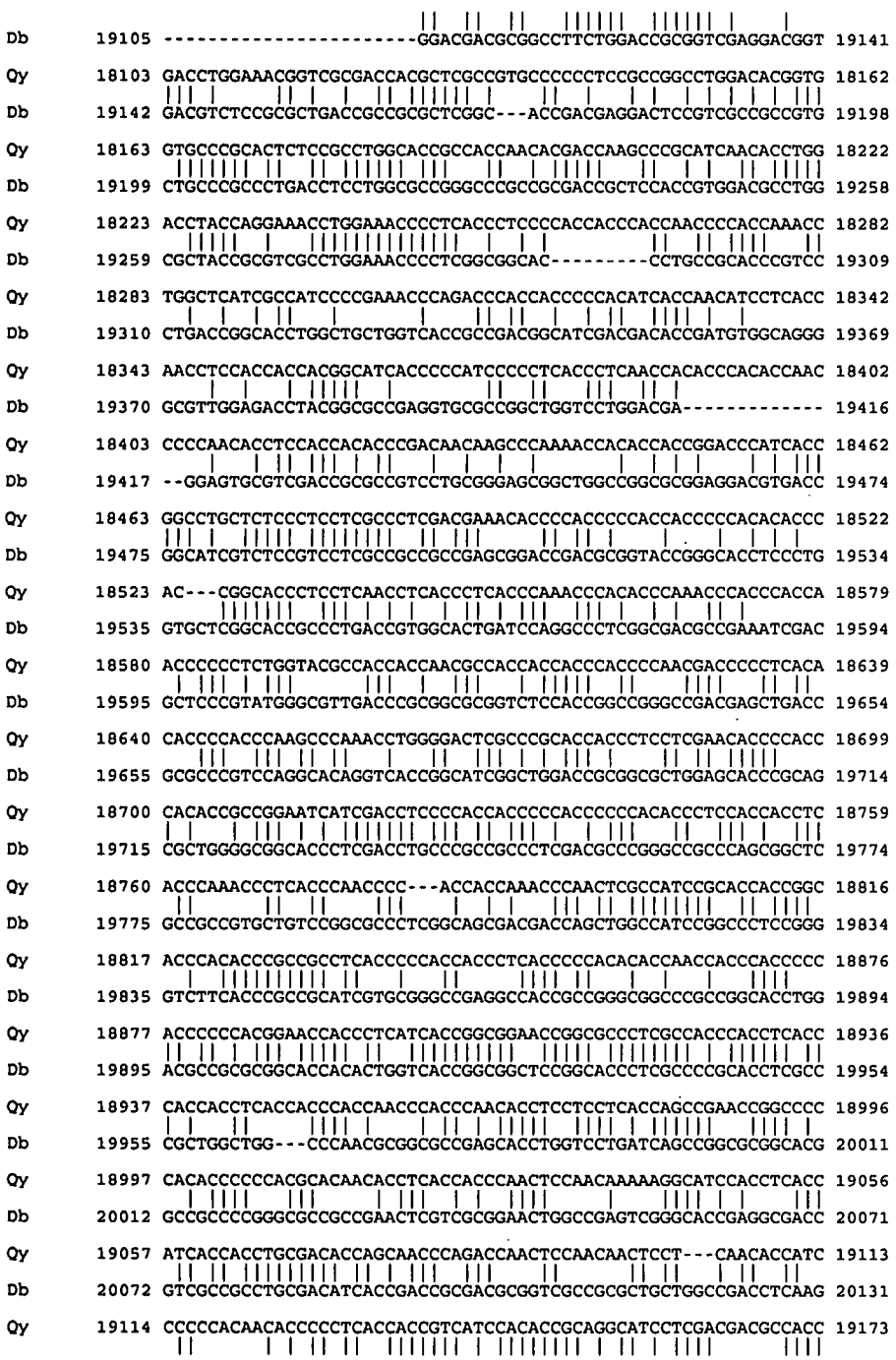


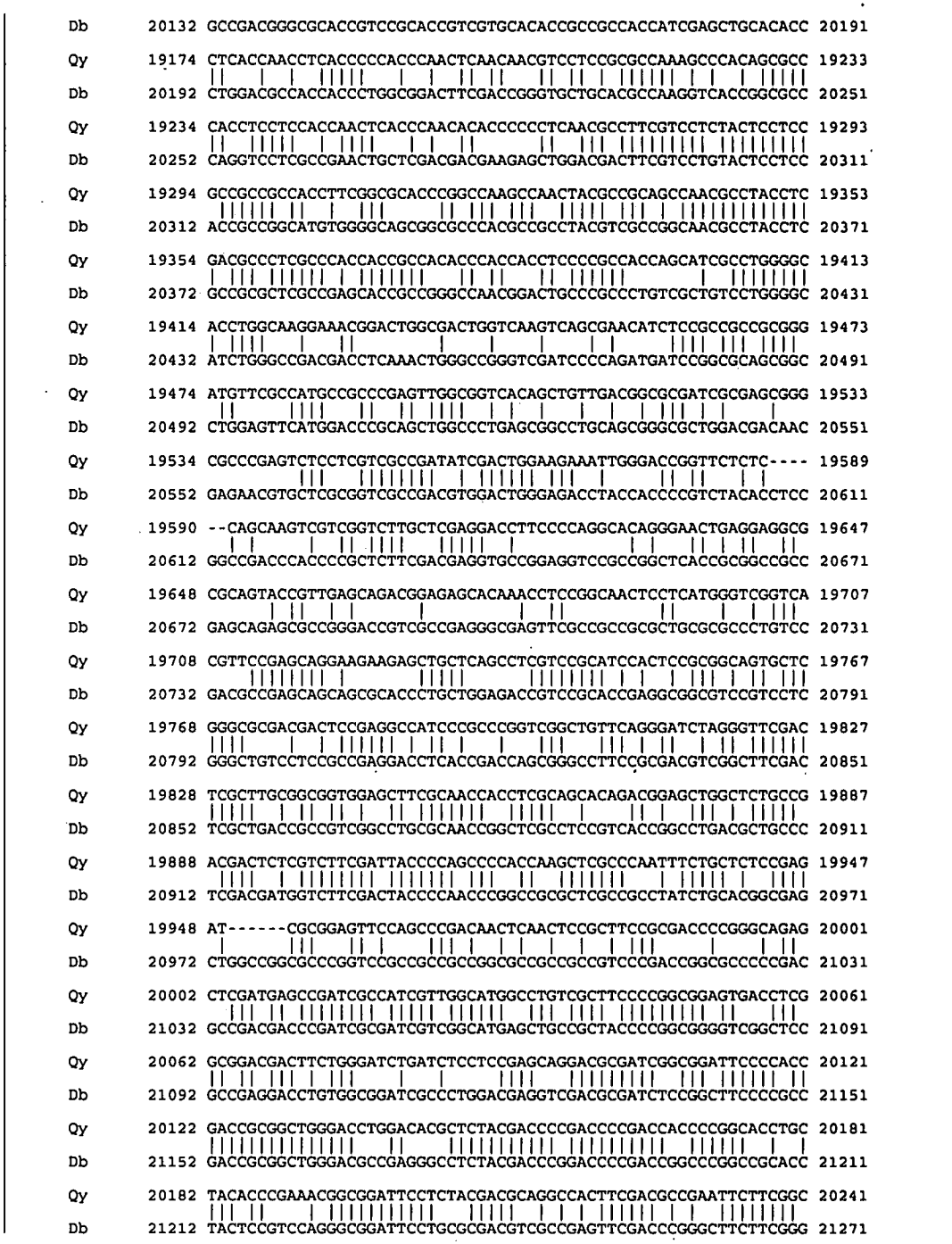


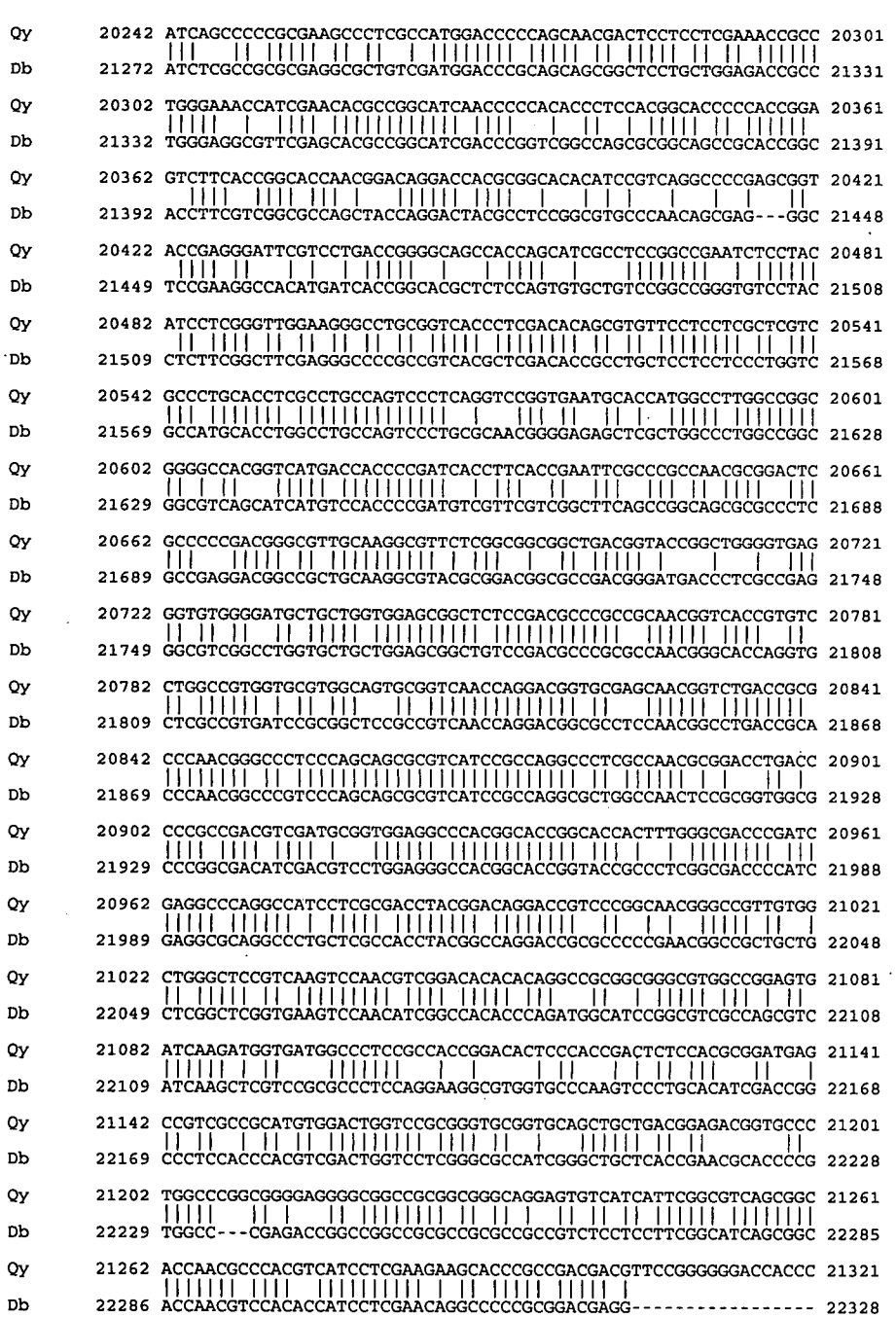


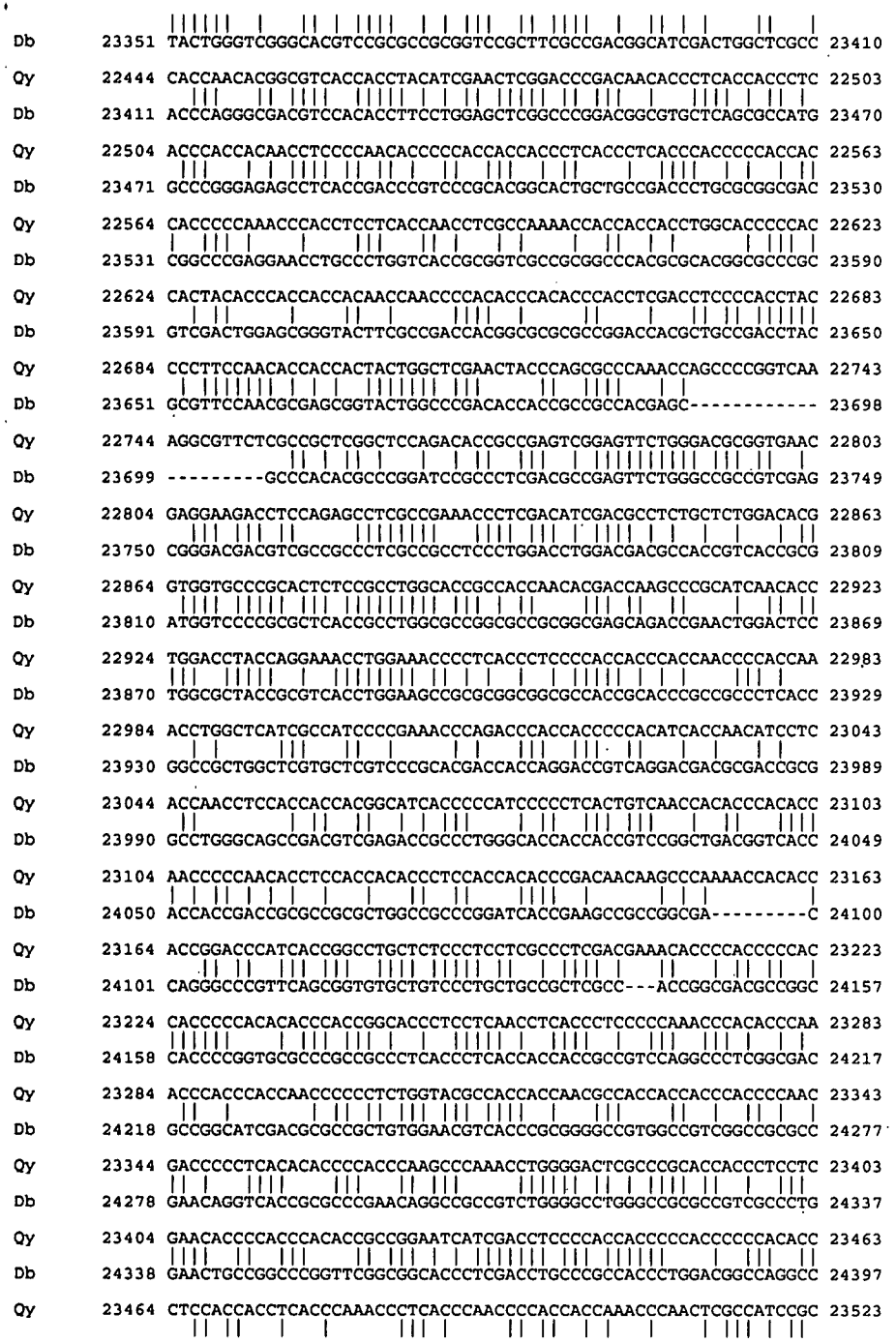


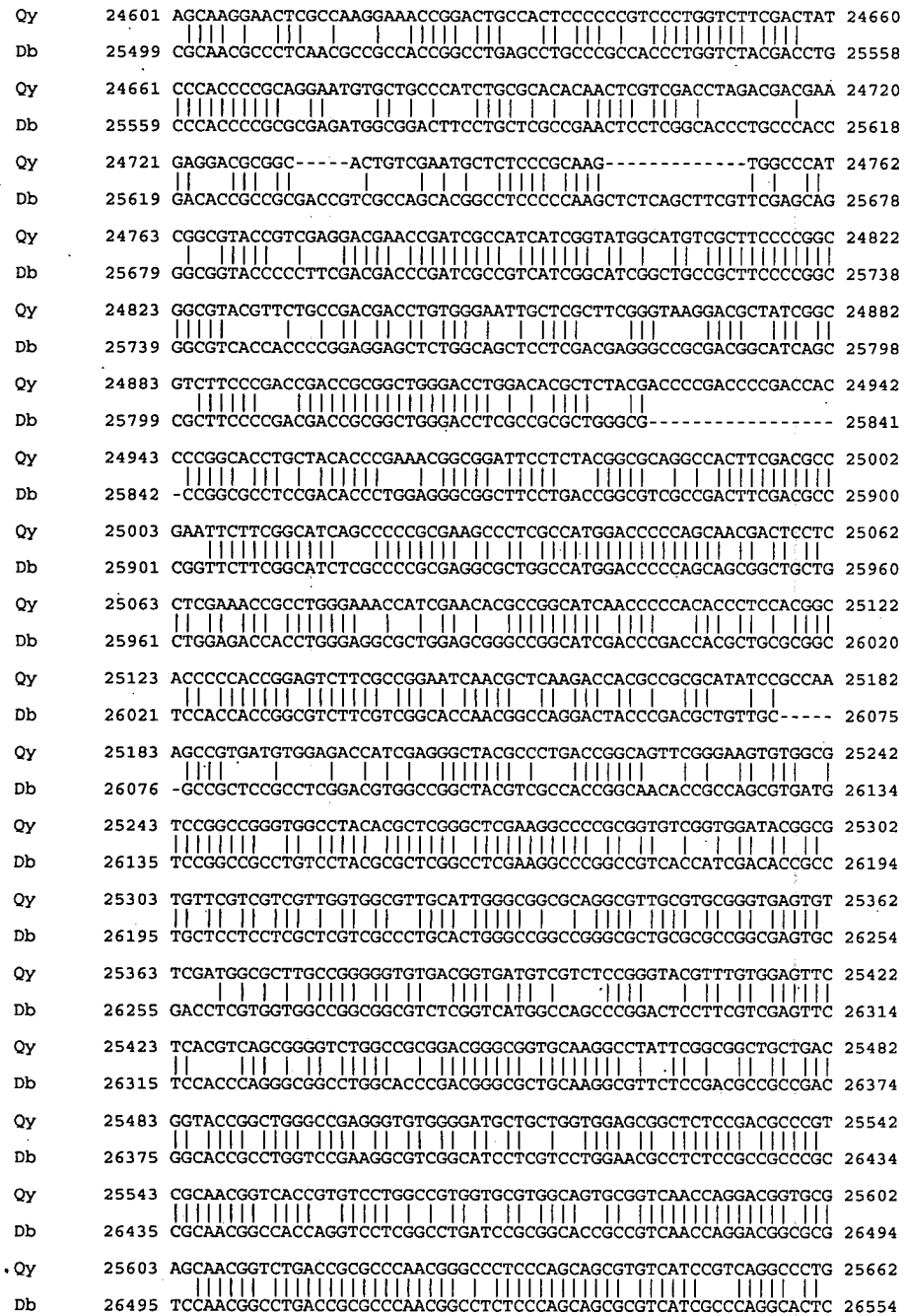



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  AUTHORS   August,P.R., Tang,L., Yoon,Y.J., Ning,S., Mueller,R., Yu,T.W.,
            Taylor,M., Hoffmann,D., Kim,C.G., Zhang,X., Hutchinson,C.R. and
            Floss,H.G.
  TITLE     Biosynthesis of the ansamycin antibiotic rifamycin: deductions from
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  JOURNAL   Chem. Biol. 5 (2), 69-79 (1998)
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  AUTHORS   Kim,C.G., Yu,T.W., Fryhle,C.B., Handa,S. and Floss,H.G.
  TITLE     3-Amino-5-hydroxybenzoic acid synthase, the terminal enzyme in the
            formation of the precursor of mC7N units in rifamycin and related
            antibiotics
  JOURNAL   J. Biol. Chem. 273 (11), 6030-6040 (1998)
  MEDLINE   98165773
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REFERENCE   3  (bases 1 to 90445)
  AUTHORS   Yu,T.W., Muller,R., Muller,M., Zhang,X., Draeger,G., Kim,C.G.,
            Leistner,E. and Floss,H.G.
  TITLE     Mutational analysis and reconstituted expression of the
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            3-amino-5-hydroxybenzoic acid, the starter unit of rifamycin
            biosynthesis in amycolatopsis Mediterranei S699
  JOURNAL   J. Biol. Chem. 276 (16), 12546-12555 (2001)
  MEDLINE   21201076
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  AUTHORS   August,P.R., Tang,L., Yoon,Y.J., Ning,S., Mueller,R.,
            Hutchinson,C.R. and Floss,H.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-DEC-1997) Dept. of Chemistry, University of
            Washington, Box 351700, Seattle, WA 98195-1700, USA
REFERENCE   5  (bases 1 to 90445)
  AUTHORS   August,P.R., Tang,L., Yoon,Y.J., Ning,S., Mueller,R.,
            Hutchinson,C.R. and Floss,H.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JAN-2001) Dept. of Chemistry, University of
            Washington, Box 351700, Seattle, WA 98195-1700, USA
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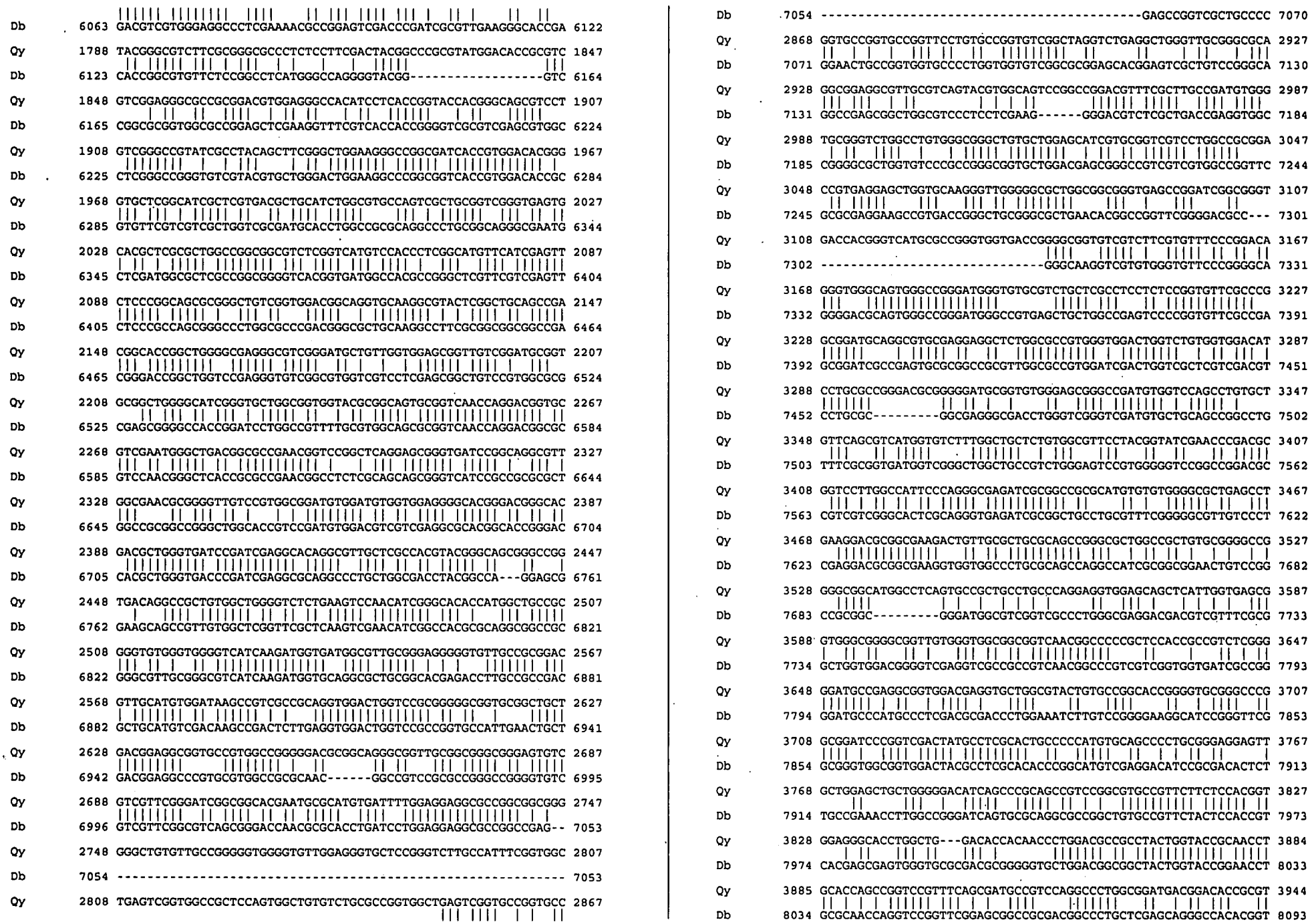
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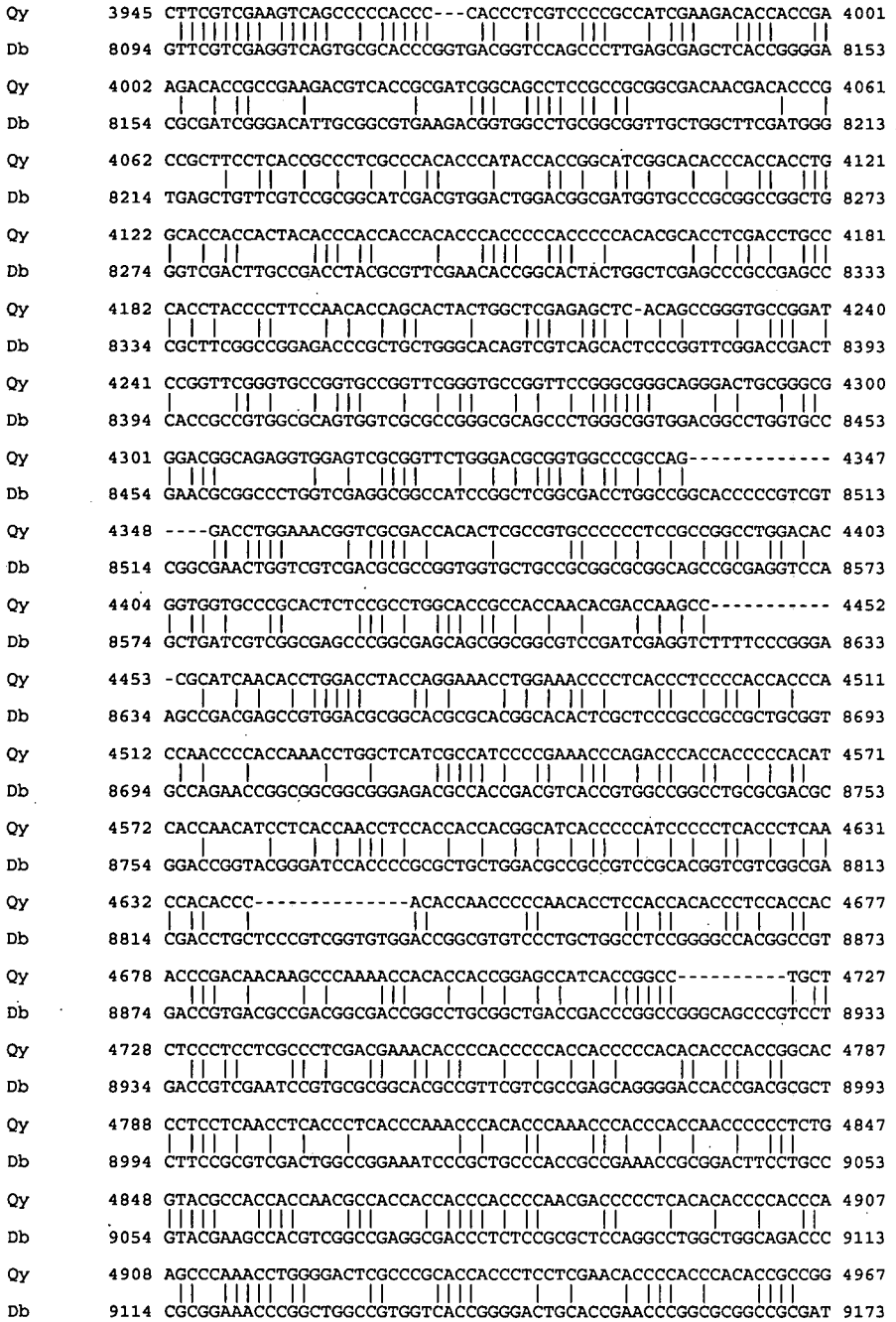
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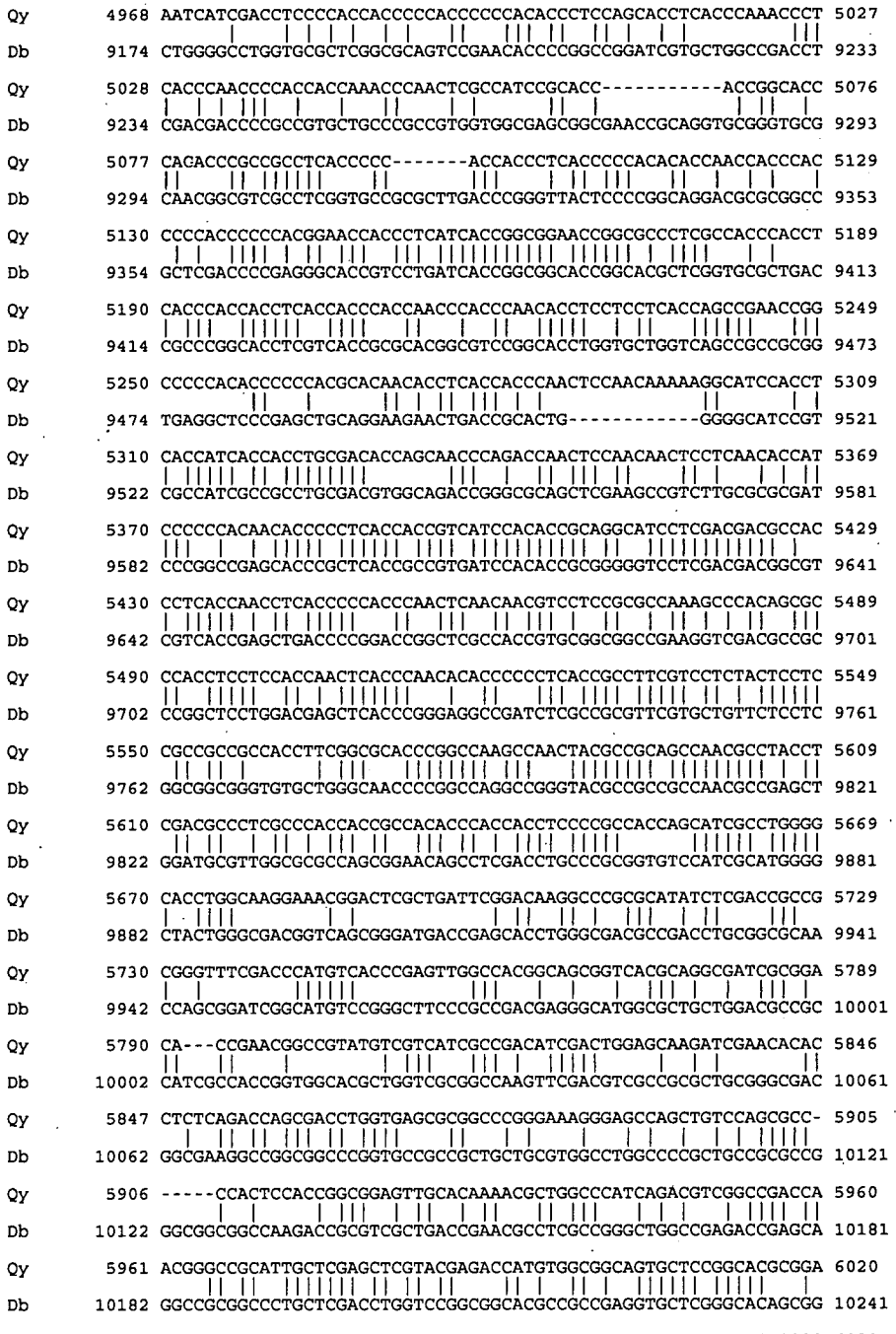
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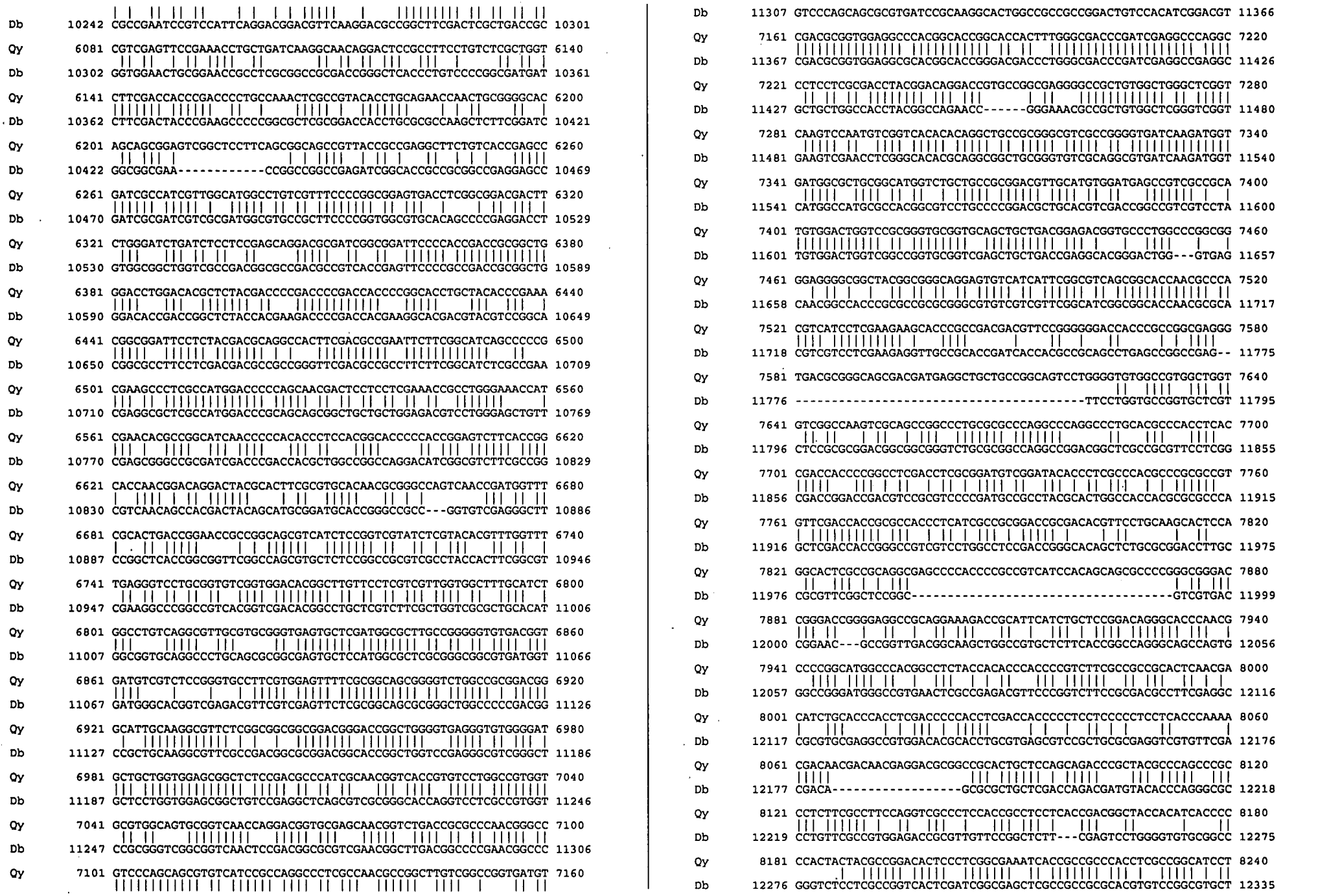
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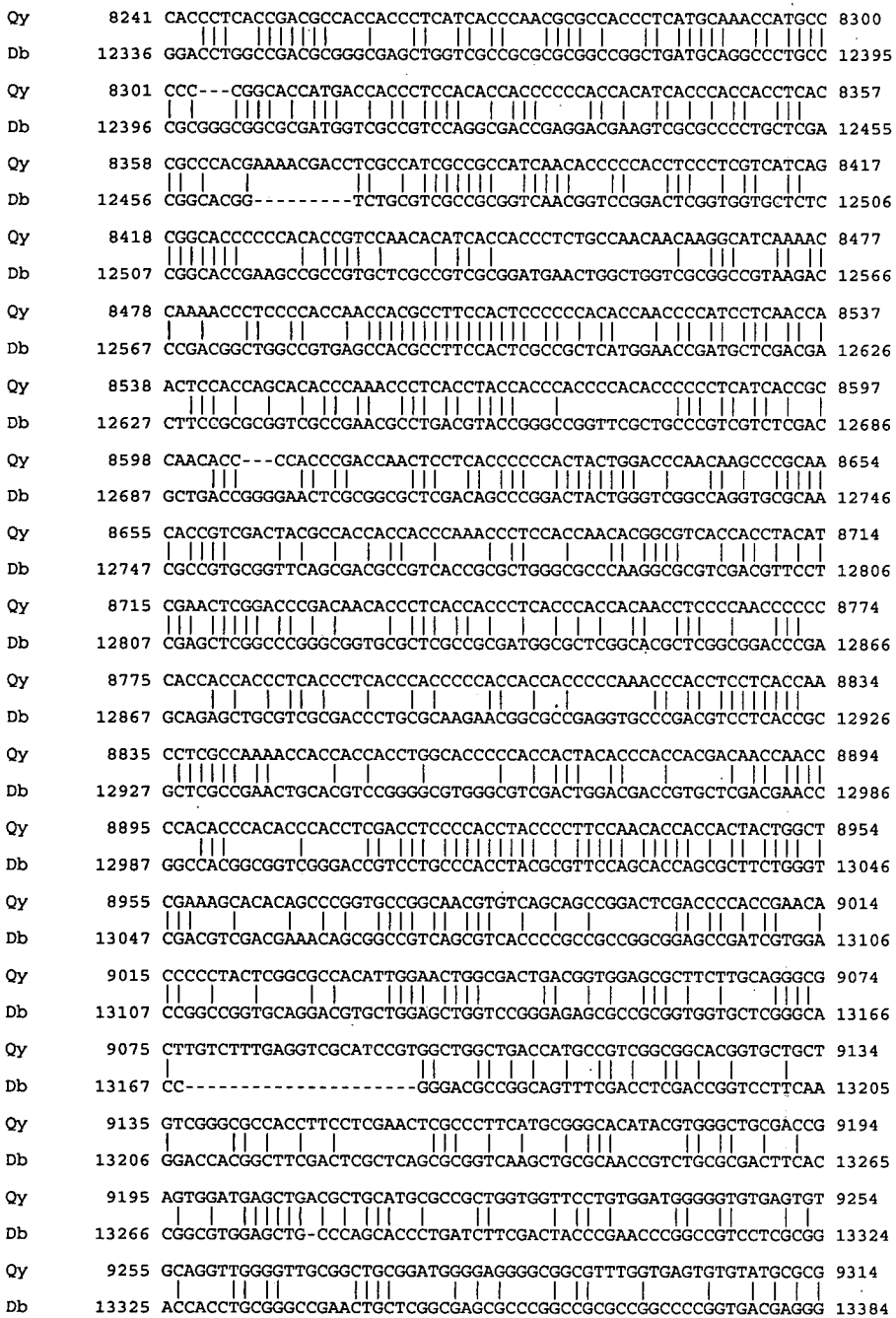
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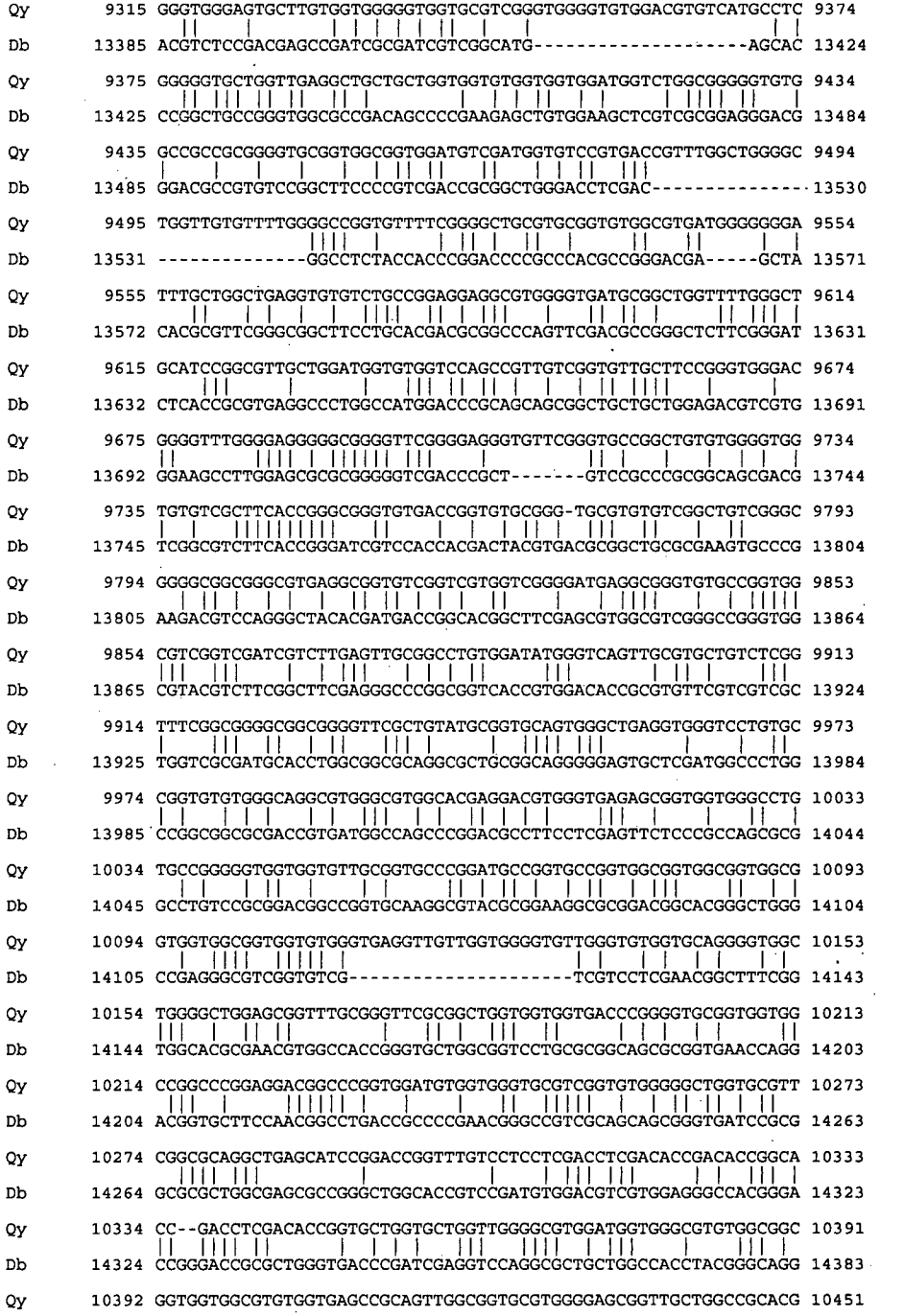


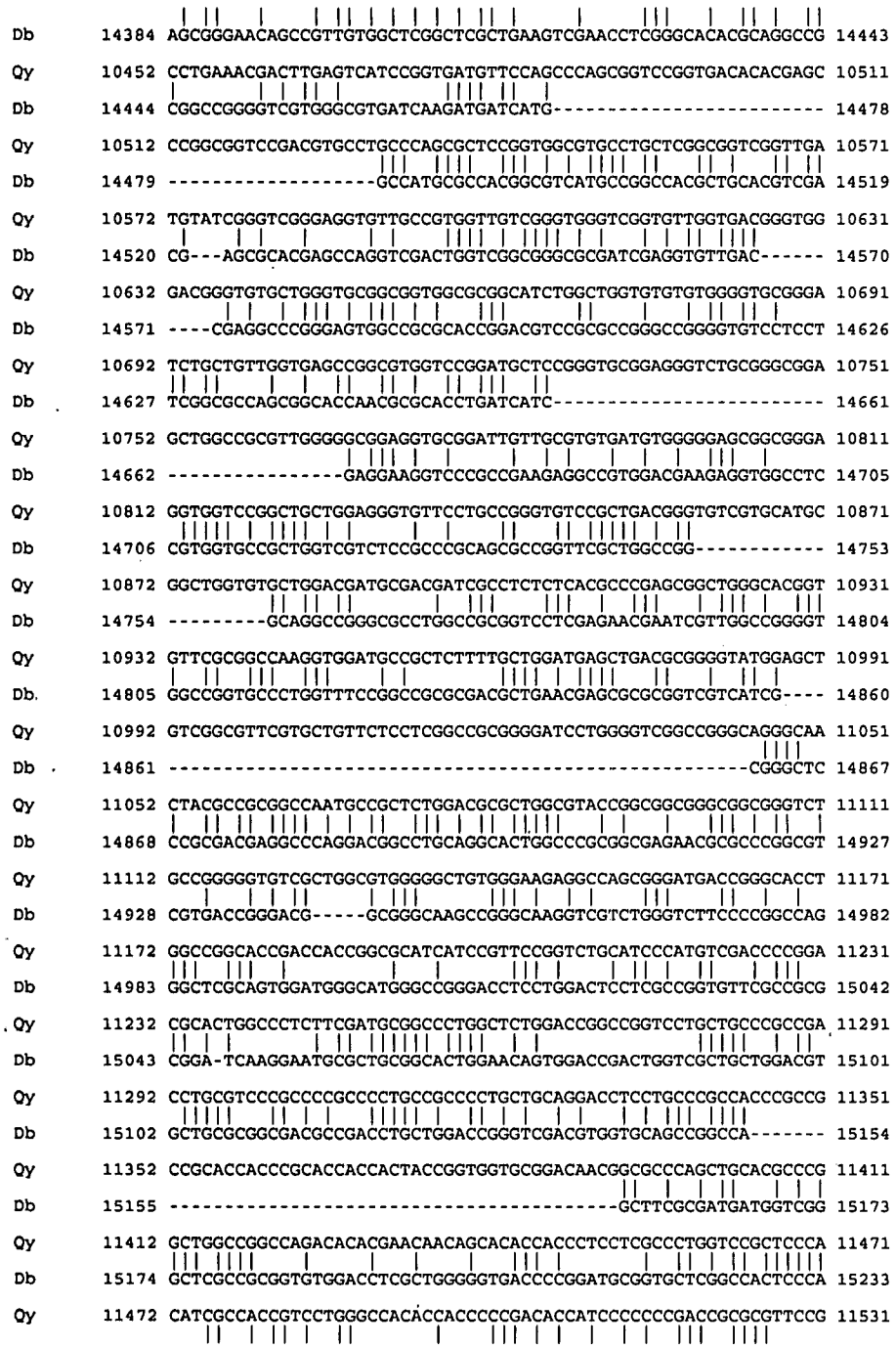


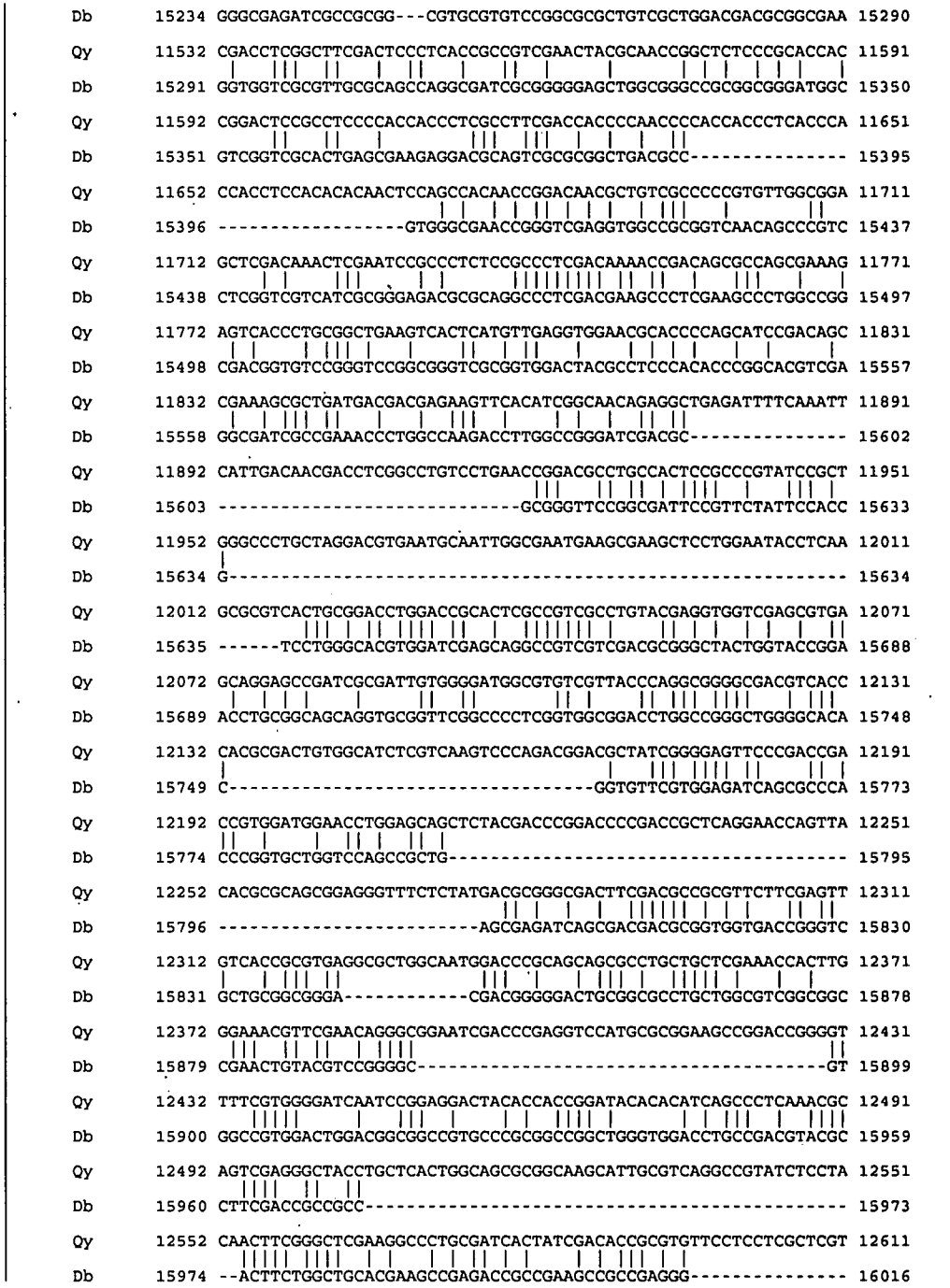


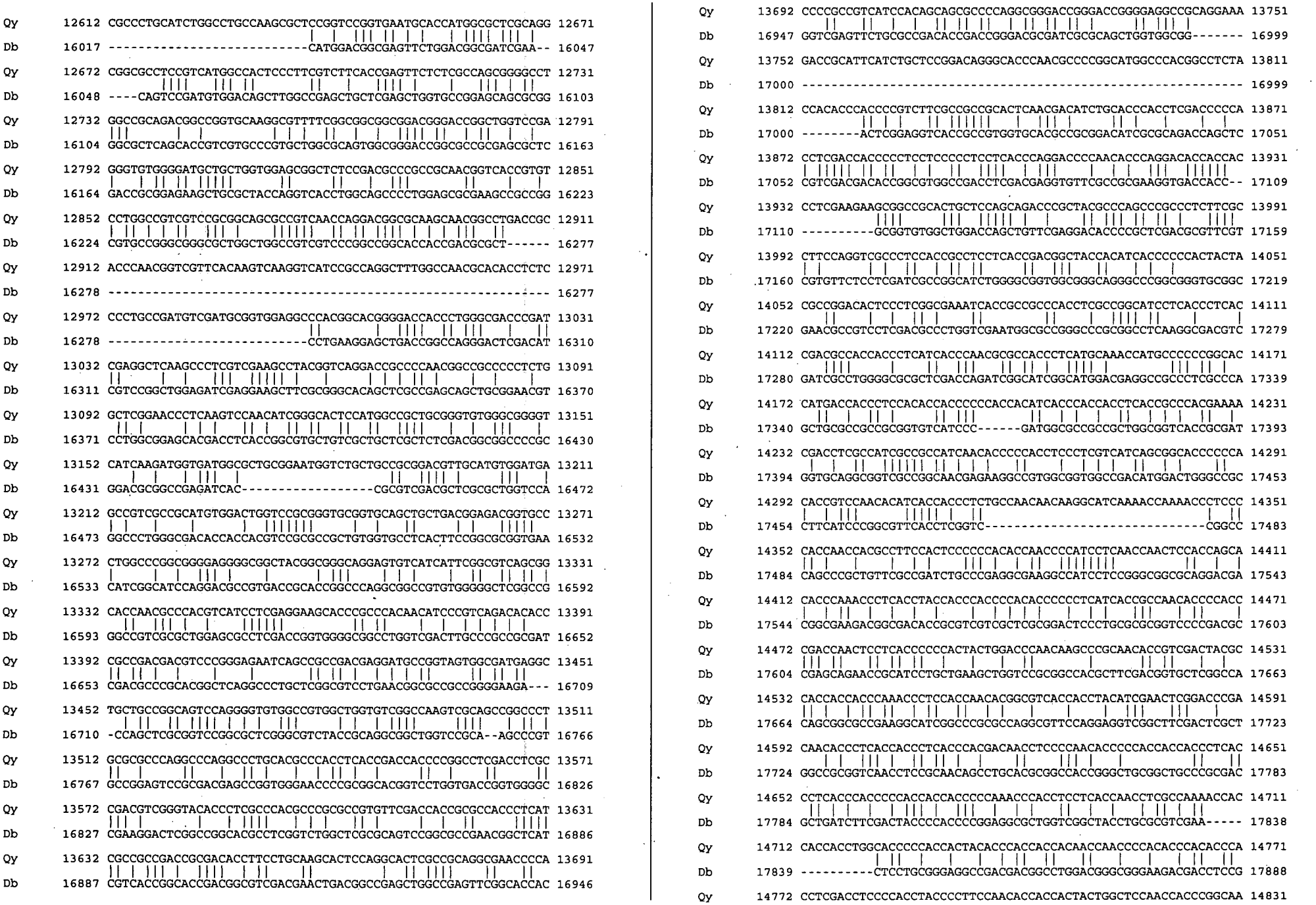


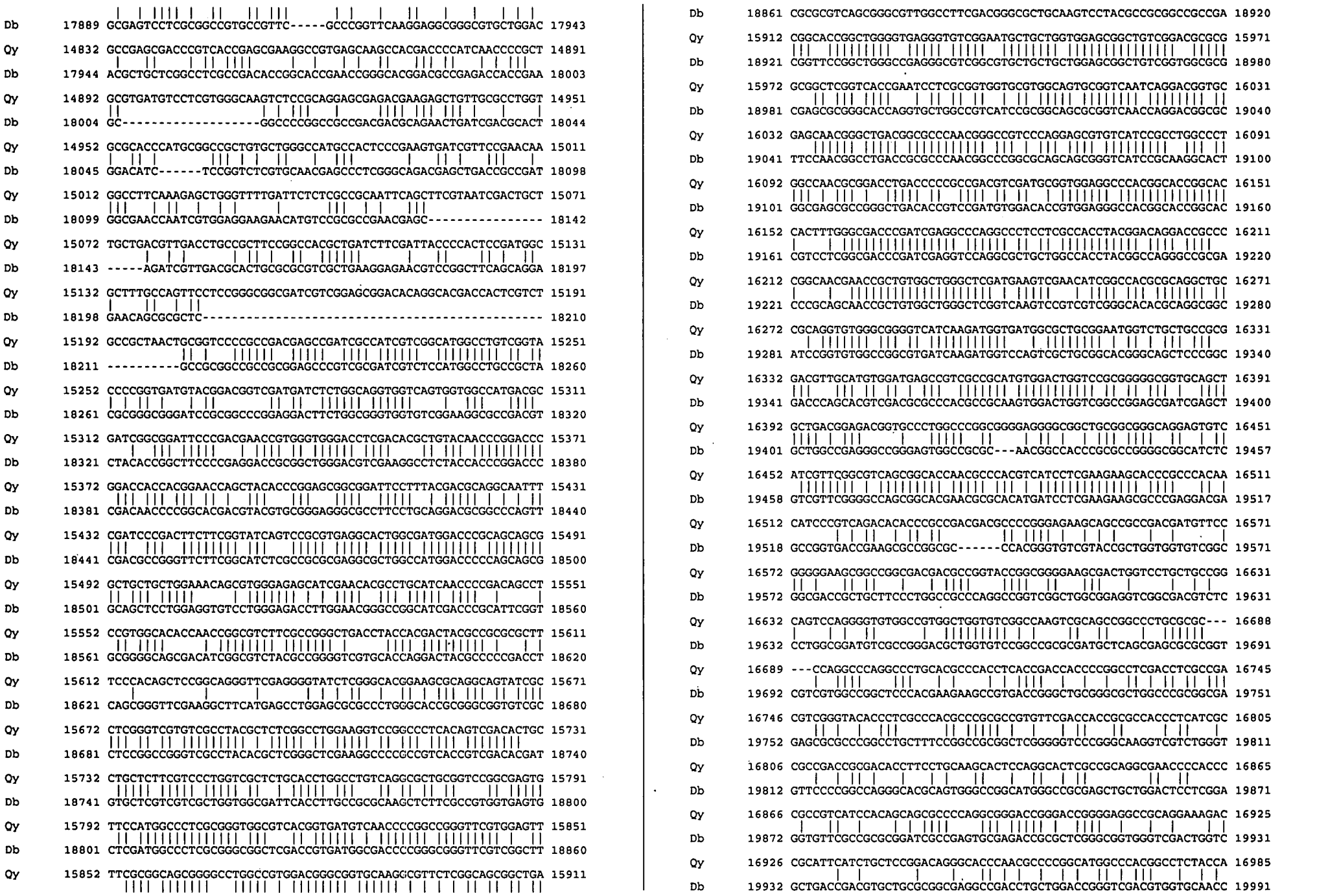


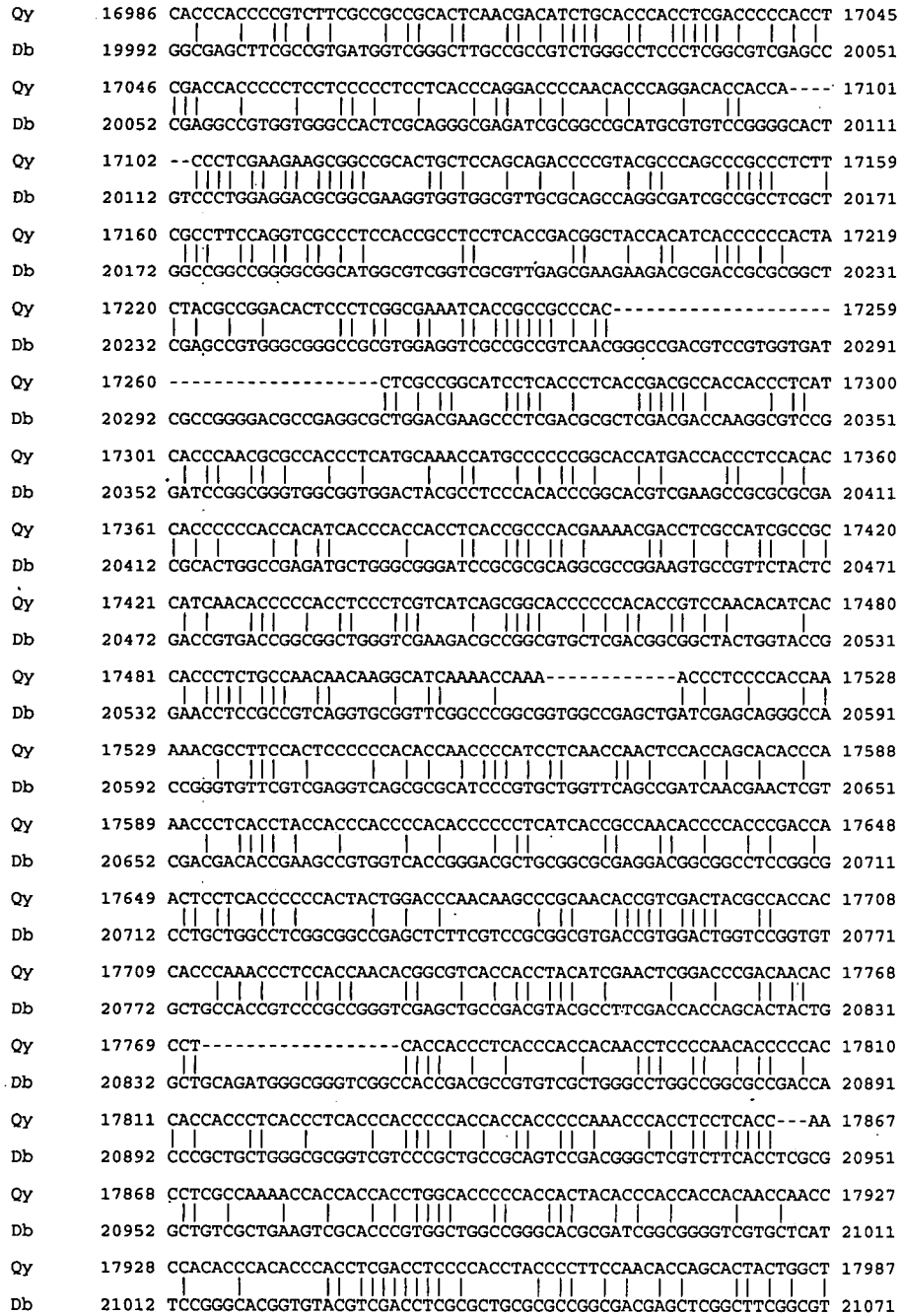


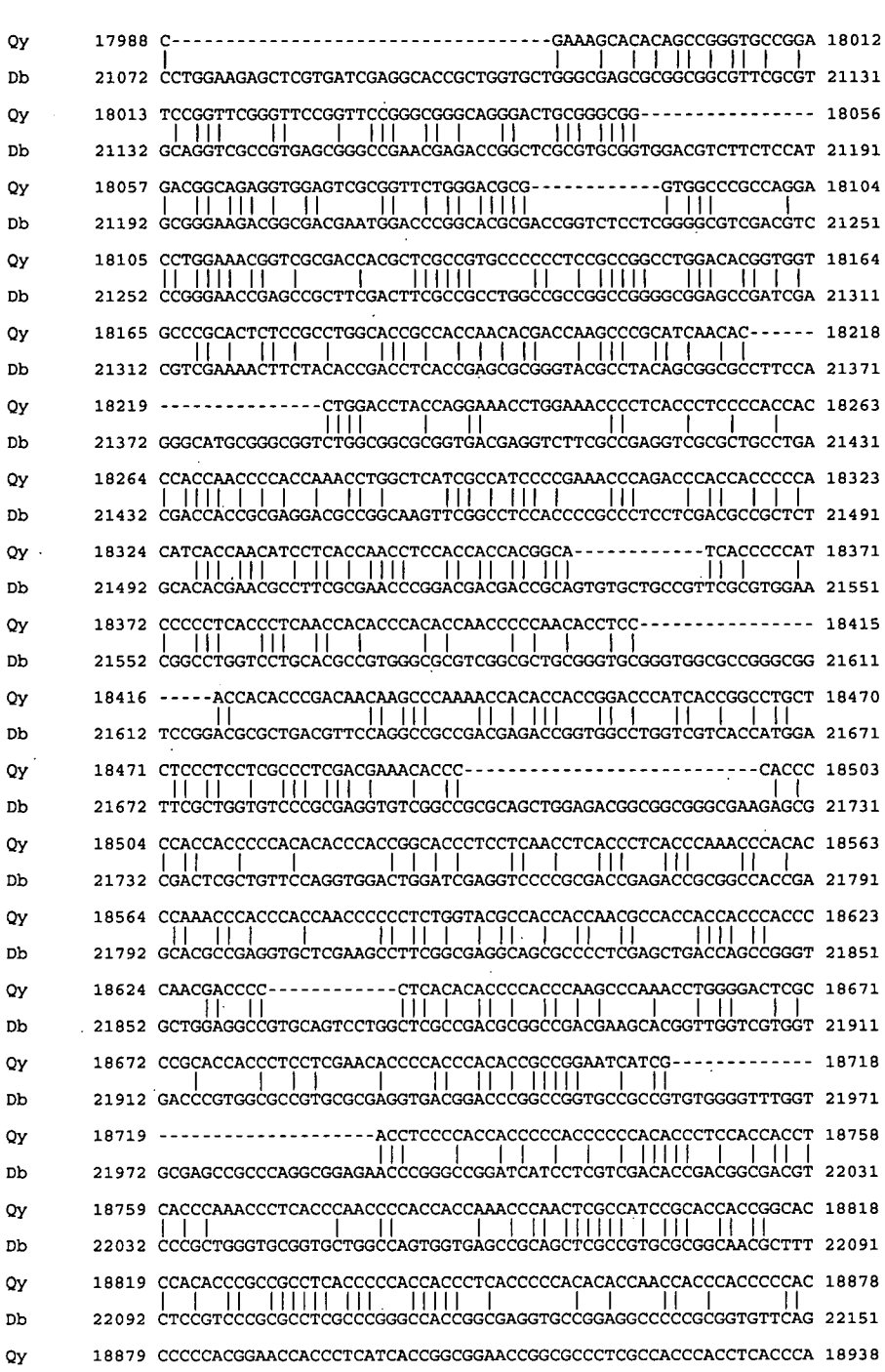


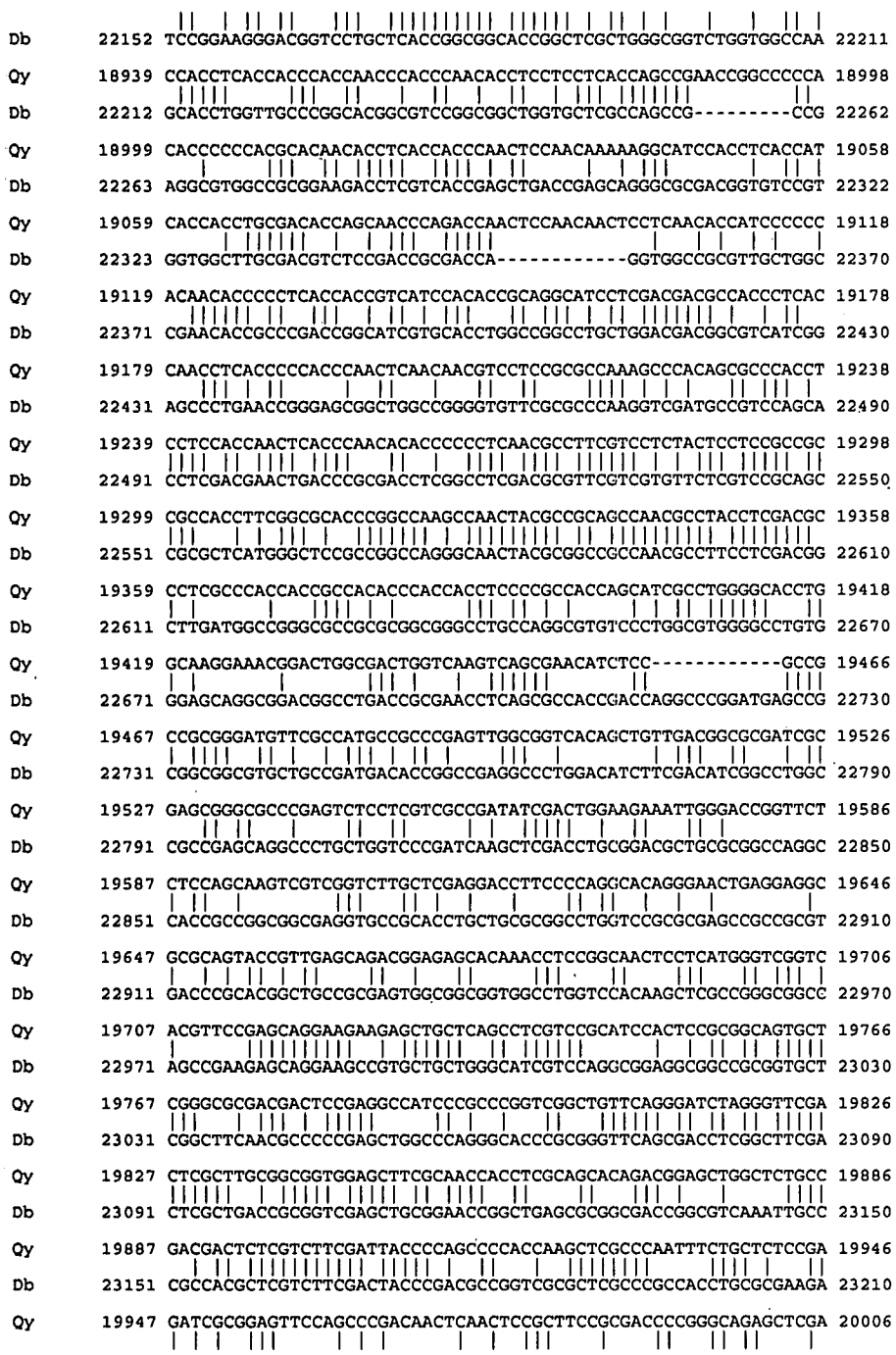


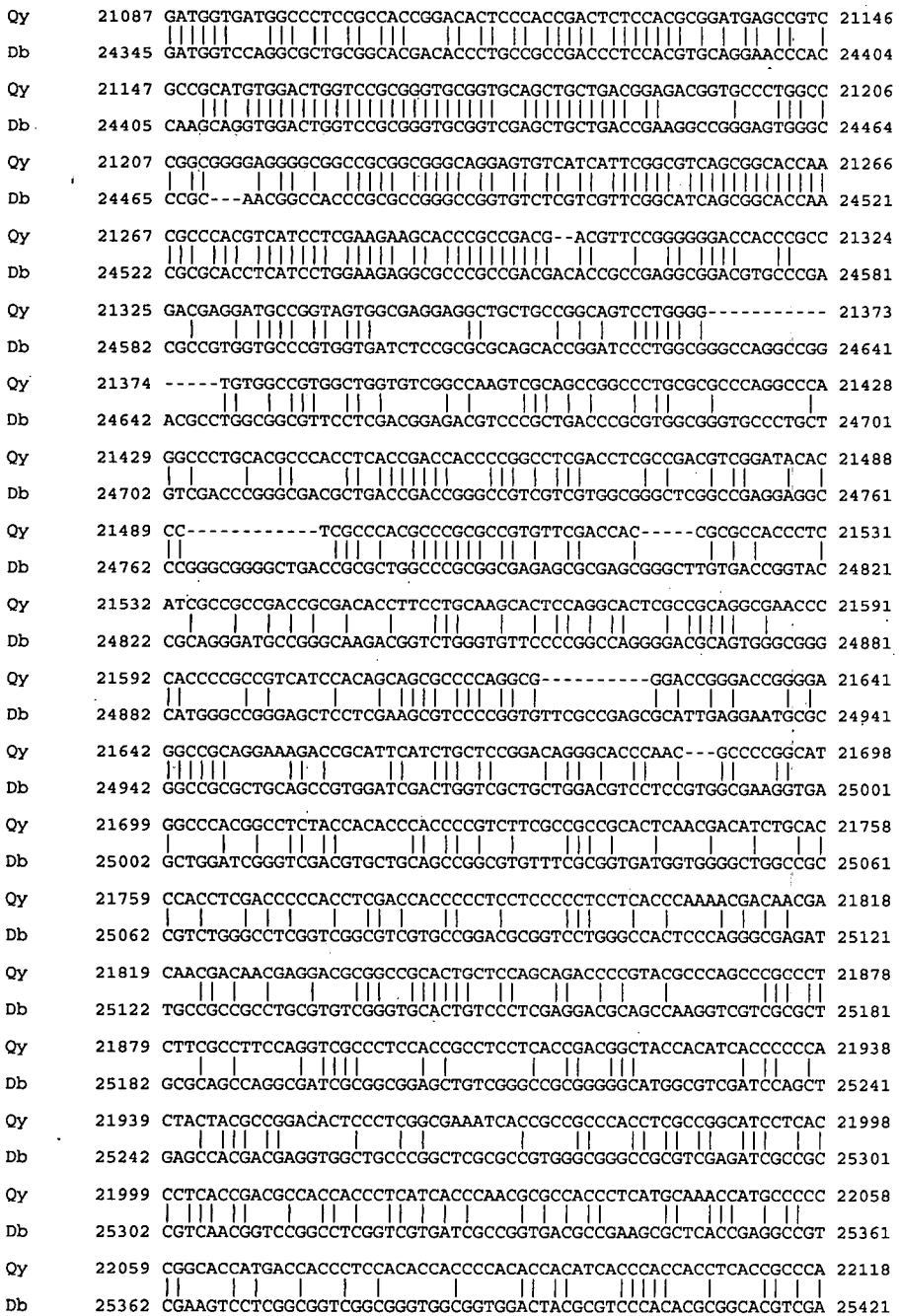


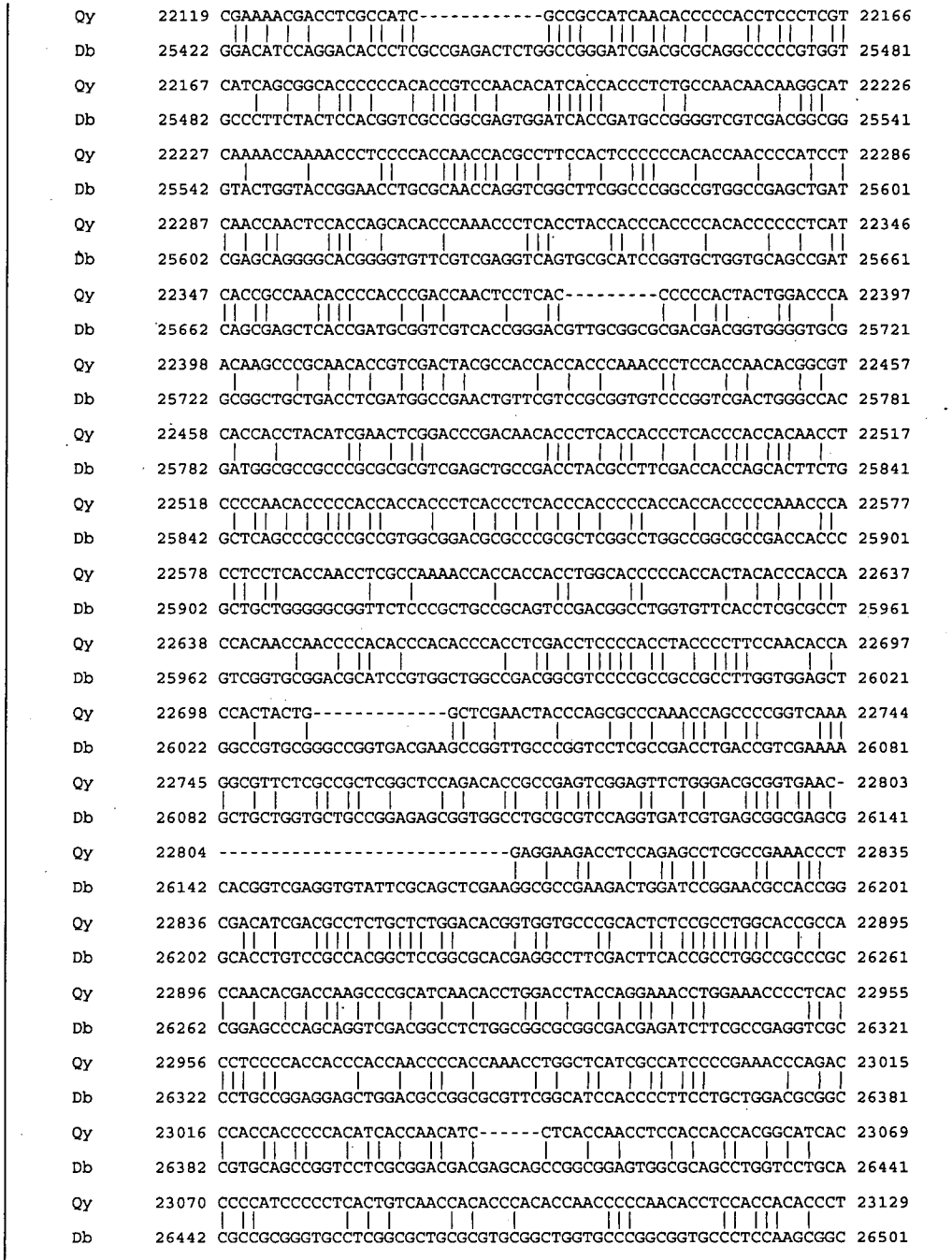


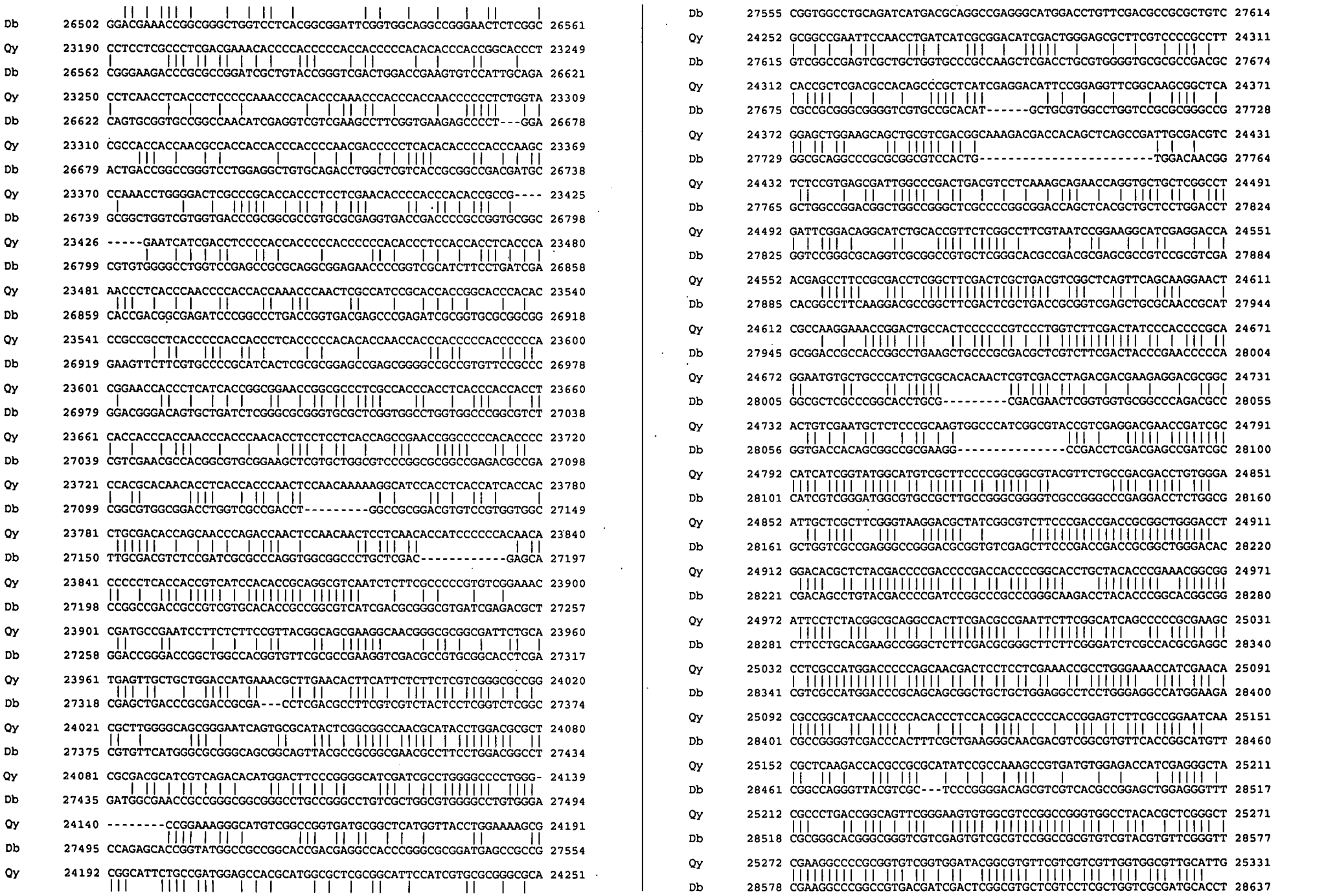


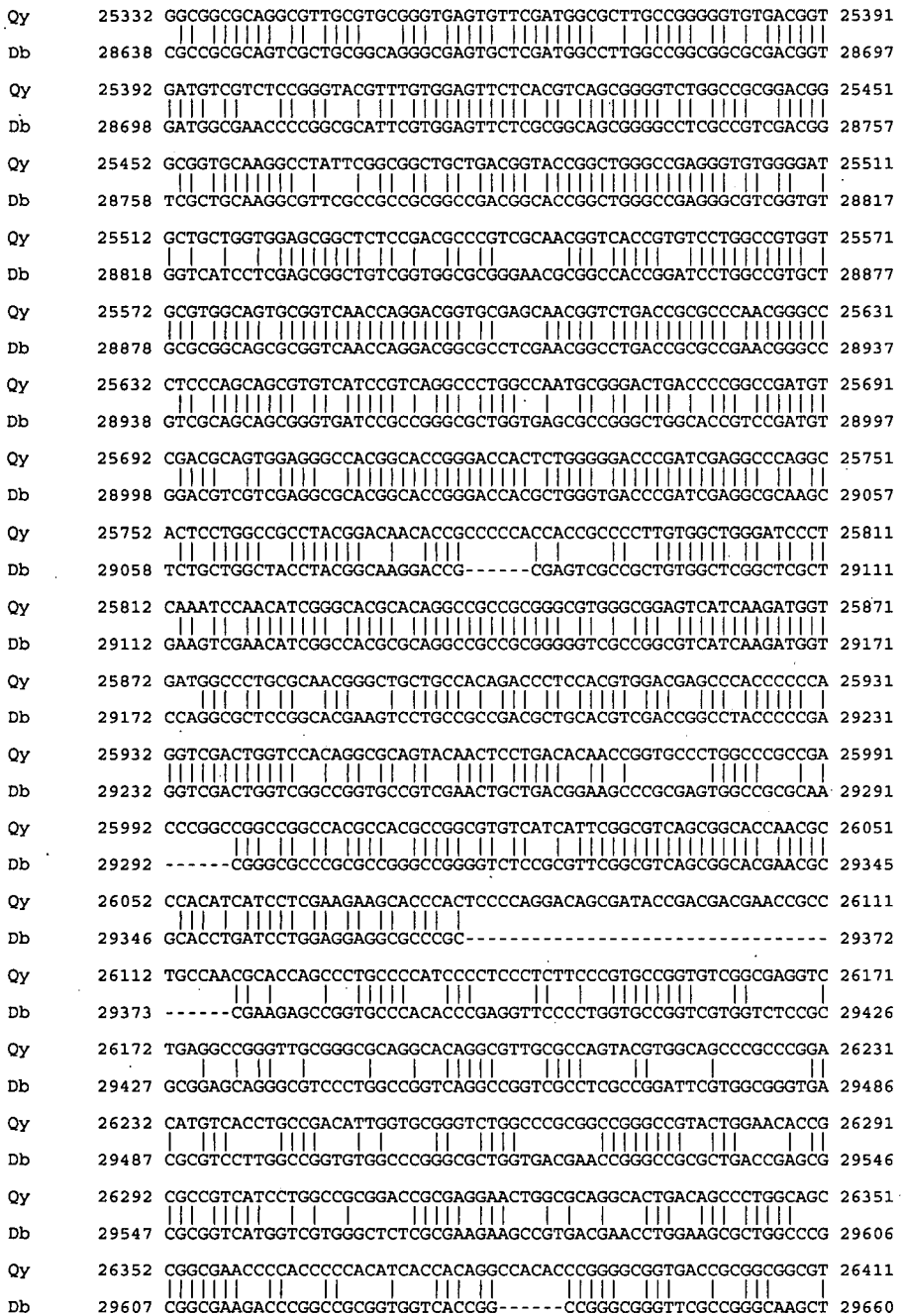


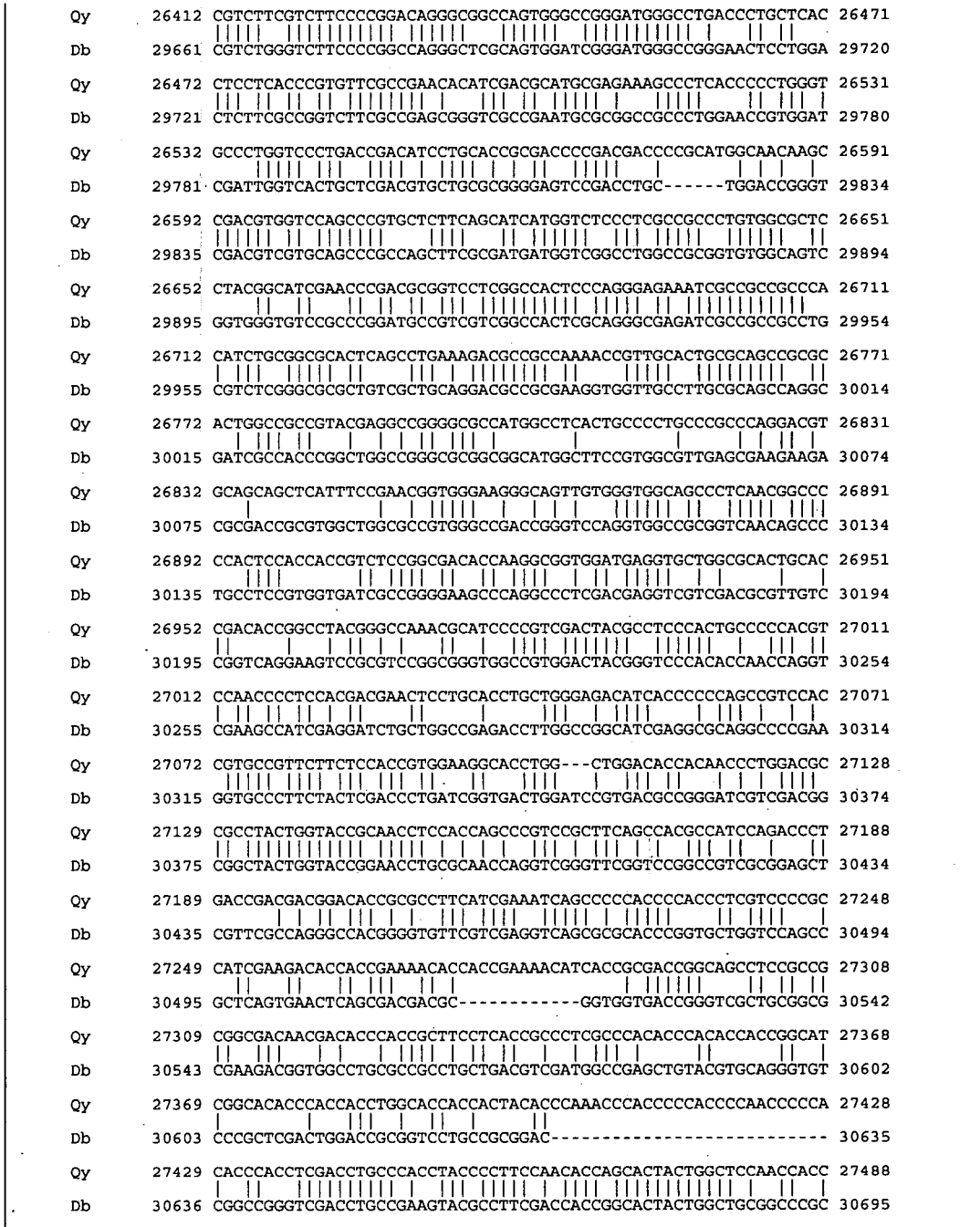

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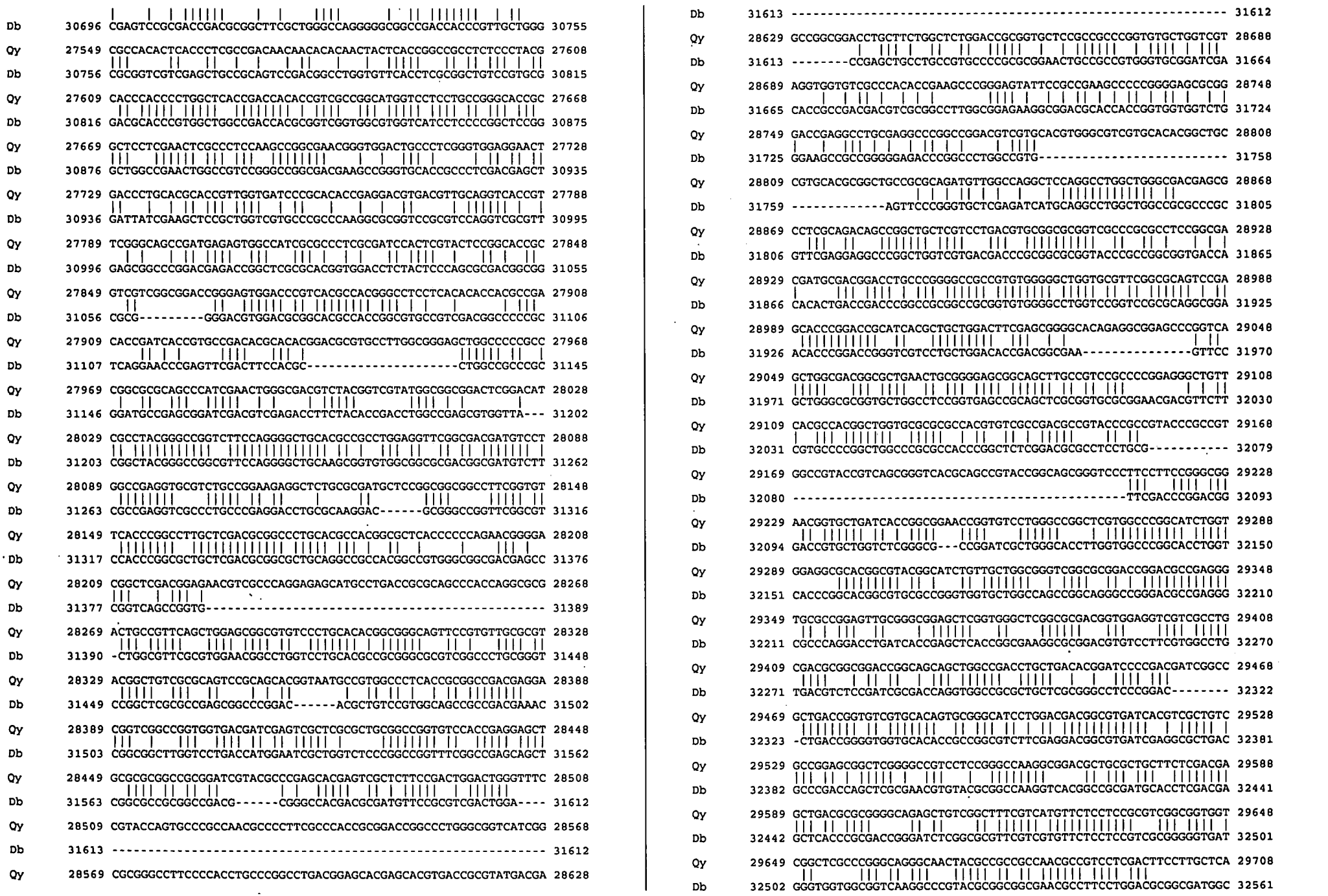












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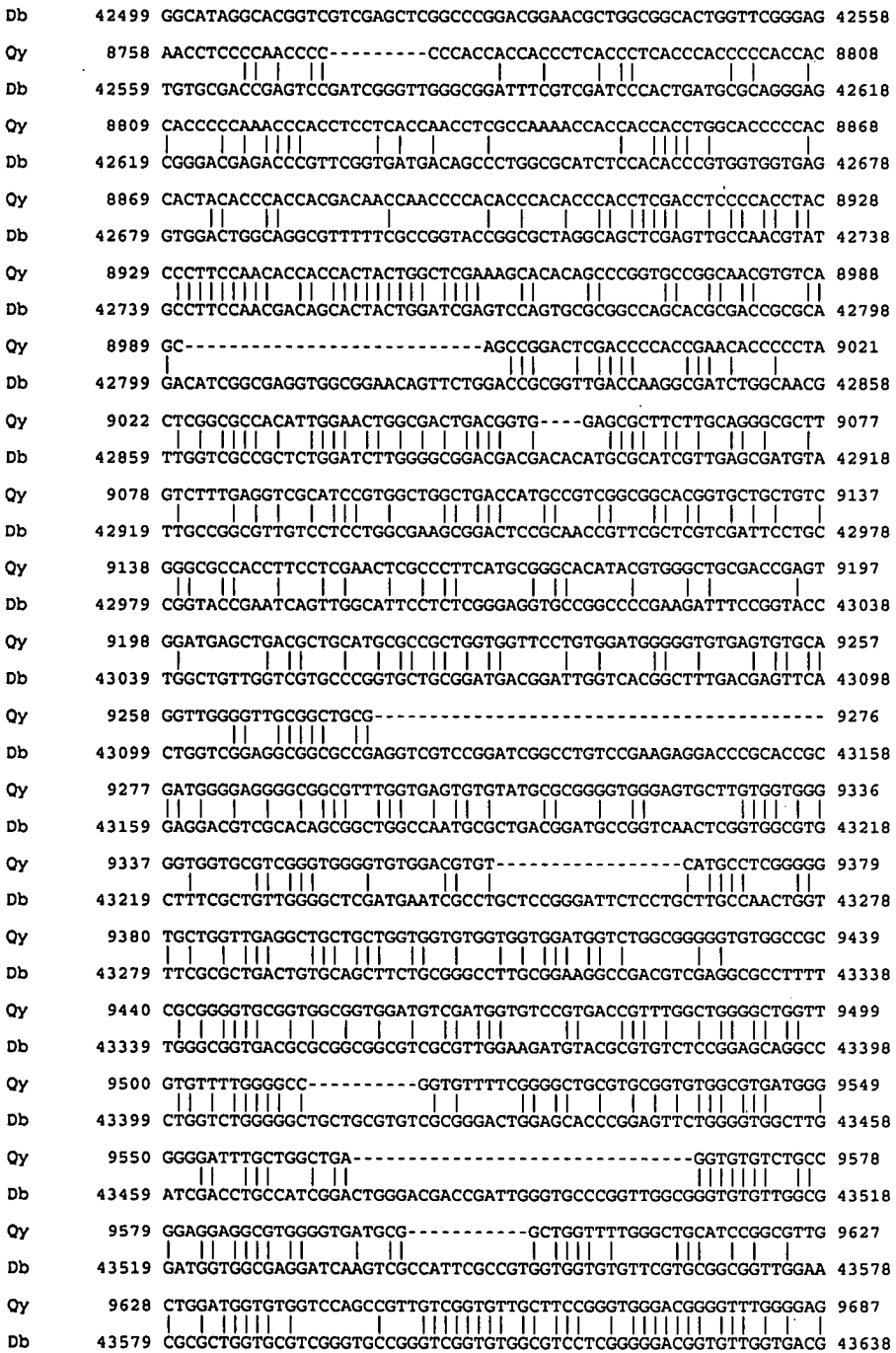
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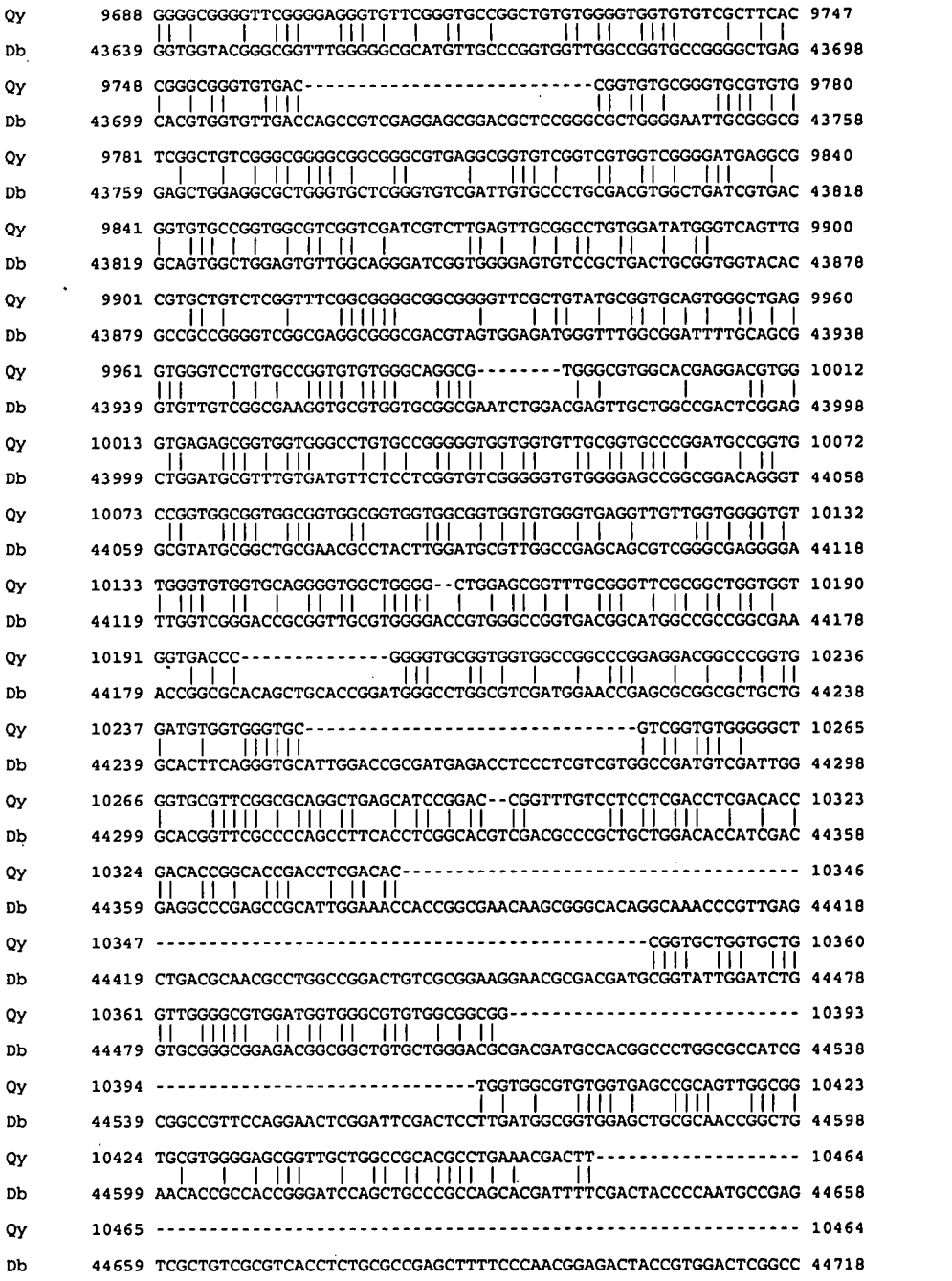
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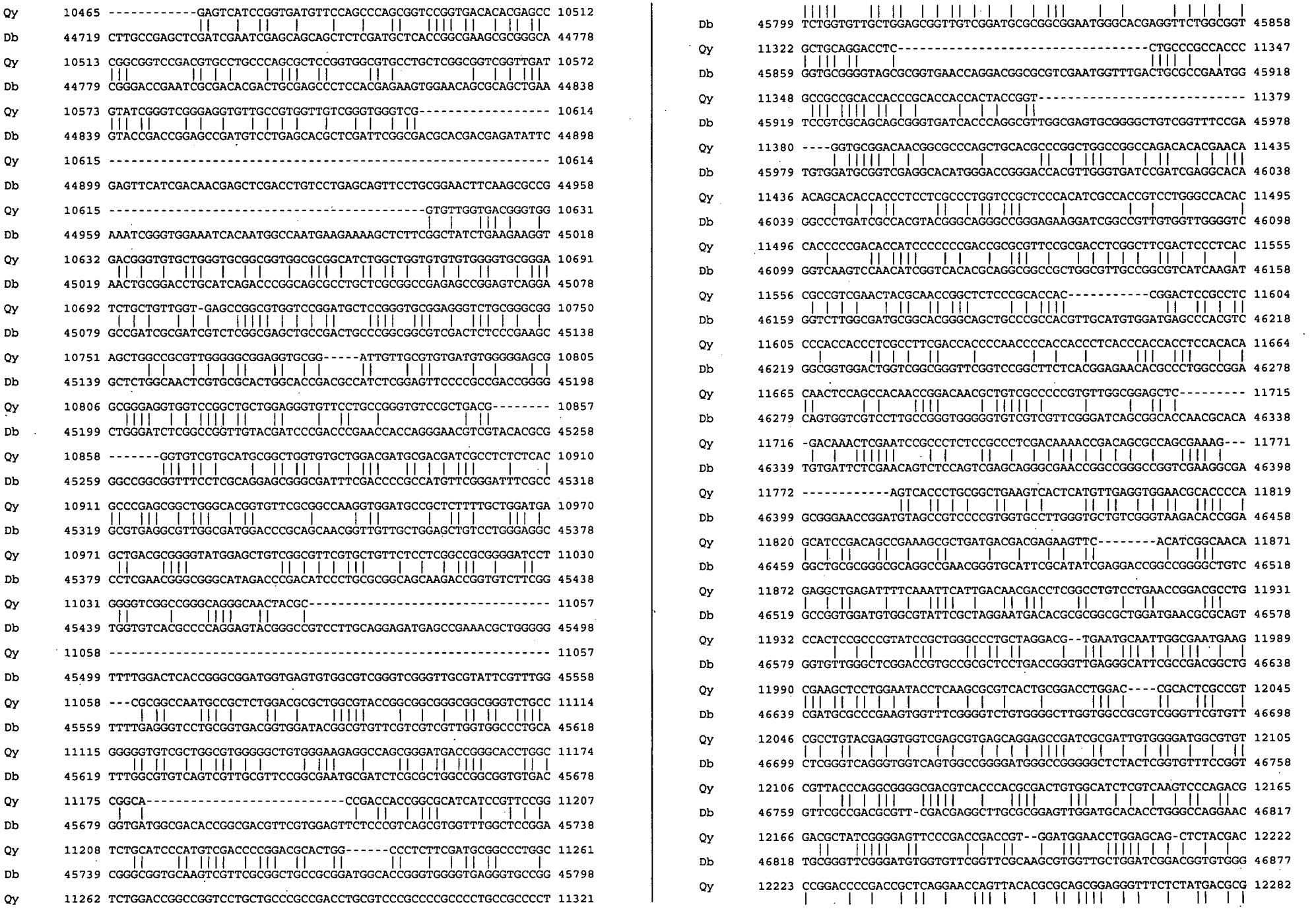
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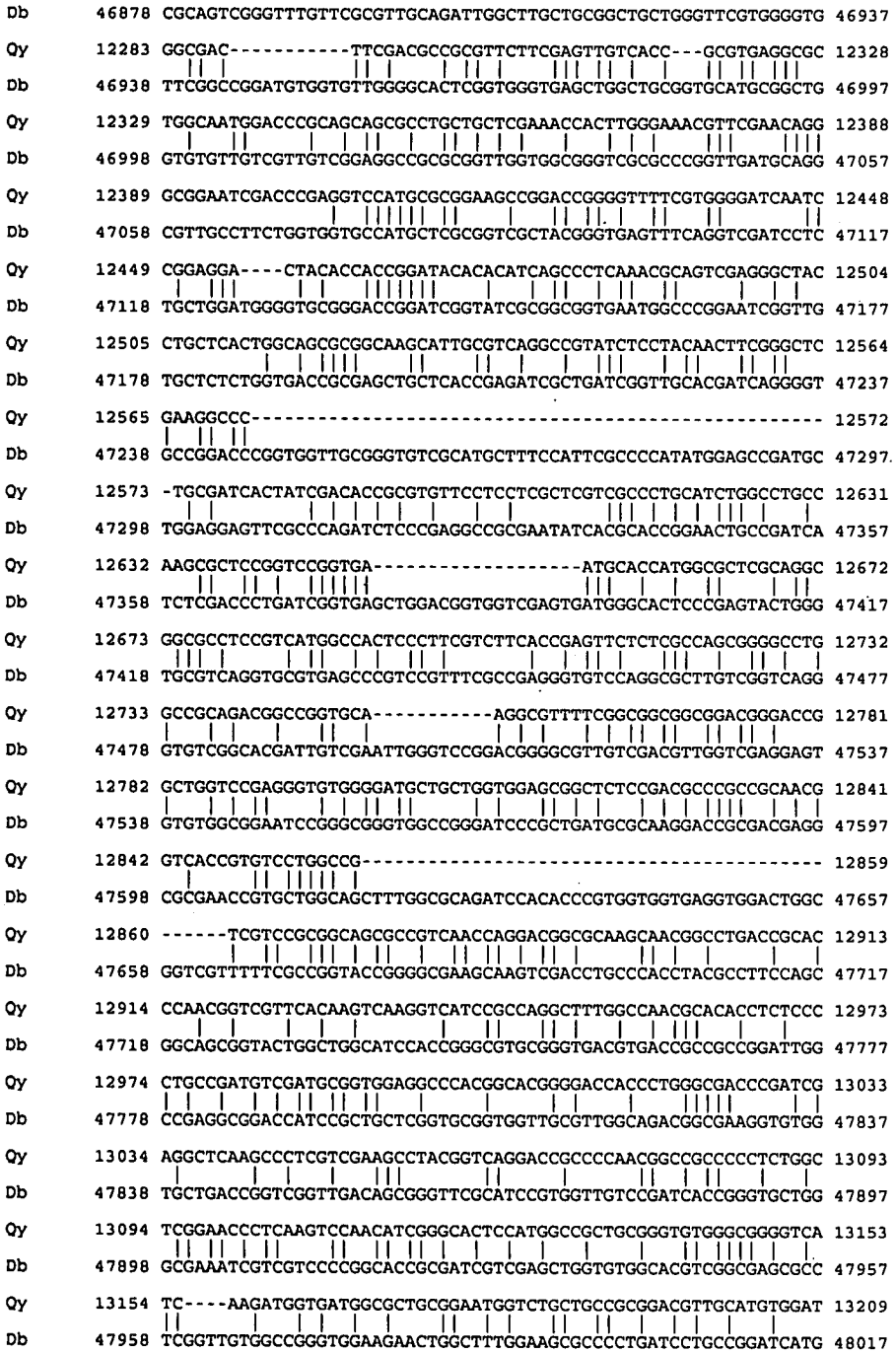
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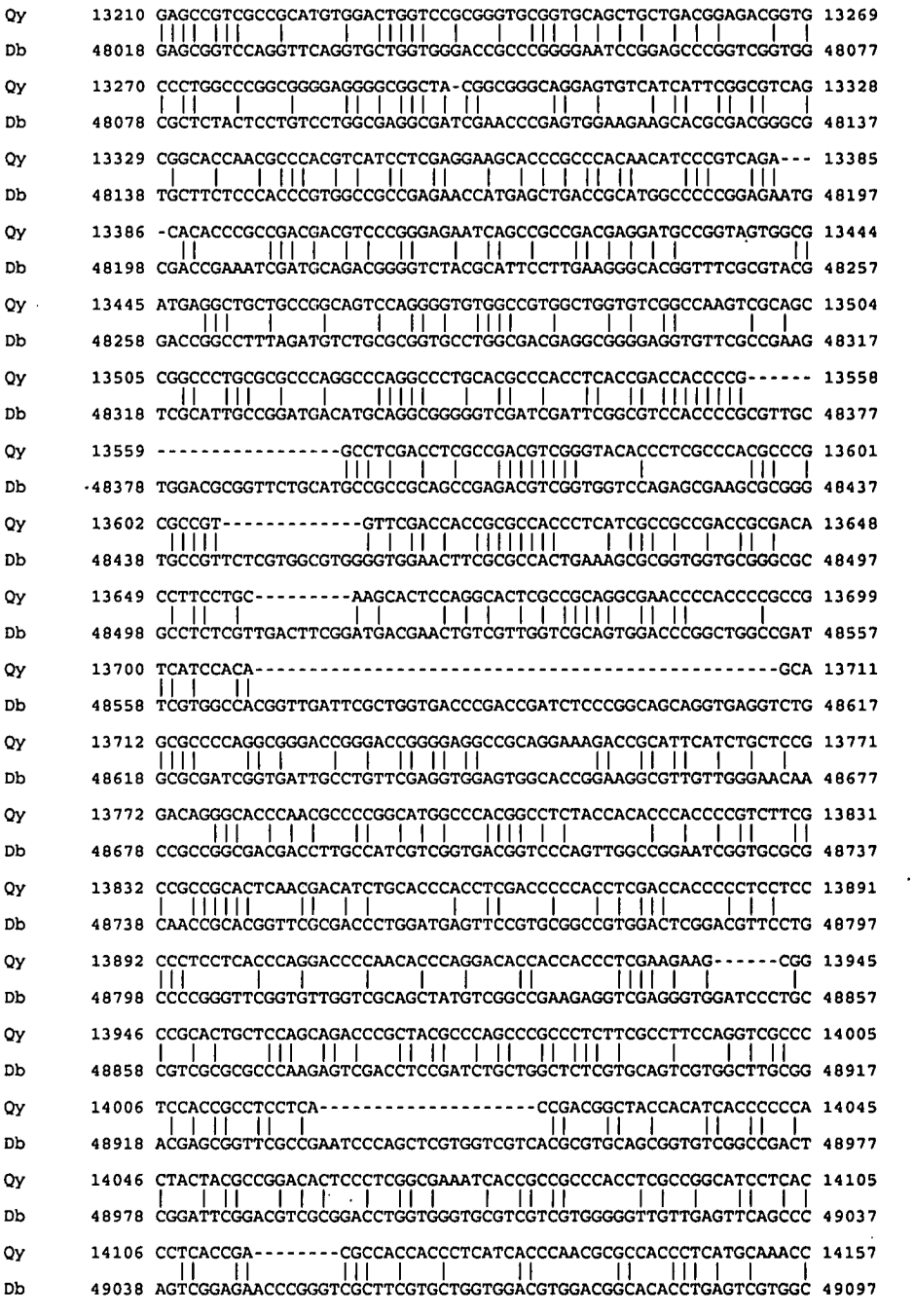
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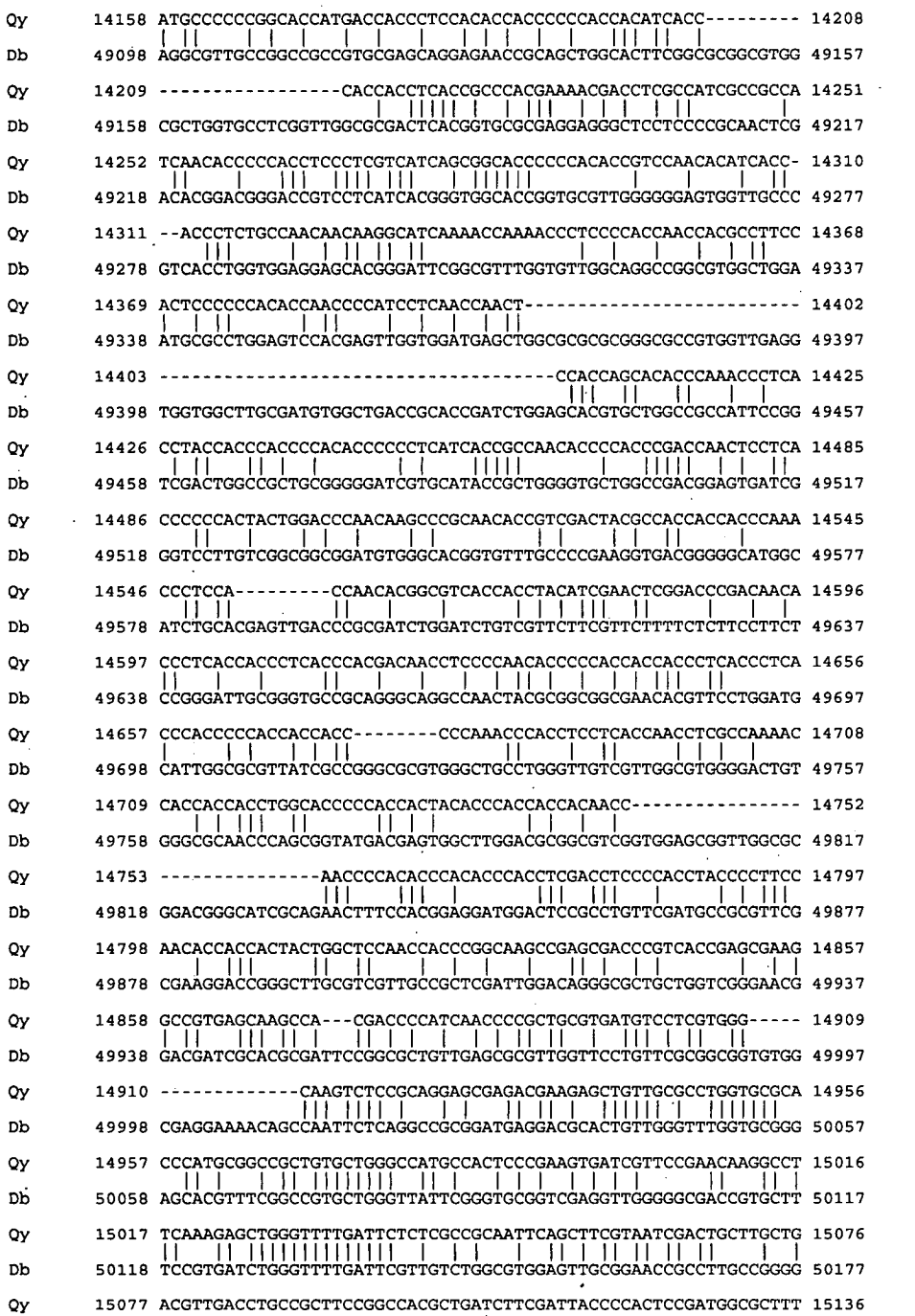


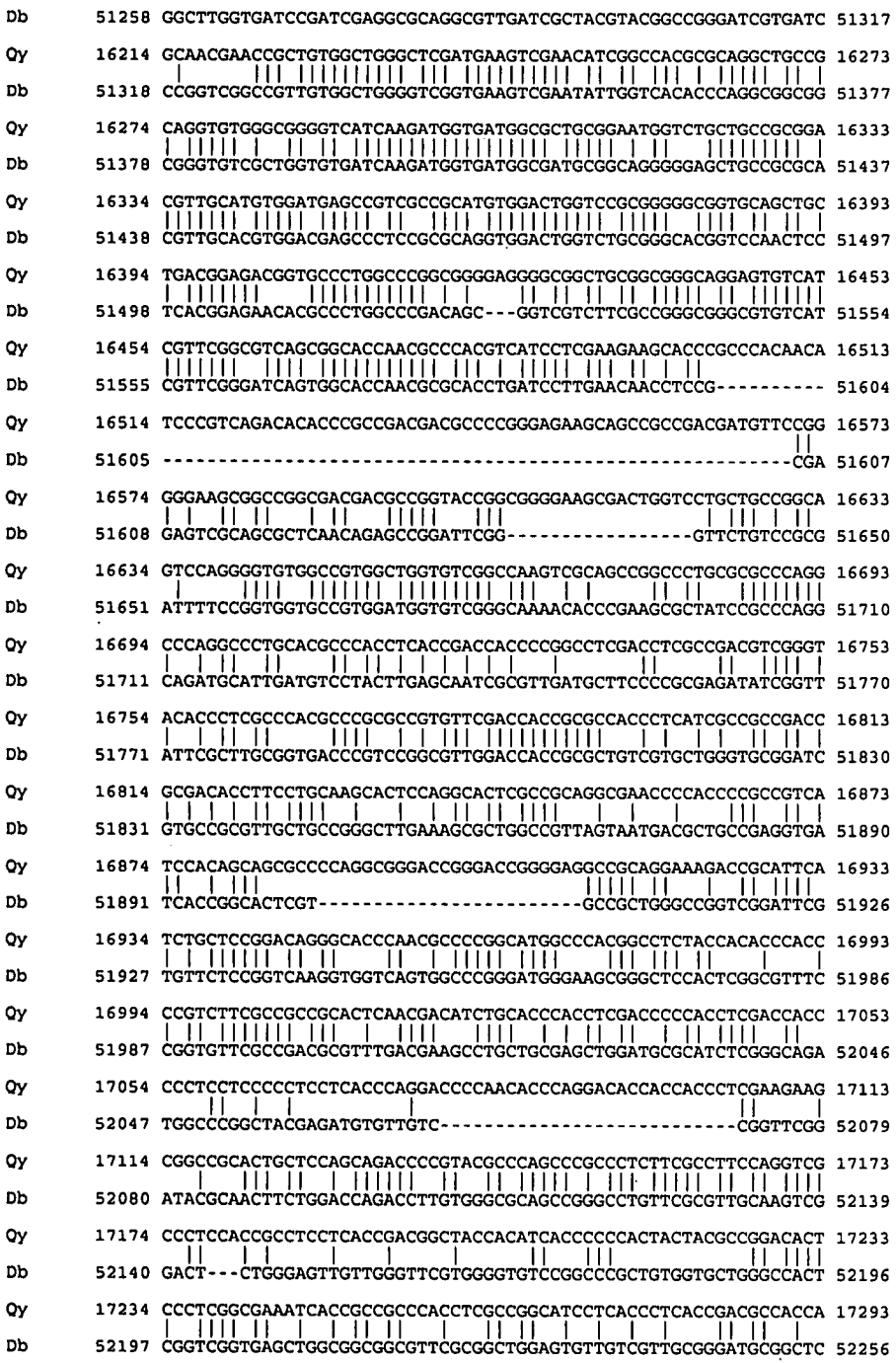


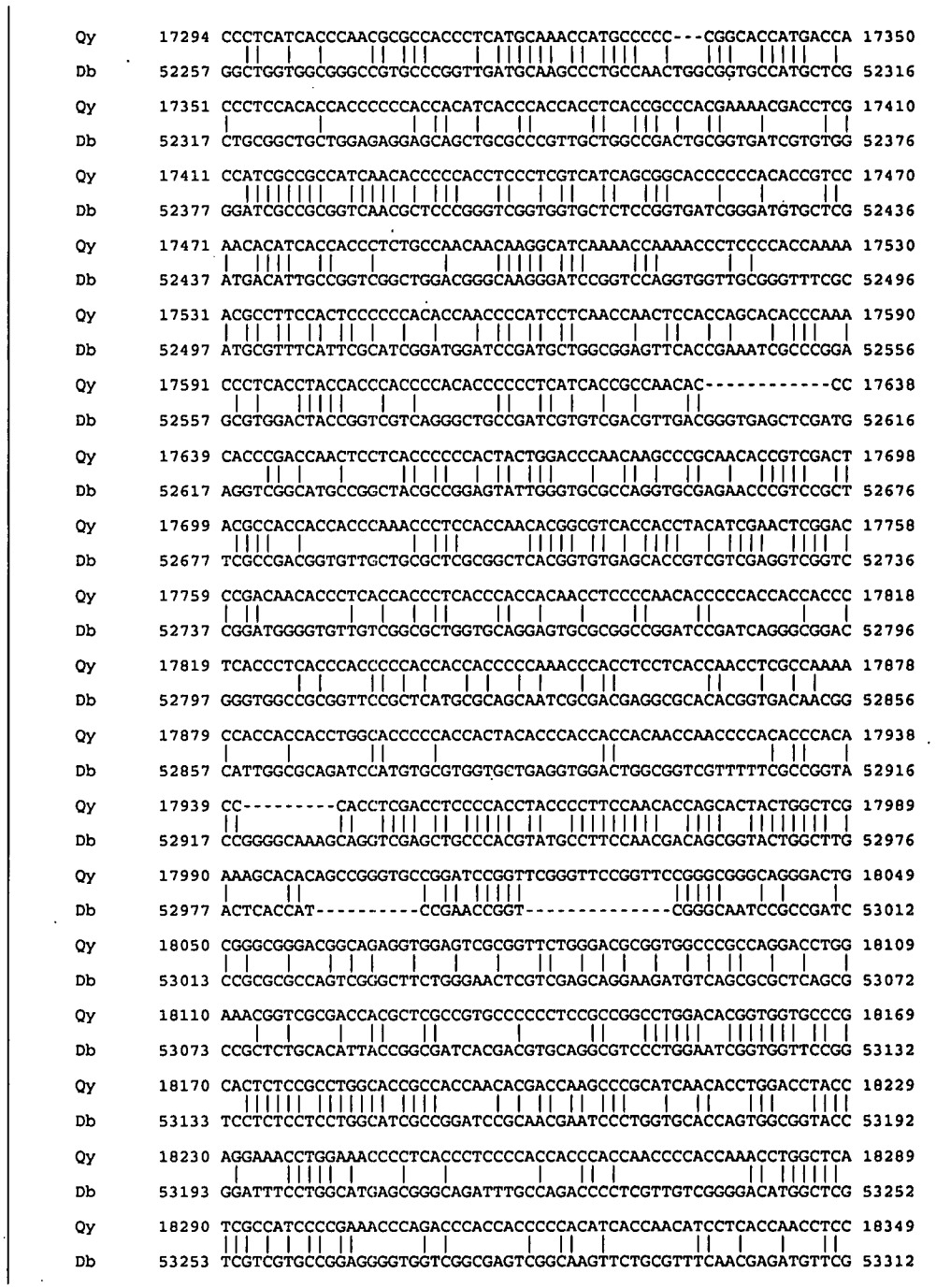


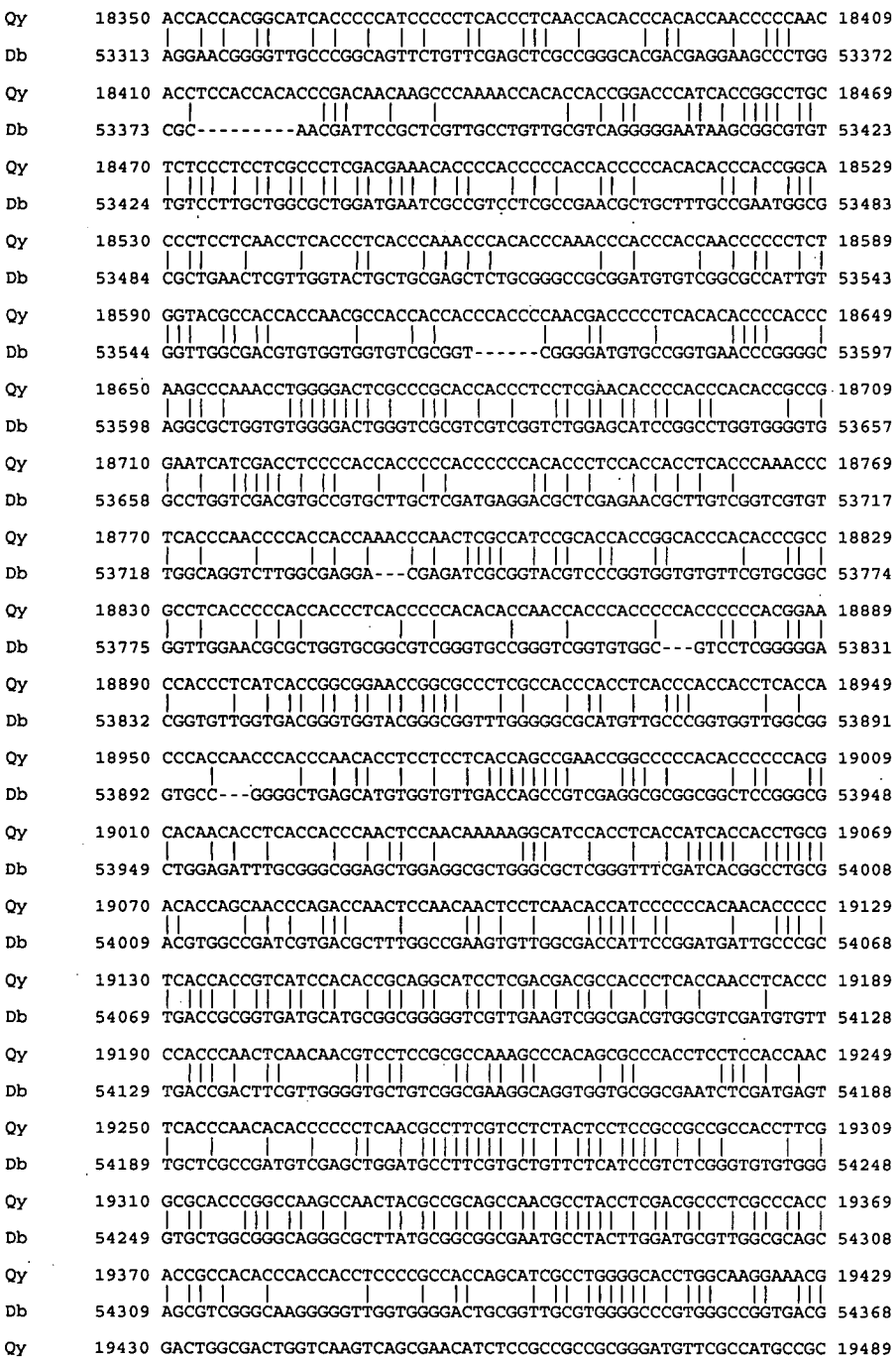


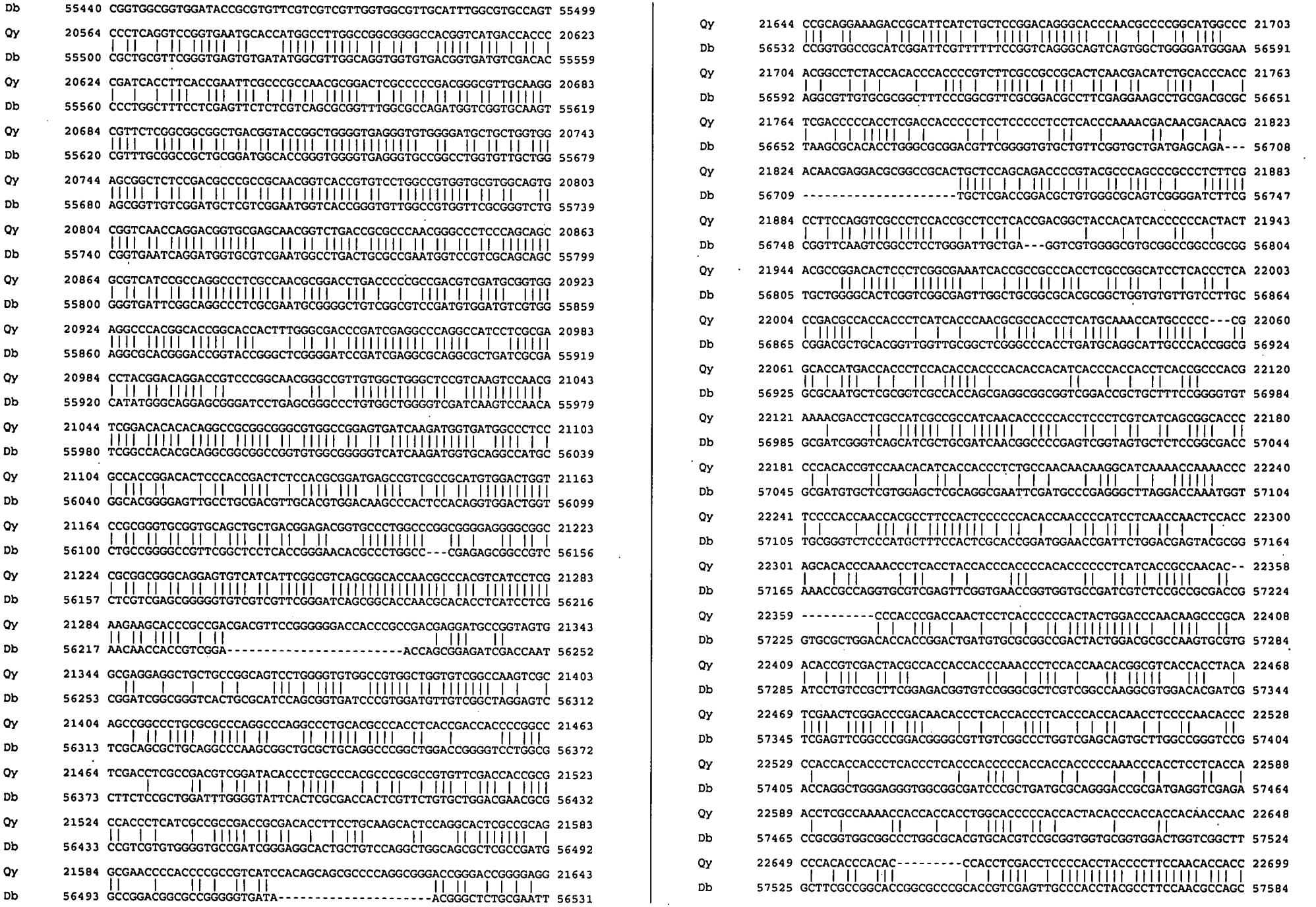


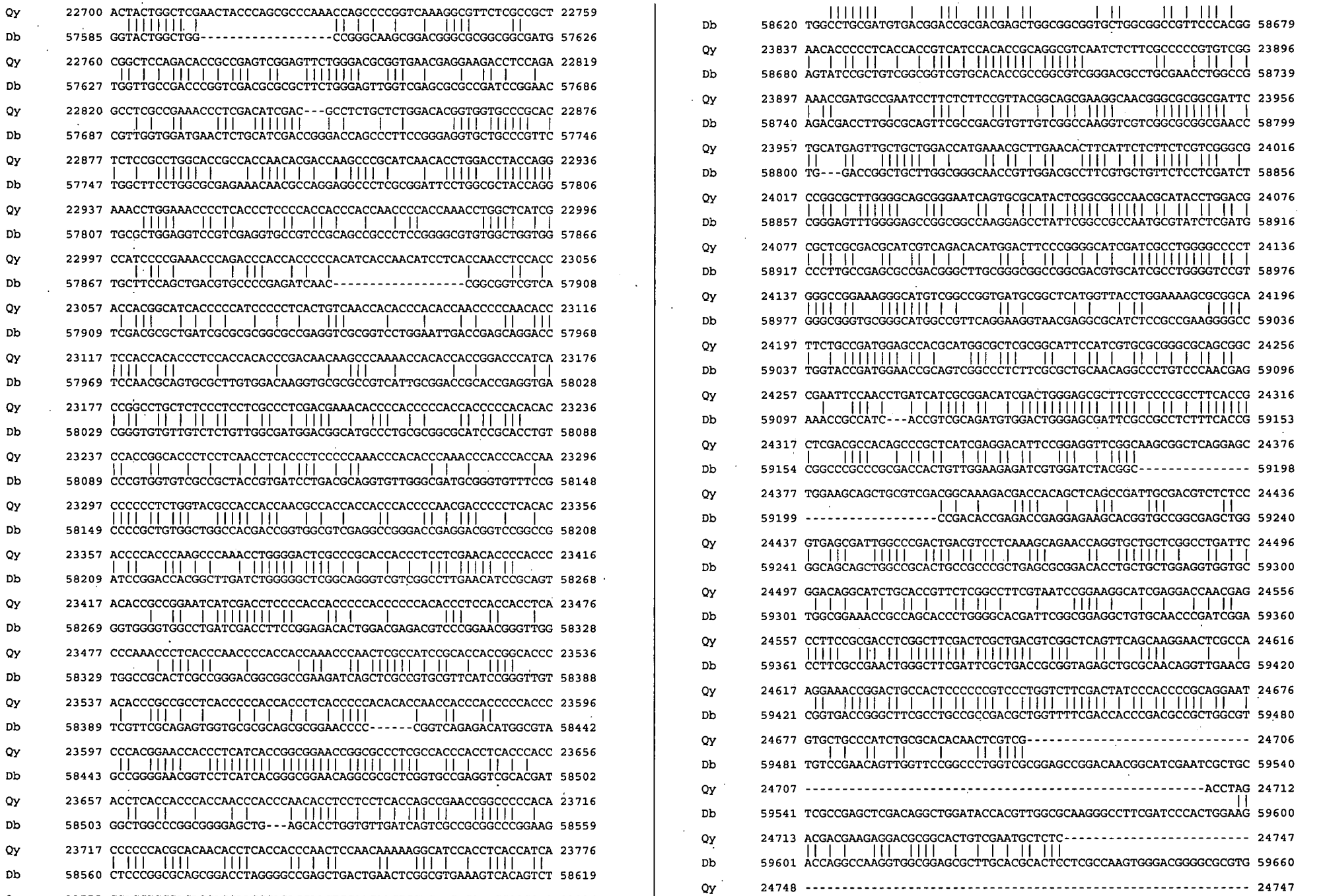

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	30690	100.0	30690	22	AAH79277	Streptomyces averm
2	30672.4	99.9	30690	21	AAA92301	S. avermitilis ave
3	11914.4	38.8	11916	22	AAH79279	Streptomyces averm
4	11548	37.6	12381	21	AAZ58381	Streptomyces averm
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6	6437.2	21.0	31422	22	AAH79278	Streptomyces averm
7	4347.6	14.2	125401	22	AAD17186	Streptomyces nours
8	3788.2	12.3	65140	22	AAD17184	Streptomyces nours
9	3443.4	11.2	27541	22	AAD17185	Streptomyces nours
10	3399.8	11.1	53789	19	AAV21187	Amycolatopsis medi
11	3194.8	10.4	49377	19	AAV05287	The soraphen biosy
12	3142	10.2	50000	22	AAF88313	S. spinosa DNA fra
13	3142	10.2	50000	22	AAF88316	S. spinosa DNA fra
14	3142	10.2	80161	20	AAZ21501	DNA fragment of Sa
15	3140.6	10.2	28958	18	AAT89956	Sorangium cellulos
16	3140.6	10.2	28958	21	AAA75299	DNA sequence of So
17	3071.8	10.0	28598	17	AAT06769	Sorangium cellulos
18	2956.6	9.6	38506	21	AAA75633	Nucleotide sequenc
19	2956.6	9.6	38506	21	AAZ56001	Recombinant cosmid
20	2951.8	9.6	37948	21	AAZ87285	S. venezuelae pik
21	2951.4	9.6	36778	21	AAZ87318	S. venezuelae pik
22	2939.8	9.6	43280	18	AAT80413	Tylactone synthase
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24	2663	8.7	44377	18	AAT78508	Platenolide syntha
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c 26	2545	8.3	77536	21	AAA14651	Nucleotide sequenc
27	2340	7.6	13842	21	AAZ87297	S. venezuelae macr
28	2304.2	7.5	50937	21	AAA09469	Streptococcus olea
29	2270	7.4	29879	14	AAQ46806	eryA region of S.
30	2188.4	7.1	15872	21	AAZ87283	S. venezuelae vep
31	2180.4	7.1	15872	18	AAT68715	Streptomyces venez
32	2179.4	7.1	47981	22	AAF30757	Micromonospora meg
33	2140.6	7.0	11220	21	AAZ87298	S. venezuelae macr
34	2000.8	6.5	77536	21	AAA14651	Nucleotide sequenc
35	1854.8	6.0	9513	22	AAF88337	S. spinosa DNA fra
36	1852.8	6.0	13987	18	AAT80415	Hybrid srmG/tylG O
37	1800.8	5.9	33529	23	AAS17367	DNA sequence of S.
38	1706.4	5.6	14775	22	AAF88338	S. spinosa DNA fra
39	1698	5.5	16767	22	AAF88339	S. spinosa DNA fra
40	1071	3.5	12249	21	AAC55840	Complete Mitomycin
41	1071	3.5	18331	21	AAC55857	Complete nucleotid
42	1010.2	3.3	3978	21	AAC55785	Type I polyketide
43	1007	3.3	71989	21	AAA29349	Sorangium cellulos
44	1004.4	3.3	4041	21	AAZ87300	S. venezuelae macr
45	1004.4	3.3	4818	21	AAA14669	Nucleotide sequenc

ALIGNMENTS

RESULT 1
AAH79277
ID AAH79277 standard; DNA; 30690 BP.
XX
AC AAH79277;
XX
DT 04-DEC-2001 (first entry)
XX
DE Streptomyces avermitilis coding sequences SEQ ID NO: 1.
XX
KW Avermectin aglycone synthase; AAS; avermectin derivative;
KW drug production; vetinary drug; pesticide; ds.
XX
OS Streptomyces avermitilis.
XX
FH Key Location/Qualifiers
FT CDS 1..11919
FT /*tag= a
FT /product= "AAG65264"
FT /partial
FT CDS 11971..30690
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XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-JP01381.
XX
PR 24-FEB-2000; 2000JP-0047405.
XX

PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (KITA) KITASATO INST.
XX
PI Endo H, Yamaguchi H, Kanda Y, Hashimoto S, Omura S, Ikeda H;
XX
DR WPI; 2001-582053/65.
DR P-PSDB; AAG65264, AAG65265.
XX
PT New modified avermectin aglycone synthase derived from Streptomyces
PT avermectilis used in production of 22,23-dihydroavermectin B1a used in
PT drugs and pesticides -
XX
PS Example 2; Page 58-123; 257pp; Japanese.
XX
CC The present invention relates to the production of modified derivatives
CC of avermectin aglycone synthase (AAS) derived from Streptomyces
CC avermitilis. The activity of an acyl carrier protein (ACP),
CC beta-ketoacyl carrier protein synthase (KS), acyltransferase (AT),
CC beta-ketoacyl carrier protein reductase (KR), dehydratase (DH), enoyl
CC reductase (ER) and/or thioesterase (TE) domain may be reduced or
CC suppressed. The process can be used in the production of drugs, vetinary
CC drugs and pesticides. The present sequence is a fragment of the S.
CC avermitilis genome.
XX
SQ Sequence 30690 BP; 5355 A; 12455 C; 8617 G; 4263 T; 0 other;

Query Match 100.0%; Score 30690; DB 22; Length 30690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 30690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 GGCATGGGAAGGGAACTTCTCGACGCTTCCGACGTCTTCCGGGAGAGCGTCCGCGCCTGC 180
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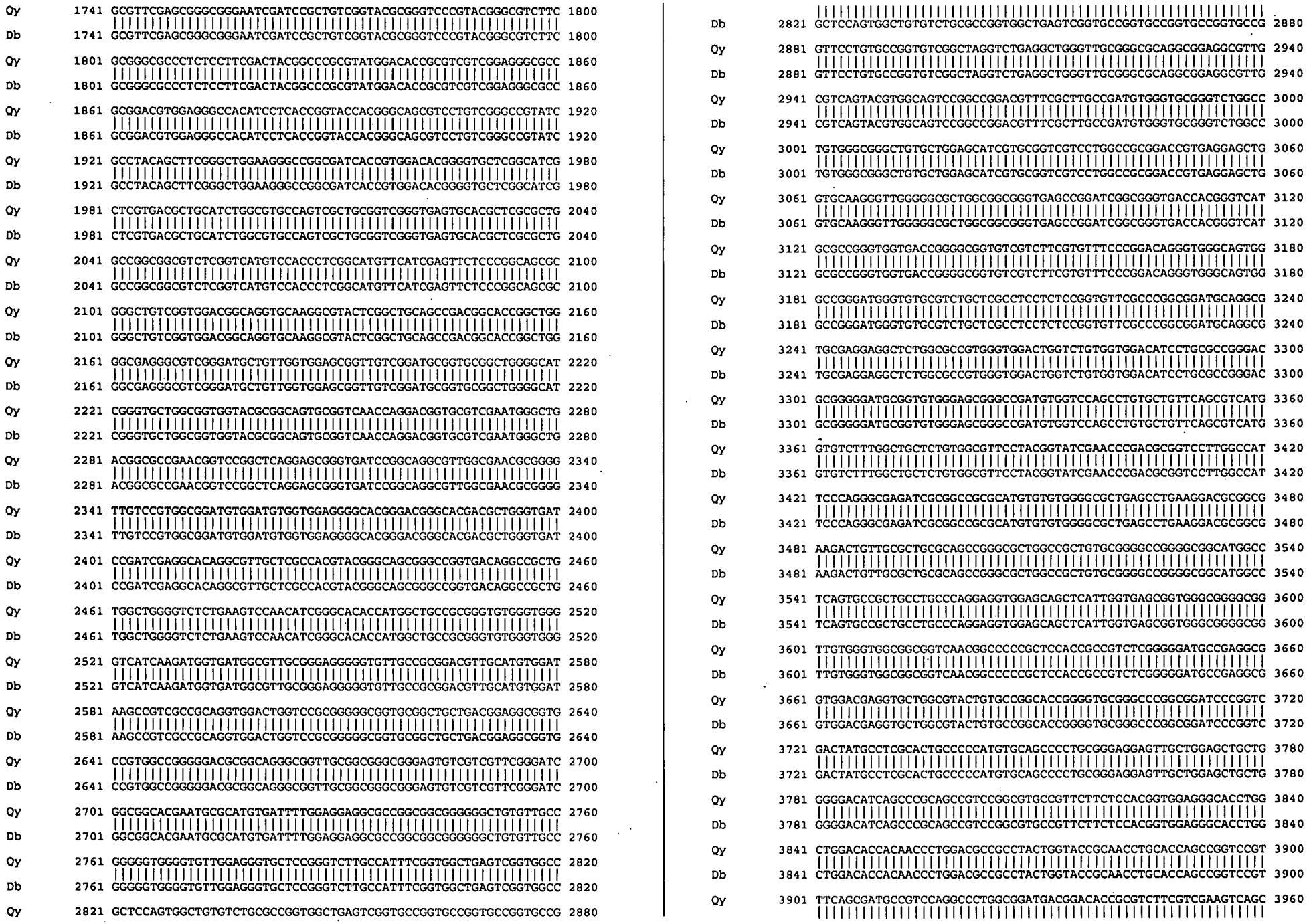
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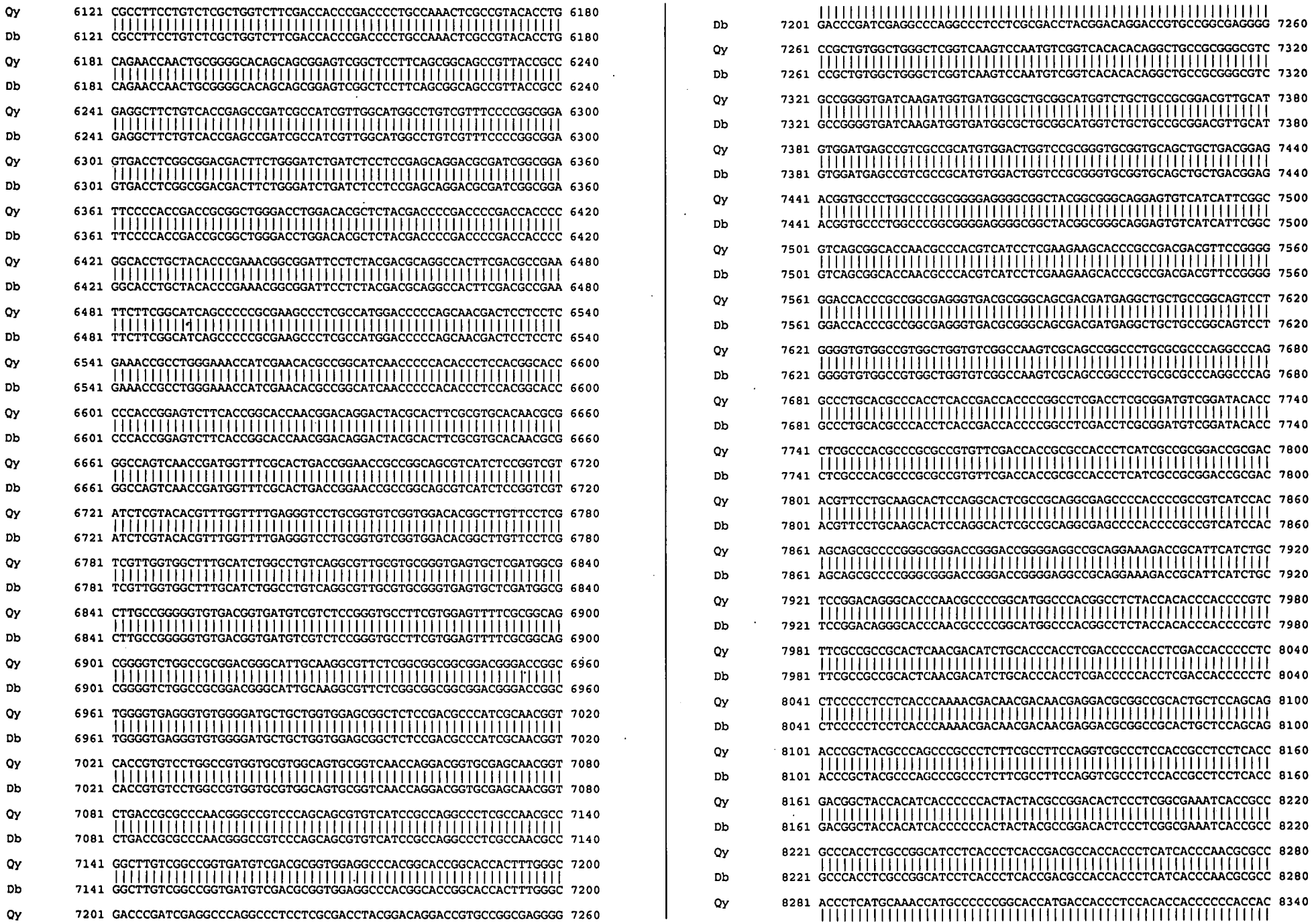
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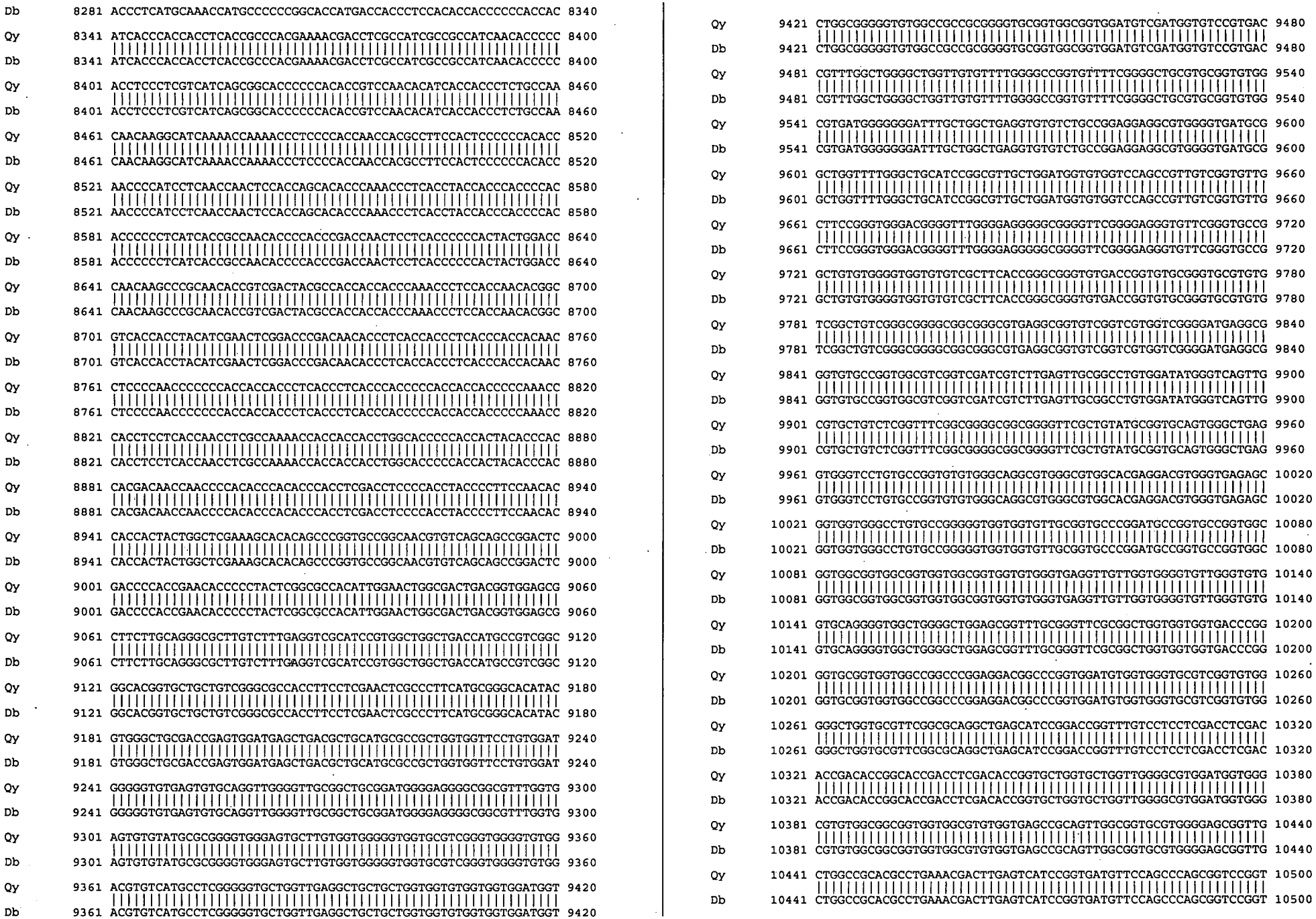
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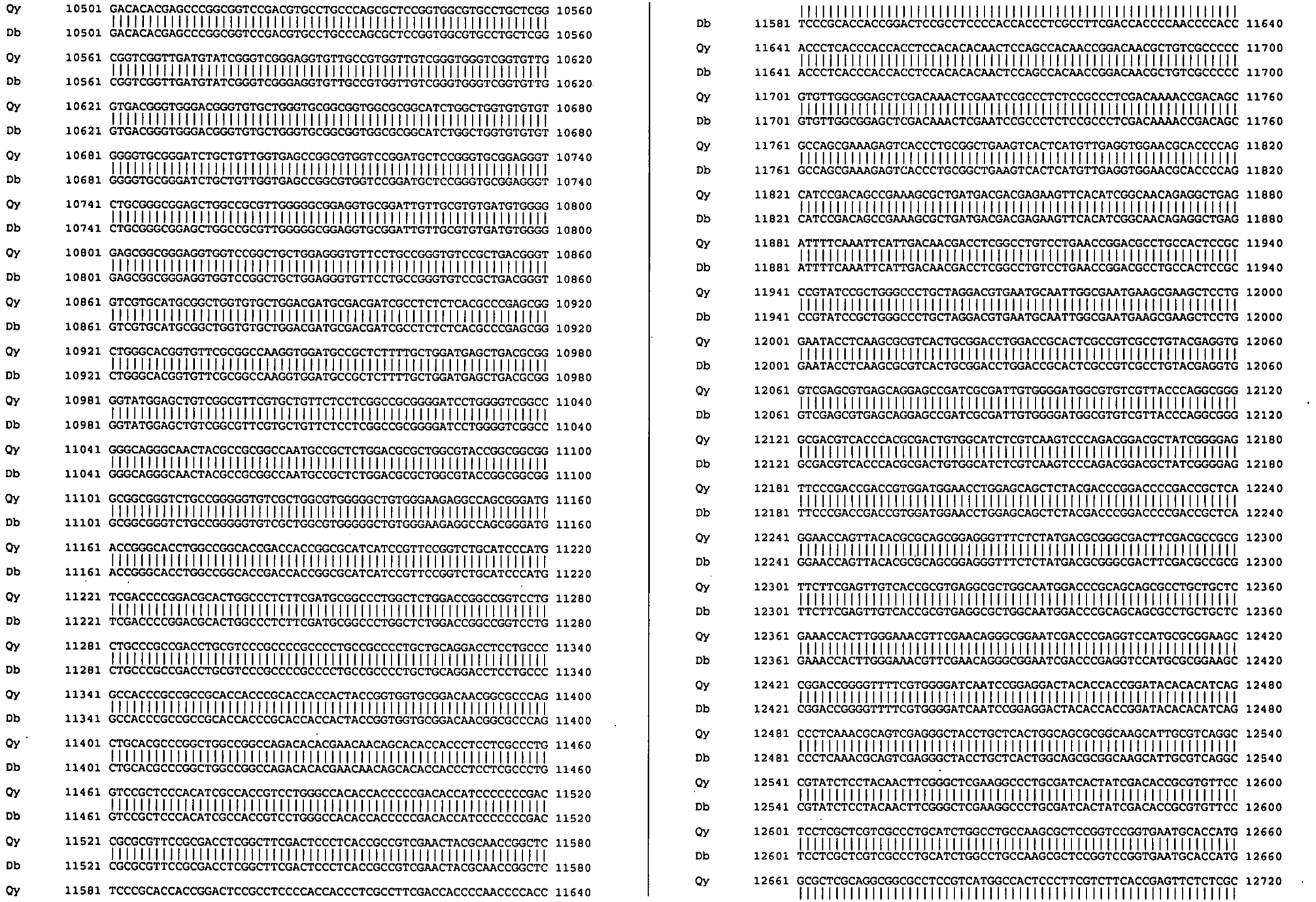
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Db      13261 GAGACGGTGCCCTGGCCCGGCGGGGAGGGGCGGCTACGGCGGGCAGGAGTGTCATCATTC 13320

Qy      13321 GGCGTCAGCGGCACCAACGCCCACGTCATCCTCGAGGAAGCACCCGCCCACAACATCCCG 13380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13321 GGCGTCAGCGGCACCAACGCCCACGTCATCCTCGAGGAAGCACCCGCCCACAACATCCCG 13380

Qy      13381 TCAGACACACCCGCCGACGACGTCCCGGGAGAATCAGCCGCCGACGAGGATGCCGGTAGT 13440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13381 TCAGACACACCCGCCGACGACGTCCCGGGAGAATCAGCCGCCGACGAGGATGCCGGTAGT 13440

Qy      13441 GGCGATGAGGCTGCTGCCGGCAGTCCAGGGGTGTGGCCGTGGCTGGTGTCGGCCAAGTCG 13500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      13501 CAGCCGGCCCTGCGCGCCCAGGCCCAGGCCCTGCACGCCCACCTCACCGACCACCCCGGC 13560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13501 CAGCCGGCCCTGCGCGCCCAGGCCCAGGCCCTGCACGCCCACCTCACCGACCACCCCGGC 13560

Qy      13561 CTCGACCTCGCCGACGTCGGGTACACCCTCGCCCACGCCCGCGCCGTGTTCGACCACCGC 13620
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Qy      13621 GCCACCCTCATCGCCGCCGACCGCGACACCTTCCTGCAAGCACTCCAGGCACTCGCCGCA 13680
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Db      13621 GCCACCCTCATCGCCGCCGACCGCGACACCTTCCTGCAAGCACTCCAGGCACTCGCCGCA 13680

Qy      13681 GGCGAACCCCACCCCGCCGTCATCCACAGCAGCGCCCCAGGCGGGACCGGGACCGGGGAG 13740
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Db      13681 GGCGAACCCCACCCCGCCGTCATCCACAGCAGCGCCCCAGGCGGGACCGGGACCGGGGAG 13740

Qy      13741 GCCGCAGGAAAGACCGCATTCATCTGCTCCGGACAGGGCACCCAACGCCCCGGCATGGCC 13800
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Qy      13801 CACGGCCTCTACCACACCCACCCCGTCTTCGCCGCCGCACTCAACGACATCTGCACCCAC 13860
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Db      13801 CACGGCCTCTACCACACCCACCCCGTCTTCGCCGCCGCACTCAACGACATCTGCACCCAC 13860

Qy      13861 CTCGACCCCCACCTCGACCACCCCCTCCTCCCCCTCCTCACCCAGGACCCCAACACCCAG 13920
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Qy      13921 GACACCACCACCCTCGAAGAAGCGGCCGCACTGCTCCAGCAGACCCGCTACGCCCAGCCC 13980
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Qy      13981 GCCCTCTTCGCCTTCCAGGTCGCCCTCCACCGCCTCCTCACCGACGGCTACCACATCACC 14040
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Qy      14041 CCCCACTACTACGCCGGACACTCCCTCGGCGAAATCACCGCCGCCCACCTCGCCGGCATC 14100
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Qy      14101 CTCACCCTCACCGACGCCACCACCCTCATCACCCAACGCGCCACCCTCATGCAAACCATG 14160
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Qy      14161 CCCCCCGGCACCATGACCACCCTCCACACCACCCCCCACCACATCACCCACCACCTCACC 14220
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Db      14161 CCCCCCGGCACCATGACCACCCTCCACACCACCCCCCACCACATCACCCACCACCTCACC 14220

Qy      14221 GCCCACGAAAACGACCTCGCCATCGCCGCCATCAACACCCCCACCTCCCTCGTCATCAGC 14280
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Qy      14281 GGCACCCCCCACACCGTCCAACACATCACCACCCTCTGCCAACAACAAGGCATCAAAACC 14340
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Qy      14341 AAAACCCTCCCCACCAACCACGCCTTCCACTCCCCCCACACCAACCCCCATCCTCAACCAA 14400
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Db      14341 AAAACCCTCCCCACCAACCACGCCTTCCACTCCCCCCACACCAACCCCATCCTCAACCAA 14400

Qy      14401 CTCCACCAGCACACCCAAACCCTCACCTACCACCCACCCCACACCCCCCTCATCACCGCC 14460
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Db      14401 CTCCACCAGCACACCCAAACCCTCACCTACCACCCACCCCACACCCCCCTCATCACCGCC 14460

Qy      14461 AACACCCCACCCGACCAACTCCTCACCCCCCACTACTGGACCCAACAAGCCCGCAACACC 14520
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Qy      14521 GTCGACTACGCCACCACCACCCAAACCCTCCACCAACACGGCGTCACCACCTACATCGAA 14580
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Qy      14581 CTCGGACCCGACAACACCCTCACCACCCTCACCCACGACAACCTCCCCAACACCCCCACC 14640
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Qy      14641 ACCACCCTCACCCTCACCCACCCCCACCACCACCCCCAAACCCACCTCCTCACCAACCTC 14700
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Qy      14701 GCCAAAACCACCACCACCTGGCACCCCCACCACTACACCCACCACCACAACCAACCCCAC 14760
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Qy      14761 ACCCACACCCACCTCGACCTCCCCACCTACCCCTTCCAACACCACCACTACTGGCTCCAA 14820
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Qy      14821 CCACCCGGCAAGCCGAGCGACCCGTCACCGAGCGAAGGCCGTGAGCAAGCCACGACCCCA 14880
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Qy      14881 TCAACCCCGCTGCGTGATGTCCTCGTGGGCAAGTCTCCGCAGGAGCGAGACGAAGAGCTG 14940
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Qy      14941 TTGCGCCTGGTGCGCACCCATGCGGCCGCTGTGCTGGGCCATGCCACTCCCGAAGTGATC 15000
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Qy      15001 GTTCCGAACAAGGCCTTCAAAGAGCTGGGTTTTGATTCTCTCGCCGCAATTCAGCTTCGT 15060
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Qy      15061 AATCGACTGCTTGCTGACGTTGACCTGCCGCTTCCGGCCACGCTGATCTTCGATTACCCC 15120
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Qy      15121 ACTCCGATGGCGCTTTGCCAGTTCCTCCGGGCGGCGATCGTCGGAGCGGACACAGGCACG 15180
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Db      15121 ACTCCGATGGCGCTTTGCCAGTTCCTCCGGGCGGCGATCGTCGGAGCGGACACAGGCACG 15180

Qy      15181 ACCACTCGTCTGCCGCTAACTGCGGTCCCCGCCGACGAGCCGATCGCCATCGTCGGCATG 15240
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Db      15181 ACCACTCGTCTGCCGCTAACTGCGGTCCCCGCCGACGAGCCGATCGCCATCGTCGGCATG 15240

Qy      15241 GCCTGTCGGTACCCCGGTGATGTACGGACGGTCGATGATCTCTGGCAGGTGGTCAGTGGT 15300
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Qy      15301 GGCCATGACGCGATCGGCGGATTCCCGACGAACCGTGGGTGGGACCTCGACACGCTGTAC 15360
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Qy      15361 AACCCGGACCCGGACCACCACGGAACCAGCTACACCCGGAGCGGCGGATTCCTTTACGAC 15420
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Db      15361 AACCCGGACCCGGACCACCACGGAACCAGCTACACCCGGAGCGGCGGATTCCTTTACGAC 15420

Qy      15421 GCAGGCAATTTCGATCCCGACTTCTTCGGTATCAGTCCGCGTGAGGCACTGGCGATGGAC 15480
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Db      15421 GCAGGCAATTTCGATCCCGACTTCTTCGGTATCAGTCCGCGTGAGGCACTGGCGATGGAC 15480

Qy      15481 CCGCAGCAGCGGCTGCTGCTGGAAACAGCGTGGGAGAGCATCGAACACGCCTGCATCAAC 15540
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Qy      15541 CCCGACAGCCTCCGTGGCACACCAACCGGCGTCTTCGCCGGGCTGACCTACCACGACTAC 15600
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Qy      15601 GCCGCGCGCTTTCCCACAGCTCCGGCAGGGTTCGAGGGGTATCTCGGGCACGGAAGCGCA 15660
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Qy      15661 GGCAGTATCGCCTCGGGTCGTGTCGCCTACGCTCTCGGCCTGGAAGGTCCGGCCCTCACA 15720
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Qy      15721 GTCGACACTGCCTGCTCTTCGTCCCTGGTCGCTCTGCACCTGGCCTGTCAGGCGCTGCGG 15780
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Qy      15781 TCCGGCGAGTGTTCCATGGCCCTCGCGGGTGGCGTCACGGTGATGTCAACCCCGGCCGGG 15840
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Qy      15841 TTCGTGGAGTTTTCGCGGCAGCGGGGCCTGGCCGTGGACGGGCGGTGCAAGGCGTTCTCG 15900
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Qy      15901 GCAGCGGCTGACGGCACCGGCTGGGGTGAGGGTGTCGGAATGCTGCTGGTGGAGCGGCTG 15960
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Qy      15961 TCGGACGCGCGGCGGCTCGGTCACCGAATCCTCGCGGTGGTGCGTGGCAGTGCGGTCAAT 16020
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Db      15961 TCGGACGCGCGGCGGCTCGGTCACCGAATCCTCGCGGTGGTGCGTGGCAGTGCGGTCAAT 16020

Qy      16021 CAGGACGGTGCGAGCAACGGGCTGACGGCGCCCAACGGGCCGTCCCAGGAGCGTGTCATC 16080
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Qy      16141 GGCACCGGCACCACTTTGGGCGACCCGATCGAGGCCCAGGCCCTCCTCGCCACCTACGGA 16200
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Qy      16261 GCGCAGGCTGCCGCAGGTGTGGGCGGGGTCATCAAGATGGTGATGGCGCTGCGGAATGGT 16320
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Qy      16321 CTGCTGCCGCGGACGTTGCATGTGGATGAGCCGTCGCCGCATGTGGACTGGTCCGCGGGG 16380
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Qy      16381 GCGGTGCAGCTGCTGACGGAGACGGTGCCCTGGCCCGGCGGGGAGGGGCGGCTGCGGCGG 16440
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Qy      16441 GCAGGAGTGTCATCGTTCGGCGTCAGCGGCACCAACGCCCACGTCATCCTCGAAGAAGCA 16500
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Qy      16501 CCCGCCCACAACATCCCGTCAGACACACCCGCCGACGACGCCCCGGGAGAAGCAGCCGCC 16560
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Db      16501 CCCGCCCACAACATCCCGTCAGACACACCCGCCGACGACGCCCCGGGAGAAGCAGCCGCC 16560

Qy      16561 GACGATGTTCCGGGGGGAAGCGGCCGGCGACGACGCCGGTACCGGCGGGGAAGCGACTGGT 16620
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Db      16561 GACGATGTTCCGGGGGGAAGCGGCCGGCGACGACGCCGGTACCGGCGGGGAAGCGACTGGT 16620

Qy      16621 CCTGCTGCCGGCAGTCCAGGGGTGTGGCCGTGGCTGGTGTCGGCCAAGTCGCAGCCGGCC 16680
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Qy      16681 CTGCGCGCCCAGGCCCAGGCCCTGCACGCCCACCTCACCGACCACCCCGGCCTCGACCTC 16740
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Qy      16741 GCCGACGTCGGGTACACCCTCGCCCACGCCCGCGCCGTGTTCGACCACCGCGCCCACCCTC 16800
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Qy      16981 TACCACACCCACCCCGTCTTCGCCGCCGCACTCAACGACATCTGCACCCACCTCGACCCC 17040
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Qy      17041 CACCTCGACCACCCCCTCCTCCCCCTCCTCACCCAGGACCCCAACACCCAGGACACCACC 17100
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Db      17041 CACCTCGACCACCCCCTCCTCCCCCTCCTCACCCAGGACCCCAACACCCAGGACACCACC 17100
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Qy      17221 TACGCCGGACACTCCCTCGGCGAAATCACCGCCGCCCACCTCGCCGGCATCCTCACCCTC 17280
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Qy      17281 ACCGACGCCACCACCCTCATCACCCAACGCGCCACCCTCATGCAAACCATGCCCCCCGGC 17340
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Qy      17701 GCCACCACCACCCAAACCCTCCACCAACACGGCGTCACCACCTACATCGAACTCGGACCC 17760
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Qy      18301 GAAACCCAGACCCACCACCCCCACATCACCAACATCCTCACCAACCTCCACCACCACGGC 18360
Db      18301 GAAACCCAGACCCACCACCCCCACATCACCAACATCCTCACCAACCTCCACCACCACGGC 18360
Qy      18361 ATCACCCCCATCCCCCTCACCCTCAACCACACCCACACCAACCCCCCAACACCTCCACCAC 18420
Db      18361 ATCACCCCCATCCCCCTCACCCTCAACCACACCCACACCAACCCCCCAACACCTCCACCAC 18420
Qy      18421 ACCCGACAACAAGCCCAAAACCACACCACCGGACCCATCACCGGCCTGCTCTCCCTCCTC 18480
Db      18421 ACCCGACAACAAGCCCAAAACCACACCACCGGACCCATCACCGGCCTGCTCTCCCTCCTC 18480
Qy      18481 GCCCTCGACGAAACACCCCACCCCCACCACCCCCACACACCCACCGGCACCCTCCTCAAC 18540
Db      18481 GCCCTCGACGAAACACCCCACCCCCACCACCCCCACACACCCACCGGCACCCTCCTCAAC 18540
Qy      18541 CTCACCCTCACCCAAACCCACACCCAAACCCACCCACCAACCCCCCTCTGGTACGCCACC 18600
Db      18541 CTCACCCTCACCCAAACCCACACCCAAACCCACCCACCAACCCCCCTCTGGTACGCCACC 18600
Qy      18601 ACCAACGCCACCACCACCCACCCCAACGACCCCCTCACACACCCCACCCAAGCCCAAACC 18660
Db      18601 ACCAACGCCACCACCACCCACCCCAACGACCCCCTCACACACCCCACCCAAGCCCAAACC 18660
Qy      18661 TGGGGACTCGCCCGCACCACCCTCCTCGAACACCCCACCCACACCGCCGGAATCATCGAC 18720
Db      18661 TGGGGACTCGCCCGCACCACCCTCCTCGAACACCCCACCCACACCGCCGGAATCATCGAC 18720
Qy      18721 CTCCCCACCACCCCCACCCCCCACACCCTCCACCACCTCACCCAAACCCTCACCCAACCC 18780
Db      18721 CTCCCCACCACCCCCACCCCCCACACCCTCCACCACCTCACCCAAACCCTCACCCAACCC 18780
Qy      18781 CACCACCAAACCCAACTCGCCATCCGCACCACCGGCACCCACACCCGCCGCCTCACCCCC 18840
Db      18781 CACCACCAAACCCAACTCGCCATCCGCACCACCGGCACCCACACCCGCCGCCTCACCCCC 18840
Qy      18841 ACCACCCTCACCCCCACACACCAACCACCCACCCCCACCCCCCACGGAACCACCCTCATC 18900
Db      18841 ACCACCCTCACCCCCACACACCAACCACCCACCCCCACCCCCCACGGAACCACCCTCATC 18900
Qy      18901 ACCGGCGGAACCGGCGCCCTCGCCACCCACCTCACCCACCACCTCACCACCCACCAACCC 18960
Db      18901 ACCGGCGGAACCGGCGCCCTCGCCACCCACCTCACCCACCACCTCACCACCCACCAACCC 18960
Qy      18961 ACCCAACACCTCCTCCTCACCAGCCGAACCGGCCCCCACACCCCCCACGCACAACACCTC 19020
Db      18961 ACCCAACACCTCCTCCTCACCAGCCGAACCGGCCCCCACACCCCCCACGCACAACACCTC 19020
Qy      19021 ACCACCCAACTCCAACAAAAAGGCATCCACCTCACCATCACCACCTGCGACACCAGCAAC 19080
Db      19021 ACCACCCAACTCCAACAAAAAGGCATCCACCTCACCATCACCACCTGCGACACCAGCAAC 19080
Qy      19081 CCAGACCAACTCCAACAACTCCTCAACACCATCCCCCCACAACACCCCCTCACCACCGTC 19140
Db      19081 CCAGACCAACTCCAACAACTCCTCAACACCATCCCCCCACAACACCCCCTCACCACCGTC 19140
Qy      19141 ATCCACACCGCAGGCATCCTCGACGACGCCCACCCTCACCAACCTCACCCCCACCCAACTC 19200
Db      19141 ATCCACACCGCAGGCATCCTCGACGACGCCCACCCTCACCAACCTCACCCCCACCCAACTC 19200
Qy      19201 AACAACGTCCTCCGCGCCAAAGCCCACAGCGCCCACCTCCTCCACCAACTCACCCAACAC 19260
Db      19201 AACAACGTCCTCCGCGCCAAAGCCCACAGCGCCCACCTCCTCCACCAACTCACCCAACAC 19260
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Qy      19261 ACCCCCCTCAACGCCTTCGTCCTCTACTCCTCCGCCGCCGCCACCTTCGGCGCACCCGGC 19320
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Db      19261 ACCCCCCTCAACGCCTTCGTCCTCTACTCCTCCGCCGCCGCCACCTTCGGCGCACCCGGC 19320

Qy      19321 CAAGCCAACTACGCCGCAGCCAACGCCTACCTCGACGCCCTCGCCCACCACCGCCACACC 19380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19321 CAAGCCAACTACGCCGCAGCCAACGCCTACCTCGACGCCCTCGCCCACCACCGCCACACC 19380

Qy      19381 CACCACCTCCCCGCCACCAGCATCGCCTGGGGCACCTGGCAAGGAAACGGACTGGCGACT 19440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19381 CACCACCTCCCCGCCACCAGCATCGCCTGGGGCACCTGGCAAGGAAACGGACTGGCGACT 19440

Qy      19441 GGTCAAGTCAGCGAACATCTCCGCCGCCGCGGGATGTTCGCCATGCCGCCCGAGTTGGCG 19500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19441 GGTCAAGTCAGCGAACATCTCCGCCGCCGCGGGATGTTCGCCATGCCGCCCGAGTTGGCG 19500

Qy      19501 GTCACAGCTGTTGACGGCGCGATCGCGAGCGGGCGCCCGAGTCTCCTCGTCGCCGATATC 19560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19501 GTCACAGCTGTTGACGGCGCGATCGCGAGCGGGCGCCCGAGTCTCCTCGTCGCCGATATC 19560

Qy      19561 GACTGGAAGAAATTGGGACCGGTTCTCTCCAGCAAGTCGTCGGTCTTGCTCGAGGACCTT 19620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19561 GACTGGAAGAAATTGGGACCGGTTCTCTCCAGCAAGTCGTCGGTCTTGCTCGAGGACCTT 19620

Qy      19621 CCCCAGGCACAGGGAACTGAGGAGGCGCGCAGTACCGTTGAGCAGACGGAGAGCACAAAC 19680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19621 CCCCAGGCACAGGGAACTGAGGAGGCGCGCAGTACCGTTGAGCAGACGGAGAGCACAAAC 19680

Qy      19681 CTCCGGCAACTCCTCATGGGTCGGTCACGTTCCGAGCAGGAAGAAGAGCTGCTCAGCCTC 19740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19681 CTCCGGCAACTCCTCATGGGTCGGTCACGTTCCGAGCAGGAAGAAGAGCTGCTCAGCCTC 19740

Qy      19741 GTCCGCATCCACTCCGCGGCAGTGCTCGGGCGCGACGACTCCGAGGCCATCCCGCCCGGT 19800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19741 GTCCGCATCCACTCCGCGGCAGTGCTCGGGCGCGACGACTCCGAGGCCATCCCGCCCGGT 19800

Qy      19801 CGGCTGTTCAGGGATCTAGGGTTCGACTCGCTTGCGGCGGTGGAGCTTCGCAACCACCTC 19860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19801 CGGCTGTTCAGGGATCTAGGGTTCGACTCGCTTGCGGCGGTGGAGCTTCGCAACCACCTC 19860

Qy      19861 GCAGCACAGACGGAGCTGGCTCTGCCGACGACTCTCGTCTTCGATTACCCCAGCCCCACC 19920
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Db      19861 GCAGCACAGACGGAGCTGGCTCTGCCGACGACTCTCGTCTTCGATTACCCCAGCCCCACC 19920

Qy      19921 AAGCTCGCCCAATTTCTGCTCTCCGAGATCGCGGAGTTCCAGCCCGACAACTCAACTCCG 19980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19921 AAGCTCGCCCAATTTCTGCTCTCCGAGATCGCGGAGTTCCAGCCCGACAACTCAACTCCG 19980

Qy      19981 CTTCCGCGACCCCGGGCAGAGCTCGATGAGCCGATCGCCATCGTTGGCATGGCCTGTCGC 20040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19981 CTTCCGCGACCCCGGGCAGAGCTCGATGAGCCGATCGCCATCGTTGGCATGGCCTGTCGC 20040

Qy      20041 TTCCCCGGCGGAGTGACCTCGGCGGACGACTTCTGGGATCTGATCTCCTCCGAGCAGGAC 20100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20041 TTCCCCGGCGGAGTGACCTCGGCGGACGACTTCTGGGATCTGATCTCCTCCGAGCAGGAC 20100

Qy      20101 GCGATCGGCGGATTCCCCACCGACCGCGGCTGGGACCTGGACACGCTCTACGACCCCGAC 20160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20101 GCGATCGGCGGATTCCCCACCGACCGCGGCTGGGACCTGGACACGCTCTACGACCCCGAC 20160

Qy      20161 CCCGACCACCCCGGCACCTGCTACACCCGAAACGGCGGATTCCTCTACGACGCAGGCCAC 20220
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Db      20161 CCCGACCACCCCGGCACCTGCTACACCCGAAACGGCGGATTCCTCTACGACGCAGGCCAC 20220

Qy      20221 TTCGACGCCGAATTCTTCGGCATCAGCCCCCGCGAAGCCCTCGCCATGGACCCCCAGCAA 20280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20221 TTCGACGCCGAATTCTTCGGCATCAGCCCCCGCGAAGCCCTCGCCATGGACCCCCAGCAA 20280

Qy      20281 CGACTCCTCCTCGAAACCGCCTGGGAAACCATCGAACACGCCGGCATCAACCCCCACACC 20340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20281 CGACTCCTCCTCGAAACCGCCTGGGAAACCATCGAACACGCCGGCATCAACCCCCACACC 20340

Qy      20341 CTCCACGGCACCCCCACCGGAGTCTTCACCGGCACCAACGGACAGGACCACGCGGCACAC 20400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20341 CTCCACGGCACCCCCACCGGAGTCTTCACCGGCACCAACGGACAGGACCACGCGGCACAC 20400

Qy      20401 ATCCGTCAGGCCCCGAGCGGTACCGAGGGATTCGTCCTGACCGGGGCAGCCACCAGCATC 20460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20401 ATCCGTCAGGCCCCGAGCGGTACCGAGGGATTCGTCCTGACCGGGGCAGCCACCAGCATC 20460

Qy      20461 GCCTCCGGCCGAATCTCCTACATCCTCGGGTTGGAAGGGCCTGCGGTCACCCTCGACACA 20520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20461 GCCTCCGGCCGAATCTCCTACATCCTCGGGTTGGAAGGGCCTGCGGTCACCCTCGACACA 20520

Qy      20521 GCGTGTTCCTCCTCGCTCGTCGCCCTGCACCTCGCCTGCCAGTCCCTCAGGTCCGGTGAA 20580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20521 GCGTGTTCCTCCTCGCTCGTCGCCCTGCACCTCGCCTGCCAGTCCCTCAGGTCCGGTGAA 20580

Qy      20581 TGCACCATGGCCTTGGCCGGCGGGGCCACGGTCATGACCACCCCGATCACCTTCACCGAA 20640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20581 TGCACCATGGCCTTGGCCGGCGGGGCCACGGTCATGACCACCCCGATCACCTTCACCGAA 20640

Qy      20641 TTCGCCCGCCAACGCGGACTCGCCCCCGACGGGCGTTGCAAGGCGTTCTCGGCGGCGGCT 20700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20641 TTCGCCCGCCAACGCGGACTCGCCCCCGACGGGCGTTGCAAGGCGTTCTCGGCGGCGGCT 20700

Qy      20701 GACGGTACCGGCTGGGGTGAGGGTGTGGGGATGCTGCTGGTGGAGCGGCTCTCCGACGCC 20760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20701 GACGGTACCGGCTGGGGTGAGGGTGTGGGGATGCTGCTGGTGGAGCGGCTCTCCGACGCC 20760

Qy      20761 CGCCGCAACGGTCACCGTGTCCTGGCCGTGGTGCGTGGCAGTGCGGTCAACCAGGACGGT 20820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20761 CGCCGCAACGGTCACCGTGTCCTGGCCGTGGTGCGTGGCAGTGCGGTCAACCAGGACGGT 20820

Qy      20821 GCGAGCAACGGTCTGACCGCGCCCAACGGGCCCTCCCAGCAGCGCGTCATCCGCCAGGCC 20880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20821 GCGAGCAACGGTCTGACCGCGCCCAACGGGCCCTCCCAGCAGCGCGTCATCCGCCAGGCC 20880

Qy      20881 CTCGCCAACGCGGACCTGACCCCCGCCGACGTCGATGCGGTGGAGGCCCACGGCACCGGC 20940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20881 CTCGCCAACGCGGACCTGACCCCCGCCGACGTCGATGCGGTGGAGGCCCACGGCACCGGC 20940

Qy      20941 ACCACTTTGGGCGACCCGATCGAGGCCCAGGCCATCCTCGCGACCTACGGACAGGACCGT 21000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20941 ACCACTTTGGGCGACCCGATCGAGGCCCAGGCCATCCTCGCGACCTACGGACAGGACCGT 21000

Qy      21001 CCCGGCAACGGGCCGTTGTGGCTGGGCTCCGTCAAGTCCAACGTCGGACACACACAGGCC 21060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21001 CCCGGCAACGGGCCGTTGTGGCTGGGCTCCGTCAAGTCCAACGTCGGACACACACAGGCC 21060

Qy      21061 GCGGCGGGCGTGGCCGGAGTGATCAAGATGGTGATGGCCCTCCGCCACCGGACACTCCCA 21120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21061 GCGGCGGGCGTGGCCGGAGTGATCAAGATGGTGATGGCCCTCCGCCACCGGACACTCCCA 21120

Qy      21121 CCGACTCTCCACGCGGATGAGCCGTCGCCGCATGTGGACTGGTCCGCGGGTGCGGTGCAG 21180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21121 CCGACTCTCCACGCGGATGAGCCGTCGCCGCATGTGGACTGGTCCGCGGGTGCGGTGCAG 21180

Qy      21181 CTGCTGACGGAGACGGTGCCCTGGCCCGGCGGGGAGGGGCGGCCGCGGCGGGCAGGAGTG 21240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21181 CTGCTGACGGAGACGGTGCCCTGGCCCGGCGGGGAGGGGCGGCCGCGGCGGGCAGGAGTG 21240

Qy      21241 TCATCATTCGGCGTCAGCGGCACCAACGCCCACGTCATCCTCGAAGAAGCACCCGCCGAC 21300
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Db      21241 TCATCATTCGGCGTCAGCGGCACCAACGCCCACGTCATCCTCGAAGAAGCACCCGCCGAC 21300

Qy      21301 GACGTTCCGGGGGGACCACCCGCCGACGAGGATGCCGGTAGTGGCGAGGAGGCTGCTGCC 21360
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Db      21301 GACGTTCCGGGGGGACCACCCGCCGACGAGGATGCCGGTAGTGGCGAGGAGGCTGCTGCC 21360

Qy      21361 GGCAGTCCTGGGGTGTGGCCGTGGCTGGTGTCGGCCAAGTCGCAGCCGGCCCTGCGCGCC 21420
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Db      21361 GGCAGTCCTGGGGTGTGGCCGTGGCTGGTGTCGGCCAAGTCGCAGCCGGCCCTGCGCGCC 21420

Qy      21421 CAGGCCCAGGCCCTGCACGCCCACCTCACCGACCACCCCGGCCTCGACCTCGCCGACGTC 21480
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Db      21421 CAGGCCCAGGCCCTGCACGCCCACCTCACCGACCACCCCGGCCTCGACCTCGCCGACGTC 21480
Qy      21481 GGATACACCCTCGCCCACGCCCGCGCCGTGTTCGACCACCGCGCCACCCTCATCGCCGCC 21540
Db      21481 GGATACACCCTCGCCCACGCCCGCGCCGTGTTCGACCACCGCGCCACCCTCATCGCCGCC 21540
Qy      21541 GACCGCGACACCTTCCTGCAAGCACTCCAGGCACTCGCCGCAGGCGAACCCCACCCCGCC 21600
Db      21541 GACCGCGACACCTTCCTGCAAGCACTCCAGGCACTCGCCGCAGGCGAACCCCACCCCGCC 21600
Qy      21601 GTCATCCACAGCAGCGCCCCAGGCGGGACCGGGACCGGGGAGGCCGCAGGAAAGACCGCA 21660
Db      21601 GTCATCCACAGCAGCGCCCCAGGCGGGACCGGGACCGGGGAGGCCGCAGGAAAGACCGCA 21660
Qy      21661 TTCATCTGCTCCGGACAGGGCACCCAACGCCCCGGCATGGCCCACGGCCTCTACCACACC 21720
Db      21661 TTCATCTGCTCCGGACAGGGCACCCAACGCCCCGGCATGGCCCACGGCCTCTACCACACC 21720
Qy      21721 CACCCCGTCTTCGCCGCCGCACTCAACGACATCTGCACCCACCTCGACCCCCACCTCGAC 21780
Db      21721 CACCCCGTCTTCGCCGCCGCACTCAACGACATCTGCACCCACCTCGACCCCCACCTCGAC 21780
Qy      21781 CACCCCCTCCTCCCCCTCCTCACCCAAAACGACAACGACAACGACAACGAGGACGCGGCC 21840
Db      21781 CACCCCCTCCTCCCCCTCCTCACCCAAAACGACAACGACAACGACAACGAGGACGCGGCC 21840
Qy      21841 GCACTGCTCCAGCAGACCCCGTACGCCCAGCCCGCCCTCTTCGCCTTCCAGGTCGCCCTC 21900
Db      21841 GCACTGCTCCAGCAGACCCCGTACGCCCAGCCCGCCCTCTTCGCCTTCCAGGTCGCCCTC 21900
Qy      21901 CACCGCCTCCTCACCGACGGCTACCACATCACCCCCCACTACTACGCCGGACACTCCCTC 21960
Db      21901 CACCGCCTCCTCACCGACGGCTACCACATCACCCCCCACTACTACGCCGGACACTCCCTC 21960
Qy      21961 GGCGAAATCACCGCCGCCCACCTCGCCGGCATCCTCACCCTCACCGACGCCACCACCCTC 22020
Db      21961 GGCGAAATCACCGCCGCCCACCTCGCCGGCATCCTCACCCTCACCGACGCCACCACCCTC 22020
Qy      22021 ATCACCCAACGCGCCACCCTCATGCAAACCATGCCCCCCGGCACCATGACCACCCTCCAC 22080
Db      22021 ATCACCCAACGCGCCACCCTCATGCAAACCATGCCCCCCGGCACCATGACCACCCTCCAC 22080
Qy      22081 ACCACCCCACACCACATCACCCACCACCTCACCGCCCACGAAAACGACCTCGCCATCGCC 22140
Db      22081 ACCACCCCACACCACATCACCCACCACCTCACCGCCCACGAAAACGACCTCGCCATCGCC 22140
Qy      22141 GCCATCAACACCCCCACCTCCCTCGTCATCAGCGGCACCCCCCACACCGTCCAACACATC 22200
Db      22141 GCCATCAACACCCCCACCTCCCTCGTCATCAGCGGCACCCCCCACACCGTCCAACACATC 22200
Qy      22201 ACCACCCTCTGCCAACAACAAGGCATCAAAACCAAAACCCTCCCCACCAACCACGCCTTC 22260
Db      22201 ACCACCCTCTGCCAACAACAAGGCATCAAAACCAAAACCCTCCCCACCAACCACGCCTTC 22260
Qy      22261 CACTCCCCCCACACCAACCCCATCCTCAACCAACTCCACCAGCACACCCAAACCCTCACC 22320
Db      22261 CACTCCCCCCACACCAACCCCATCCTCAACCAACTCCACCAGCACACCCAAACCCTCACC 22320
Qy      22321 TACCACCCACCCCACACCCCCCTCATCACCGCCAACACCCCACCCGACCAACTCCTCACC 22380
Db      22321 TACCACCCACCCCACACCCCCCTCATCACCGCCAACACCCCACCCGACCAACTCCTCACC 22380
Qy      22381 CCCCACTACTGGACCCAACAAGCCCGCAACACCGTCGACTACGCCACCACCACCCAAACC 22440
Db      22381 CCCCACTACTGGACCCAACAAGCCCGCAACACCGTCGACTACGCCACCACCACCCAAACC 22440
Qy      22441 CTCCACCAACACGGCGTCACCACCTACATCGAACTCGGACCCGACAACACCCTCACCACC 22500
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Qy      22501 CTCACCCACCACAACCTCCCCAACACCCCCACCACCACCCTCACCCTCACCCACCCCCAC 22560
Db      22501 CTCACCCACCACAACCTCCCCAACACCCCCACCACCACCCTCACCCTCACCCACCCCCAC 22560

Qy      22561 CACCACCCCCAAACCCACCTCCTCACCAACCTCGCCAAAACCACCACCACCTGGCACCCC 22620
Db      22561 CACCACCCCCAAACCCACCTCCTCACCAACCTCGCCAAAACCACCACCACCTGGCACCCC 22620
Qy      22621 CACCACTACACCCACCACCACAACCAACCCCACACCCACACCCACCTCGACCTCCCCACC 22680
Db      22621 CACCACTACACCCACCACCACAACCAACCCCACACCCACACCCACCTCGACCTCCCCACC 22680
Qy      22681 TACCCCTTCCAACACCACCACTACTGGCTCGAACTACCCAGCGCCCAAACCAGCCCCGGT 22740
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Qy      22741 CAAAGGCGTTCTCGCCGCTCGGCTCCAGACACCGCCGAGTCGGAGTTCTGGGACGCGGTG 22800
Db      22741 CAAAGGCGTTCTCGCCGCTCGGCTCCAGACACCGCCGAGTCGGAGTTCTGGGACGCGGTG 22800
Qy      22801 AACGAGGAAGACCTCCAGAGCCTCGCCGAAACCCTCGACATCGACGCCTCTGCTCTGGAC 22860
Db      22801 AACGAGGAAGACCTCCAGAGCCTCGCCGAAACCCTCGACATCGACGCCTCTGCTCTGGAC 22860
Qy      22861 ACGGTGGTGCCCGCACTCTCCGCCTGGCACCGCCACCAACACGACCAAGCCCGCATCAAC 22920
Db      22861 ACGGTGGTGCCCGCACTCTCCGCCTGGCACCGCCACCAACACGACCAAGCCCGCATCAAC 22920
Qy      22921 ACCTGGACCTACCAGGAAACCTGGAAACCCCTCACCCTCCCCACCACCCACCAACCCCAC 22980
Db      22921 ACCTGGACCTACCAGGAAACCTGGAAACCCCTCACCCTCCCCACCACCCACCAACCCCAC 22980
Qy      22981 CAAACCTGGCTCATCGCCATCCCCGAAACCCAGACCCACCACCCCCCACATCACCAACATC 23040
Db      22981 CAAACCTGGCTCATCGCCATCCCCGAAACCCAGACCCACCACCCCCCACATCACCAACATC 23040
Qy      23041 CTCACCAACCTCCACCACCACGGCATCACCCCCATCCCCCTCACTGTCAACCACACCCAC 23100
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Qy      23101 ACCAACCCCCAACACCTCCACCACACCCTCCACCACACCCGACAACAAGCCCAAAACCAC 23160
Db      23101 ACCAACCCCCAACACCTCCACCACACCCTCCACCACACCCGACAACAAGCCCAAAACCAC 23160
Qy      23161 ACCACCGGACCCATCACCGGCCTGCTCTCCCTCCTCGCCCTCGACGAAACACCCCACCCC 23220
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Qy      23221 CACCACCCCCACACACCCACCGGCACCCTCCTCAACCTCACCCTCCCCCAAACCCACACC 23280
Db      23221 CACCACCCCCACACACCCACCGGCACCCTCCTCAACCTCACCCTCCCCCAAACCCACACC 23280
Qy      23281 CAAACCCACCCACCAACCCCCCCTCTGGTACGCCACCACCAACGCCACCACCACCCACCCC 23340
Db      23281 CAAACCCACCCACCAACCCCCCTCTGGTACGCCACCACCAACGCCACCACCACCCACCCC 23340
Qy      23341 AACGACCCCCTCACACACCCCACCCAAGCCCAAACCTGGGGACTCGCCCGCACCACCCTC 23400
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Qy      23401 CTCGAACACCCCACCCACACCGCCGGAATCATCGACCTCCCCACCACCCCCACCCCCCAC 23460
Db      23401 CTCGAACACCCCACCCACACCGCCGGAATCATCGACCTCCCCACCACCCCCACCCCCCAC 23460
Qy      23461 ACCCTCCACCACCTCACCCAAACCCTCACCCAACCCCACCACCAAACCCAACTCGCCATC 23520
Db      23461 ACCCTCCACCACCTCACCCAAACCCTCACCCAACCCCACCACCAAACCCAACTCGCCATC 23520
Qy      23521 CGCACCACCGGCACCCACACCCGCCGCCTCACCCCCACCACCCTCACCCCCACACACCAA 23580
Db      23521 CGCACCACCGGCACCCACACCCGCCGCCTCACCCCCACCACCCTCACCCCCACACACCAA 23580
Qy      23581 CCACCCACCCCCACCCCCCACGGAACCACCCTCATCACCGGCGGAACCGGCGCCCTCGCC 23640
Db      23581 CCACCCACCCCCACCCCCCACGGAACCACCCTCATCACCGGCGGAACCGGCGCCCTCGCC 23640
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Qy      23641 ACCCACCTCACCCACCACCTCACCACCCACCAACCCACCCAACACCTCCTCCTCACCAGC 23700
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Db      23641 ACCCACCTCACCCACCACCTCACCACCCACCAACCCACCCAACACCTCCTCCTCACCAGC 23700

Qy      23701 CGAACCGGCCCCCACACCCCCCACGCACAACACCTCACCACCCAACTCCAACAAAAAGGC 23760
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Db      23701 CGAACCGGCCCCCACACCCCCCACGCACAACACCTCACCACCCAACTCCAACAAAAAGGC 23760

Qy      23761 ATCCACCTCACCATCACCACCTGCGACACCAGCAACCCAGACCAACTCCAACAACTCCTC 23820
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Db      23761 ATCCACCTCACCATCACCACCTGCGACACCAGCAACCCAGACCAACTCCAACAACTCCTC 23820

Qy      23821 AACACCATCCCCCCACAACACCCCCTCACCACCGTCATCCACACCGCAGGCGTCAATCTC 23880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23821 AACACCATCCCCCCACAACACCCCCTCACCACCGTCATCCACACCGCAGGCGTCAATCTC 23880

Qy      23881 TTCGCCCCCGTGTCGGAAACCGATGCCGAATCCTTCTCTTCCGTTACGGCAGCGAAGGCA 23940
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Db      23881 TTCGCCCCCGTGTCGGAAACCGATGCCGAATCCTTCTCTTCCGTTACGGCAGCGAAGGCA 23940

Qy      23941 ACGGGCGCGGCGATTCTGCATGAGTTGCTGCTGGACCATGAAACGCTTGAACACTTCATT 24000
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Db      23941 ACGGGCGCGGCGATTCTGCATGAGTTGCTGCTGGACCATGAAACGCTTGAACACTTCATT 24000

Qy      24001 CTCTTCTCGTCGGGCGCCGGCGCTTGGGGCAGCGGGAATCAGTGCGCATACTCGGCGGCC 24060
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Db      24001 CTCTTCTCGTCGGGCGCCGGCGCTTGGGGCAGCGGGAATCAGTGCGCATACTCGGCGGCC 24060

Qy      24061 AACGCATACCTGGACGCGCTCGCGACGCATCGTCAGACACATGGACTTCCCGGGGCATCG 24120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24061 AACGCATACCTGGACGCGCTCGCGACGCATCGTCAGACACATGGACTTCCCGGGGCATCG 24120

Qy      24121 ATCGCCTGGGGCCCCTGGGCCGGAAAGGGCATGTCGGCCGGTGATGCGGCTCATGGTTAC 24180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24121 ATCGCCTGGGGCCCCTGGGCCGGAAAGGGCATGTCGGCCGGTGATGCGGCTCATGGTTAC 24180

Qy      24181 CTGGAAAAGCGCGGCATTCTGCCGATGGAGCCACGCATGGCGCTCGCGGCATTCCATCGT 24240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24181 CTGGAAAAGCGCGGCATTCTGCCGATGGAGCCACGCATGGCGCTCGCGGCATTCCATCGT 24240

Qy      24241 GCGCGGGCGCAGCGGCCGAATTCCAACCTGATCATCGCGGACATCGACTGGGAGCGCTTC 24300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24241 GCGCGGGCGCAGCGGCCGAATTCCAACCTGATCATCGCGGACATCGACTGGGAGCGCTTC 24300

Qy      24301 GTCCCCGCCTTCACCGCTCGACGCCACAGCCCGCTCATCGAGGACATTCCGGAGGTTCGG 24360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24301 GTCCCCGCCTTCACCGCTCGACGCCACAGCCCGCTCATCGAGGACATTCCGGAGGTTCGG 24360

Qy      24361 CAAGCGGCTCAGGAGCTGGAAGCAGCTGCGTCGACGGCAAAGACGACCACAGCTCAGCCG 24420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24361 CAAGCGGCTCAGGAGCTGGAAGCAGCTGCGTCGACGGCAAAGACGACCACAGCTCAGCCG 24420

Qy      24421 ATTGCGACGTCTCTCCGTGAGCGATTGGCCCGACTGACGTCCTCAAAGCAGAACCAGGTG 24480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24421 ATTGCGACGTCTCTCCGTGAGCGATTGGCCCGACTGACGTCCTCAAAGCAGAACCAGGTG 24480

Qy      24481 CTGCTCGGCCTGATTCGGACAGGCATCTGCACCGTTCTCGGCCTTCGTAATCCGGAAGGC 24540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24481 CTGCTCGGCCTGATTCGGACAGGCATCTGCACCGTTCTCGGCCTTCGTAATCCGGAAGGC 24540

Qy      24541 ATCGAGGACCAACGAGCCTTCCGCGACCTCGGCTTCGACTCGCTGACGTCGGCTCAGTTC 24600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24541 ATCGAGGACCAACGAGCCTTCCGCGACCTCGGCTTCGACTCGCTGACGTCGGCTCAGTTC 24600

Qy      24601 AGCAAGGAACTCGCCAAGGAAACCGGACTGCCACTCCCCCCGTCCCTGGTCTTCGACTAT 24660
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Db      24601 AGCAAGGAACTCGCCAAGGAAACCGGACTGCCACTCCCCCCGTCCCTGGTCTTCGACTAT 24660

Qy      24661 CCCACCCCGCAGGAATGTGCTGCCCATCTGCGCACACAACTCGTCGACCTAGACGACGAA 24720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24661 CCCACCCCGCAGGAATGTGCTGCCCATCTGCGCACACAACTCGTCGACCTAGACGACGAA 24720

Qy      24721 GAGGACGCGGCACTGTCGAATGCTCTCCCGCAAGTGGCCCATCGGCGTACCGTCGAGGAC 24780
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24721 GAGGACGCGGCACTGTCGAATGCTCTCCCGCAAGTGGCCCATCGGCGTACCGTCGAGGAC 24780

Qy      24781 GAACCGATCGCCATCATCGGTATGGCATGTCGCTTCCCCGGCGGCGTACGTTCTGCCGAC 24840
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Db      24781 GAACCGATCGCCATCATCGGTATGGCATGTCGCTTCCCCGGCGGCGTACGTTCTGCCGAC 24840

Qy      24841 GACCTGTGGGAATTGCTCGCTTCGGGTAAGGACGCTATCGGCGTCTTCCCGACCGACCGC 24900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24841 GACCTGTGGGAATTGCTCGCTTCGGGTAAGGACGCTATCGGCGTCTTCCCGACCGACCGC 24900

Qy      24901 GGCTGGGACCTGGACACGCTCTACGACCCCGACCCCGACCACCCCGGCACCTGCTACACC 24960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24901 GGCTGGGACCTGGACACGCTCTACGACCCCGACCCCGACCACCCCGGCACCTGCTACACC 24960

Qy      24961 CGAAACGGCGGATTCCTCTACGGCGCAGGCCACTTCGACGCCGAATTCTTCGGCATCAGC 25020
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Db      24961 CGAAACGGCGGATTCCTCTACGGCGCAGGCCACTTCGACGCCGAATTCTTCGGCATCAGC 25020

Qy      25021 CCCCGCGAAGCCCTCGCCATGGACCCCCAGCAACGACTCCTCCTCGAAACCGCCTGGGAA 25080
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Db      25021 CCCCGCGAAGCCCTCGCCATGGACCCCCAGCAACGACTCCTCCTCGAAACCGCCTGGGAA 25080

Qy      25081 ACCATCGAACACGCCGGCATCAACCCCCACACCCTCCACGGCACCCCCACCGGAGTCTTC 25140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25081 ACCATCGAACACGCCGGCATCAACCCCCACACCCTCCACGGCACCCCCACCGGAGTCTTC 25140

Qy      25141 GCCGGAATCAACGCTCAAGACCACGCCGCGCATATCCGCCAAAGCCGTGATGTGGAGACC 25200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25141 GCCGGAATCAACGCTCAAGACCACGCCGCGCATATCCGCCAAAGCCGTGATGTGGAGACC 25200

Qy      25201 ATCGAGGGCTACGCCCTGACCGGCAGTTCGGGAAGTGTGGCGTCCGGCCGGGTGGCCTAC 25260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25201 ATCGAGGGCTACGCCCTGACCGGCAGTTCGGGAAGTGTGGCGTCCGGCCGGGTGGCCTAC 25260

Qy      25261 ACGCTCGGGCTCGAAGGCCCCGCGGTGTCGGTGGATACGGCGTGTTCGTCGTCGTTGGTG 25320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25261 ACGCTCGGGCTCGAAGGCCCCGCGGTGTCGGTGGATACGGCGTGTTCGTCGTCGTTGGTG 25320

Qy      25321 GCGTTGCATTGGGCGGCGCAGGCGTTGCGTGCGGGTGAGTGTTCGATGGCGCTTGCCGGG 25380
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Db      25321 GCGTTGCATTGGGCGGCGCAGGCGTTGCGTGCGGGTGAGTGTTCGATGGCGCTTGCCGGG 25380

Qy      25381 GGTGTGACGGTGATGTCGTCTCCGGGTACGTTTGTGGAGTTCTCACGTCAGCGGGGTCTG 25440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25381 GGTGTGACGGTGATGTCGTCTCCGGGTACGTTTGTGGAGTTCTCACGTCAGCGGGGTCTG 25440

Qy      25441 GCCGCGGACGGGCGGTGCAAGGCCTATTCGGCGGCTGCTGACGGTACCGGCTGGGCCGAG 25500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25441 GCCGCGGACGGGCGGTGCAAGGCCTATTCGGCGGCTGCTGACGGTACCGGCTGGGCCGAG 25500

Qy      25501 GGTGTGGGGATGCTGCTGGTGGAGCGGCTCTCCGACGCCCGTCGCAACGGTCACCGTGTC 25560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25501 GGTGTGGGGATGCTGCTGGTGGAGCGGCTCTCCGACGCCCGTCGCAACGGTCACCGTGTC 25560

Qy      25561 CTGGCCGTGGTGCGTGGCAGTGCGGTCAACCAGGACGGTGCGAGCAACGGTCTGACCGCG 25620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25561 CTGGCCGTGGTGCGTGGCAGTGCGGTCAACCAGGACGGTGCGAGCAACGGTCTGACCGCG 25620

Qy      25621 CCCAACGGGCCCTCCCAGCAGCGTGTCATCCGTCAGGCCCTGGCCAATGCGGGACTGACC 25680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25621 CCCAACGGGCCCTCCCAGCAGCGTGTCATCCGTCAGGCCCTGGCCAATGCGGGACTGACC 25680

Qy      25681 CCGGCCGATGTCGACGCAGTGGAGGGCCACGGCACCGGGACCACTCTGGGGGACCCGATC 25740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25681 CCGGCCGATGTCGACGCAGTGGAGGGCCACGGCACCGGGACCACTCTGGGGGACCCGATC 25740

Qy      25741 GAGGCCCAGGCACTCCTGGCCGCCTACGGACAACACCGCCCCCACCACCGCCCCTTGTGG 25800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25741 GAGGCCCAGGCACTCCTGGCCGCCTACGGACAACACCGCCCCCACCACCGCCCCTTGTGG 25800

Qy      25801 CTGGGATCCCTCAAATCCAACATCGGGCACGCACAGGCCGCCGCGGGCGTGGGCGGAGTC 25860
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Db      25801 CTGGGATCCCTCAAATCCAACATCGGGCACGCACAGGCCGCCGCGGGCGTGGGCGGAGTC 25860

Qy      25861 ATCAAGATGGTGATGGCCCTGCGCAACGGGCTGCTGCCACAGACCCTCCACGTGGACGAG 25920
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Db      25861 ATCAAGATGGTGATGGCCCTGCGCAACGGGCTGCTGCCACAGACCCTCCACGTGGACGAG 25920

Qy      25921 CCCACCCCCCCAGGTCGACTGGTCCACAGGCGCAGTACAACTCCTGACACAACCGGTGCCC 25980
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Qy      25981 TGGCCCGCCGACCCGGCCGGCCGGCCACGCCACGCCGGCGTGTCATCATTCGGCGTCAGC 26040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25981 TGGCCCGCCGACCCGGCCGGCCGGCCACGCCACGCCGGCGTGTCATCATTCGGCGTCAGC 26040

Qy      26041 GGCACCAACGCCCACATCATCCTCGAAGAAGCACCCACTCCCCAGGACAGCGATACCGAC 26100
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Db      26041 GGCACCAACGCCCACATCATCCTCGAAGAAGCACCCACTCCCCAGGACAGCGATACCGAC 26100

Qy      26101 GACGAACCGCCTGCCAACGCACCAGCCCTGCCCCATCCCCTCCCTCTTCCCGTGCCGGTG 26160
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Db      26101 GACGAACCGCCTGCCAACGCACCAGCCCTGCCCCATCCCCTCCCTCTTCCCGTGCCGGTG 26160

Qy      26161 TCGGCGAGGTCTGAGGCCGGGTTGCGGGCGCAGGCACAGGCGTTGCGCCAGTACGTGGCA 26220
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Db      26161 TCGGCGAGGTCTGAGGCCGGGTTGCGGGCGCAGGCACAGGCGTTGCGCCAGTACGTGGCA 26220

Qy      26221 GCCCGCCCGGACATGTCACCTGCCGACATTGGTGCGGGTCTGGCCCGCGGCCGGGCCGTA 26280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26221 GCCCGCCCGGACATGTCACCTGCCGACATTGGTGCGGGTCTGGCCCGCGGCCGGGCCGTA 26280

Qy      26281 CTGGAACACCGCGCCGTCATCCTGGCCGCGGACCGCGAGGAACTGGCGCAGGCACTGACA 26340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26281 CTGGAACACCGCGCCGTCATCCTGGCCGCGGACCGCGAGGAACTGGCGCAGGCACTGACA 26340

Qy      26341 GCCCTGGCAGCCGGCGAACCCCACCCCCACATCACCACAGGCCACACCCGGGGCGGTGAC 26400
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Db      26341 GCCCTGGCAGCCGGCGAACCCCACCCCCACATCACCACAGGCCACACCCGGGGCGGTGAC 26400

Qy      26401 CGCGGCGGCGTCGTCTTCGTCTTCCCCGGACAGGGCGGCCAGTGGGCCGGGATGGGCCTG 26460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26401 CGCGGCGGCGTCGTCTTCGTCTTCCCCGGACAGGGCGGCCAGTGGGCCGGGATGGGCCTG 26460

Qy      26461 ACCCTGCTCACCTCCTCACCCGTGTTCGCCGAACACATCGACGCATGCGAGAAAGCCCTC 26520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26461 ACCCTGCTCACCTCCTCACCCGTGTTCGCCGAACACATCGACGCATGCGAGAAAGCCCTC 26520

Qy      26521 ACCCCCTGGGTGCCCTGGTCCCTGACCGACATCCTGCACCGCGACCCCGACGACCCCGCA 26580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26521 ACCCCCTGGGTGCCCTGGTCCCTGACCGACATCCTGCACCGCGACCCCGACGACCCCGCA 26580

Qy      26581 TGGCAACAAGCCGACGTGGTCCAGCCCGTGCTCTTCAGCATCATGGTCTCCCTCGCCGCC 26640
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Db      26581 TGGCAACAAGCCGACGTGGTCCAGCCCGTGCTCTTCAGCATCATGGTCTCCCTCGCCGCC 26640

Qy      26641 CTGTGGCGCTCCTACGGCATCGAACCCGACGCGGTCCTCGGCCACTCCCAGGGAGAAATC 26700
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Db      26641 CTGTGGCGCTCCTACGGCATCGAACCCGACGCGGTCCTCGGCCACTCCCAGGGAGAAATC 26700

Qy      26701 GCCGCCGCCCACATCTGCGGCGCACTCAGCCTGAAAGACGCCGCCAAAACCGTTGCACTG 26760
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Db      26701 GCCGCCGCCCACATCTGCGGCGCACTCAGCCTGAAAGACGCCGCCAAAACCGTTGCACTG 26760

Qy      26761 CGCAGCCGCGCACTGGCCGCCGTACGAGGCCGGGGCGCCATGGCCTCACTGCCCCTGCCC 26820
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Db      26761 CGCAGCCGCGCACTGGCCGCCGTACGAGGCCGGGGCGCCATGGCCTCACTGCCCCTGCCC 26820

Qy      26821 GCCCAGGACGTGCAGCAGCTCATTTCCGAACGGTGGGAAGGGCAGTTGTGGGTGGCAGCC 26880
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Db      26821 GCCCAGGACGTGCAGCAGCTCATTTCCGAACGGTGGGAAGGGCAGTTGTGGGTGGCAGCC 26880

Qy      26881 CTCAACGGCCCCCACTCCACCACCGTCTCCGGCGACACCAAGGCGGTGGATGAGGTGCTG 26940
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Db      26881 CTCAACGGCCCCCACTCCACCACCGTCTCCGGCGACACCAAGGCGGTGGATGAGGTGCTG 26940

Qy      26941 GCGCACTGCACCGACACCGGCCTACGGGCCAAACGCATCCCCGTCGACTACGCCTCCCAC 27000
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Db      26941 GCGCACTGCACCGACACCGGCCTACGGGCCAAACGCATCCCCGTCGACTACGCCTCCCAC 27000

Qy      27001 TGCCCCCACGTCCAACCCCTCCACGACGAACTCCTGCACCTGCTGGGAGACATCACCCCC 27060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      27061 CAGCCGTCCACCGTGCCGTTCTTCTCCACCGTGGAAGGCACCTGGCTGGACACCACAACC 27120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27061 CAGCCGTCCACCGTGCCGTTCTTCTCCACCGTGGAAGGCACCTGGCTGGACACCACAACC 27120

Qy      27121 CTGGACGCCGCCTACTGGTACCGCAACCTCCACCAGCCCGTCCGCTTCAGCCACGCCATC 27180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27121 CTGGACGCCGCCTACTGGTACCGCAACCTCCACCAGCCCGTCCGCTTCAGCCACGCCATC 27180

Qy      27181 CAGACCCTGACCGACGACGGACACCGCGCCTTCATCGAAATCAGCCCCCACCCCACCCTC 27240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27181 CAGACCCTGACCGACGACGGACACCGCGCCTTCATCGAAATCAGCCCCCACCCCACCCTC 27240

Qy      27241 GTCCCCGCCATCGAAGACACCACCGAAAACACCACCGAAAACATCACCGCGACCGGCAGC 27300
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Db      27241 GTCCCCGCCATCGAAGACACCACCGAAAACACCACCGAAAACATCACCGCGACCGGCAGC 27300

Qy      27301 CTCCGCCGCGGCGACAACGACACCCACCGCTTCCTCACCGCCCTCGCCCACACCCACACC 27360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27301 CTCCGCCGCGGCGACAACGACACCCACCGCTTCCTCACCGCCCTCGCCCACACCCACACC 27360

Qy      27361 ACCGGCATCGGCACACCCACCACCTGGCACCACCACTACACCCAAACCCACCCCCACCCC 27420
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Db      27361 ACCGGCATCGGCACACCCACCACCTGGCACCACCACTACACCCAAACCCACCCCCACCCC 27420

Qy      27421 AACCCCCACACCCACCTCGACCTGCCCACCTACCCCTTCCAACACCAGCACTACTGGCTC 27480
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Db      27421 AACCCCCACACCCACCTCGACCTGCCCACCTACCCCTTCCAACACCAGCACTACTGGCTC 27480

Qy      27481 CAACCACCCACCACAACAACCGACCTCACCACCACCGGCCTCACCCCCACCCACCACCCC 27540
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Db      27481 CAACCACCCACCACAACAACCGACCTCACCACCACCGGCCTCACCCCCACCCACCACCCC 27540

Qy      27541 CTCCTCACCGCCACACTCACCCTCGCCGACAACAACACACAACTACTCACCGGCCGCCTC 27600
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Db      27541 CTCCTCACCGCCACACTCACCCTCGCCGACAACAACACACAACTACTCACCGGCCGCCTC 27600

Qy      27601 TCCCTACGCACCCACCCCTGGCTCACCGACCACACCGTCGCCGGCATGGTCCTCCTGCCG 27660
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Db      27601 TCCCTACGCACCCACCCCTGGCTCACCGACCACACCGTCGCCGGCATGGTCCTCCTGCCG 27660

Qy      27661 GGCACCGCGCTCCTCGAACTCGCCCTCCAAGCCGGCGAACGGGTGGACTGCCCTCGGGTG 27720
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Db      27661 GGCACCGCGCTCCTCGAACTCGCCCTCCAAGCCGGCGAACGGGTGGACTGCCCTCGGGTG 27720

Qy      27721 GAGGAACTGACCCTGCACGCACCGTTGGTGATCCCGCACACCGAGGACGTGACGTTGCAG 27780
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Db      27721 GAGGAACTGACCCTGCACGCACCGTTGGTGATCCCGCACACCGAGGACGTGACGTTGCAG 27780

Qy      27781 GTCACCGTTCGGGCAGCCGATGAGAGTGGCCATCGCGCCCTCGCGATCCACTCGTACTCC 27840
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Qy      27841 GGCACCGCGTCGTCGGCGGACCGGGAGTGGACCCGTCACGCCACGGGCCTCCTCACACAC 27900
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Db      27841 GGCACCGCGTCGTCGGCGGACCGGGAGTGGACCCGTCACGCCACGGGCCTCCTCACACAC 27900

Qy      27901 CACGCCGACACCGATCACCGTGCCGACACGCACACGGACGCGTGCCTTGGCGGGAGCTGG 27960
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Db      27901 CACGCCGACACCGATCACCGTGCCGACACGCACACGGACGCGTGCCTTGGCGGGAGCTGG 27960

Qy      27961 CCCCCGCCCGGCGCGCAGCCCATCGAACTGGGCGACGTCTACGGTCGTATGGCGGCGGAC 28020
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Db      27961 CCCCCGCCCGGCGCGCAGCCCATCGAACTGGGCGACGTCTACGGTCGTATGGCGGCGGAC 28020
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Qy      28021 TCGGACATCGCCTACGGGCCGGTCTTCCAGGGGCTGCACGCCGCCTGGAGGTTCGGCGAC 28080
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Db      28021 TCGGACATCGCCTACGGGCCGGTCTTCCAGGGGCTGCACGCCGCCTGGAGGTTCGGCGAC 28080

Qy      28081 GATGTCCTGGCCGAGGTGCGTCTGCCGGAAGAGGCTCTGCGCGATGCTCCGGCGGCGGCC 28140
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Db      28081 GATGTCCTGGCCGAGGTGCGTCTGCCGGAAGAGGCTCTGCGCGATGCTCCGGCGGCGGCC 28140

Qy      28141 TTCGGTGTTCACCCGGCCTTGCTCGACGCGGCCCTGCACGCCACGGCGCTCACCCCCCAG 28200
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Db      28141 TTCGGTGTTCACCCGGCCTTGCTCGACGCGGCCCTGCACGCCACGGCGCTCACCCCCCAG 28200

Qy      28201 AACGGGGACGGCTCGACGGAGAACGTCGCCCAGGAGAGCATGCCTGACCGCGCAGCCCAC 28260
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Db      28201 AACGGGGACGGCTCGACGGAGAACGTCGCCCAGGAGAGCATGCCTGACCGCGCAGCCCAC 28260

Qy      28261 CAGGCGCGACTGCCGTTCAGCTGGAGCGGCGTGTCCCTGCACACGGCGGGCAGTTCCGTG 28320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28261 CAGGCGCGACTGCCGTTCAGCTGGAGCGGCGTGTCCCTGCACACGGCGGGCAGTTCCGTG 28320

Qy      28321 TTGCGCGTACGGCTGTCGCGCAGTCCGCAGCACGGTAATGCCGTGGCCCTCACCGCGGCC 28380
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Db      28321 TTGCGCGTACGGCTGTCGCGCAGTCCGCAGCACGGTAATGCCGTGGCCCTCACCGCGGCC 28380

Qy      28381 GACGAGGACGGTCGGCCGGTGGTGACGATCGAGTCGCTCGCGCTGCGGCCGGTGTCCACC 28440
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Qy      28441 GAGGAGCTGCGCGCGGCCGCGGATCGTACGCCCGAGCACGAGTCGCTCTTCCGACTGGAC 28500
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Db      28441 GAGGAGCTGCGCGCGGCCGCGGATCGTACGCCCGAGCACGAGTCGCTCTTCCGACTGGAC 28500

Qy      28501 TGGGTTTCCGTACCAGTGCCCGCCAACGCCCCTTCGCCCACCGCGGACCGGCCCTGGGCG 28560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28501 TGGGTTTCCGTACCAGTGCCCGCCAACGCCCCTTCGCCCACCGCGGACCGGCCCTGGGCG 28560

Qy      28561 GTCATCGGCGCGGGCCTTCCCCACCTGCCCGGCCTGACGGAGCACGAGCACGTGACCGCG 28620
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Qy      28621 TATGACGAGCCGGCGGACCTGCTTCTGGCTCTGGACCGCGGTGCTCCGCCGCCCGGTGTG 28680
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Qy      28681 CTGGTCGTAGGTGGTGTCGCCCACACCGAAGCCCGGGAGTATTCCGCCGAAGCCCCCGGG 28740
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Qy      28741 GAGCGCGGGACCGAGGCCTGCGAGGCCCGGCCGGACGTCGTGCACGTGGGCGTCGTGCAC 28800
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Qy      28861 GACGAGCGCCTCGCAGACAGCCGGCTGCTCGTCCTGACGTGCGGCGCGGTCGCCCGCGCC 28920
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Qy      28921 TCCGGCGACGATGCGACGGACCTGCCCGGGGCCGCCGTGTGGGGGCTGGTGCGTTCGGCG 28980
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Qy      29041 CCCGGTCAGCTGGCGACGGCGCTGAACTGCGGGGAGCGGCAGCTTGCCGTCCGCCCCGGA 29100
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RESULT 2
AAA92301
ID   AAA92301 standard; DNA; 30690 BP.
XX
AC   AAA92301;
XX
DT   10-JAN-2001  (first entry)
XX
DE   S. avermitilis avermectin aglycon synthase DNA aveAI SEQ ID NO:1.
XX
KW   Streptomyces avermitilis; avermectin aglycon synthase; biosynthesis;
KW   multifunctional enzyme; polyketide; avermectin; veterinary drug;
KW   agrochemical; ds.
XX
OS   Streptomyces avermitilis.
XX
FH   Key             Location/Qualifiers
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PR   24-FEB-1999;   99JP-0046961.
XX
PA   (KITA ) KITASATO INST.
XX
PI   Omura S,  Ikeda H;
XX
DR   WPI; 2000-565458/52.
DR   P-PSDB; AAB23749, AAB23750.
XX
PT   Avermectin aglycone synthase DNA and proteins encoded by all or part of
PT   it for the production of avermectin and its derivatives for drug and
PT   agrochemical use  -
XX
PS   Claim 2; Page 66-134; 314pp; Japanese.
XX
CC   The present sequence represents DNA which encodes avermectin aglycon
CC   synthase proteins. Also described are: (1) polypeptides encoded by all
CC   or part of the DNA; (2) expression vectors containing the DNA; (3) host
CC   cells transformed by the vectors; (4) preparation of the polypeptides
CC   by culture of the transformants; (5) preparation of avermectin aglycon
CC   or its derivatives by culture of transformed avermectin-producing
CC   microorganisms; and (6) oligonucleotides of 5-60 bases in length
CC   containing sense or antisense sequences from the avermectin aglycon
CC   synthase DNA. The enzymes are useful for the production of modified
CC   forms of avermectin and of the intermediates in its biosynthesis, for
CC   use as drugs, veterinary drugs and agrochemicals.
XX
SQ   Sequence 30690 BP; 5356 A; 12454 C; 8617 G; 4263 T; 0 other;

  Query Match             99.9%;  Score 30672.4;  DB 21;  Length 30690;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 30679;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GTGCAGAGGATGGACGGCGGGGAAGAACCCCGCCCTGCGGCAGGGGAGGTCCTCGGAGTG 60
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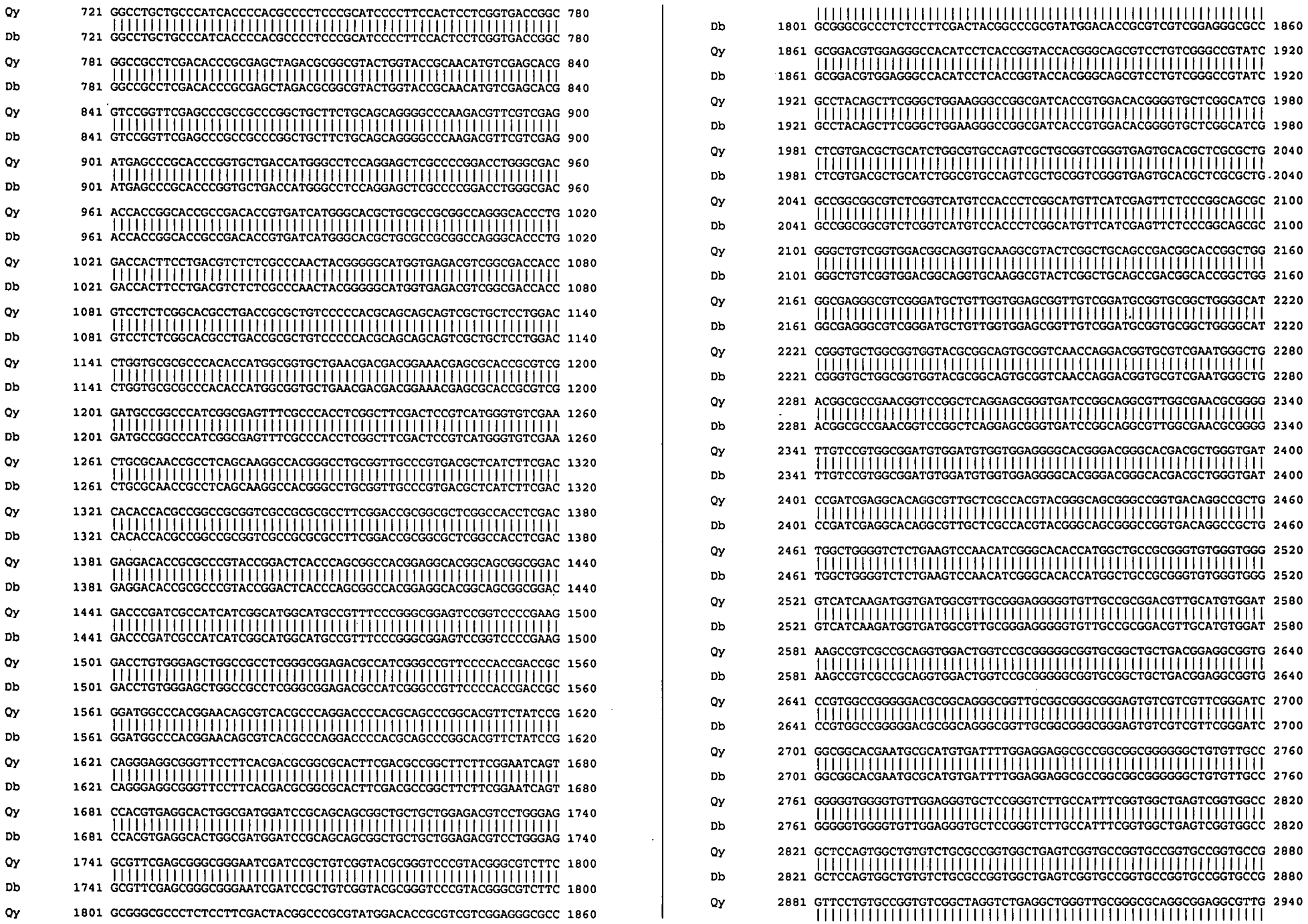
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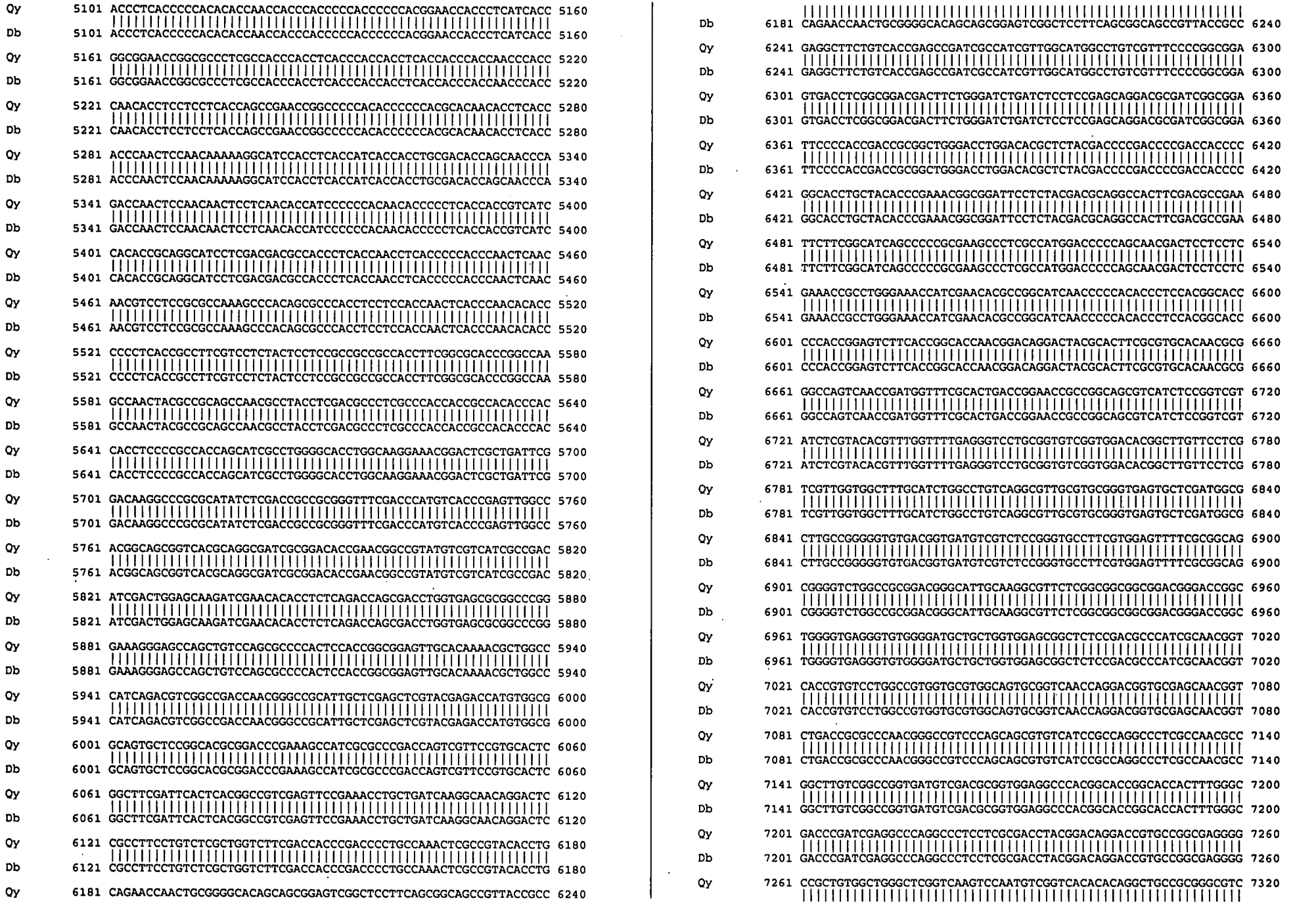
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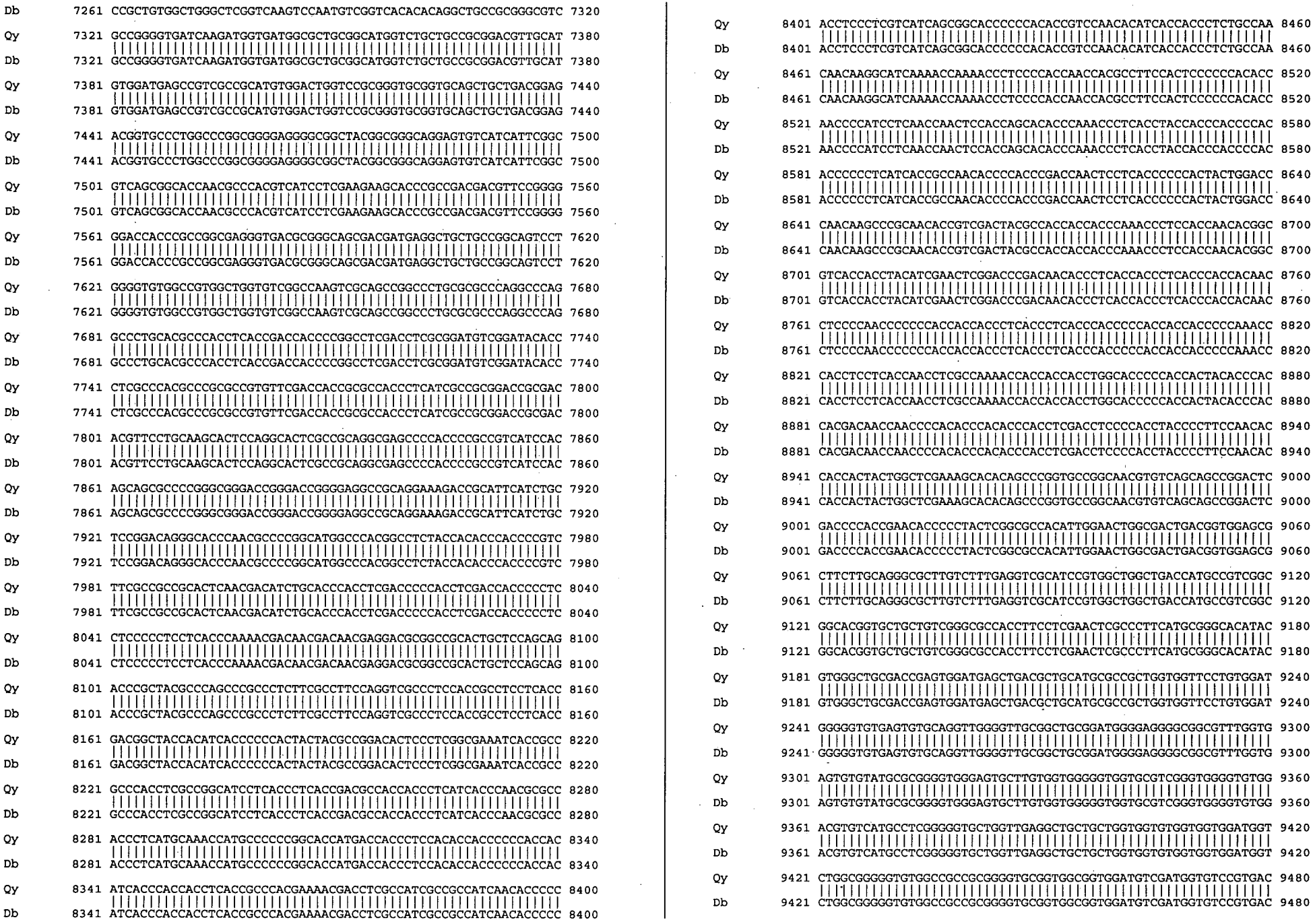
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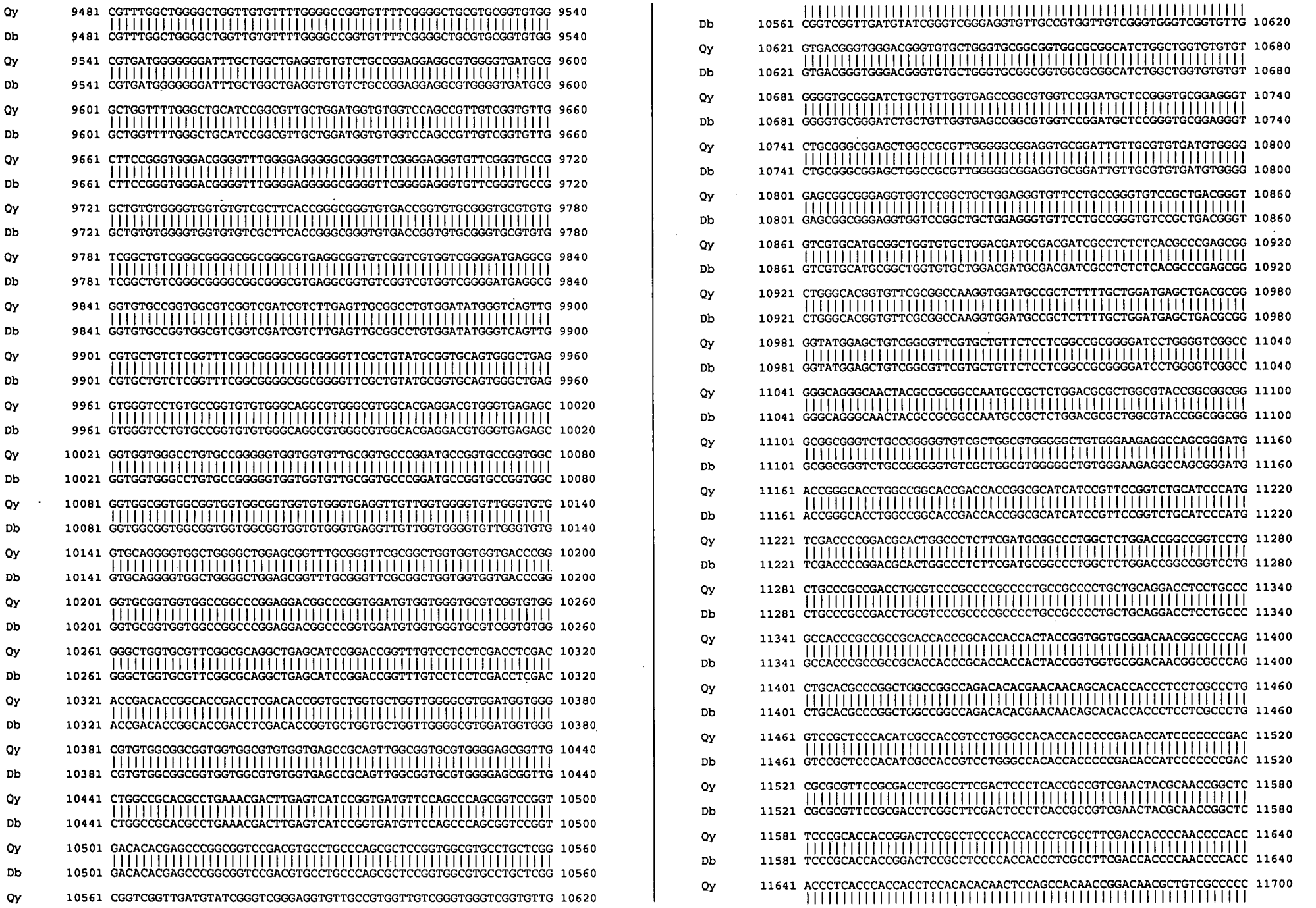

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Db 2341 TTGTCCGTGGCGGATGTGGATGTGGTGGAGGGGCACGGGACGGGCACGACGCTGGGTGAT 2400
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Db 2521 GTCATCAAGATGGTGATGGCGTTGCGGGAGGGGGTGTTGCCGCGGACGTTGCATGTGGAT 2580
Qy 2581 AAGCCGTCGCCGCAGGTGGACTGGTCCGCGGGGGCGGTGCGGCTGCTGACGGAGGCGGTG 2640
Db 2581 AAGCCGTCGCCGCAGGTGGACTGGTCCGCGGGGGCGGTGCGGCTGCTGACGGAGGCGGTG 2640
Qy 2641 CCGTGGCCGGGGGACGCGGCAGGGCGGTTGCGGCGGGCGGGAGTGTCGTCGTTCGGGATC 2700
Db 2641 CCGTGGCCGGGGGACGCGGCAGGGCGGTTGCGGCGGGCGGGAGTGTCGTCGTTCGGGATC 2700
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Qy 2761 GGGGGTGGGGTGTTGGAGGGTGCTCCGGGTCTTGCCATTTCGGTGGCTGAGTCGGTGGCC 2820
Db 2761 GGGGGTGGGGTGTTGGAGGGTGCTCCGGGTCTTGCCATTTCGGTGGCTGAGTCGGTGGCC 2820
Qy 2821 GCTCCAGTGGCTGTGTCTGCGCCGGTGGCTGAGTCGGTGCCGGTGCCGGTGCCGGTGCCG 2880
Db 2821 GCTCCAGTGGCTGTGTCTGCGCCGGTGGCTGAGTCGGTGCCGGTGCCGGTGCCGGTGCCG 2880
Qy 2881 GTTCCTGTGCCGGTGTCGGCTAGGTCTGAGGCTGGGTTGCGGGCGCAGGCGGAGGCGTTG 2940

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Qy       3001 TGTGGGCGGGCTGTGCTGGAGCATCGTGCGGTCGTCCTGGCCGCGGACCGTGAGGAGCTG 3060
Db       3001 TGTGGGCGGGCTGTGCTGGAGCATCGTGCGGTCGTCCTGGCCGCGGACCGTGAGGAGCTG 3060
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Qy       3121 GCGCCGGGTGGTGACCGGGGCGGTGTCGTCTTCGTGTTTCCCGGACAGGGTGGGCAGTGG 3180
Db       3121 GCGCCGGGTGGTGACCGGGGCGGTGTCGTCTTCGTGTTTCCCGGACAGGGTGGGCAGTGG 3180
Qy       3181 GCCGGGATGGGTGTGCGTCTGCTCGCCTCCTCTCCGGTGTTCGCCCGGCGGATGCAGGCG 3240
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Qy       3361 GTGTCTTTGGCTGCTCTGTGGCGTTCCTACGGTATCGAACCCGACGCGGTCCTTGGCCAT 3420
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Qy       3481 AAGACTGTTGCGCTGCGCAGCCGGGCGCTGGCCGCTGTGCGGGGCCGGGGCGGCATGGCC 3540
Db       3481 AAGACTGTTGCGCTGCGCAGCCGGGCGCTGGCCGCTGTGCGGGGCCGGGGCGGCATGGCC 3540
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Qy       3601 TTGTGGGTGGCGGCGGTCAACGGCCCCCGCTCCACCGCCGTCTCGGGGGATGCCGAGGCG 3660
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Db       3661 GTGGACGAGGTGCTGGCGTACTGTGCCGGCACCGGGGTGCGGGCCCGGCGGATCCCGGTC 3720
Qy       3721 GACTATGCCTCGCACTGCCCCCATGTGCAGCCCCTGCGGGAGGAGTTGCTGGAGCTGCTG 3780
Db       3721 GACTATGCCTCGCACTGCCCCCATGTGCAGCCCCTGCGGGAGGAGTTGCTGGAGCTGCTG 3780
Qy       3781 GGGGACATCAGCCCGCAGCCGTCCGGCGTGCCGTTCTTCTCCACGGTGGAGGGCACCTGG 3840
Db       3781 GGGGACATCAGCCCGCAGCCGTCCGGCGTGCCGTTCTTCTCCACGGTGGAGGGCACCTGG 3840
Qy       3841 CTGGACACCACAACCCTGGACGCCGCCTACTGGTACCGCAACCTGCACCAGCCGGTCCGT 3900
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Qy       3901 TTCAGCGATGCCGTCCAGGCCCTGGCGGATGACGGACACCGCGTCTTCGTCGAAGTCAGC 3960
Db       3901 TTCAGCGATGCCGTCCAGGCCCTGGCGGATGACGGACACCGCGTCTTCGTCGAAGTCAGC 3960
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Qy 9421 CTGGCGGGGGTGTGGCCGCCGCGGGGTGCGGTGGCGGTGGATGTCGATGGTGTCCGTGAC 9480
Db 9421 CTGGCGGGGGTGTGGCCGCCGCGGGGTGCGGTGGCGGTGGATGTCGATGGTGTCCGTGAC 9480



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Qy      11761 GCCAGCGAAAGAGTCACCCTGCGGCTGAAGTCACTCATGTTGAGGTGGAACGCACCCCAG 11820
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Qy      12181 TTCCCGACCGACCGTGGATGGAACCTGGAGCAGCTCTACGACCCGGACCCCGACCGCTCA 12240
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Qy      12541 CGTATCTCCTACAACTTCGGGCTCGAAGGCCCTGCGATCACTATCGACACCGCGTGTTCC 12600
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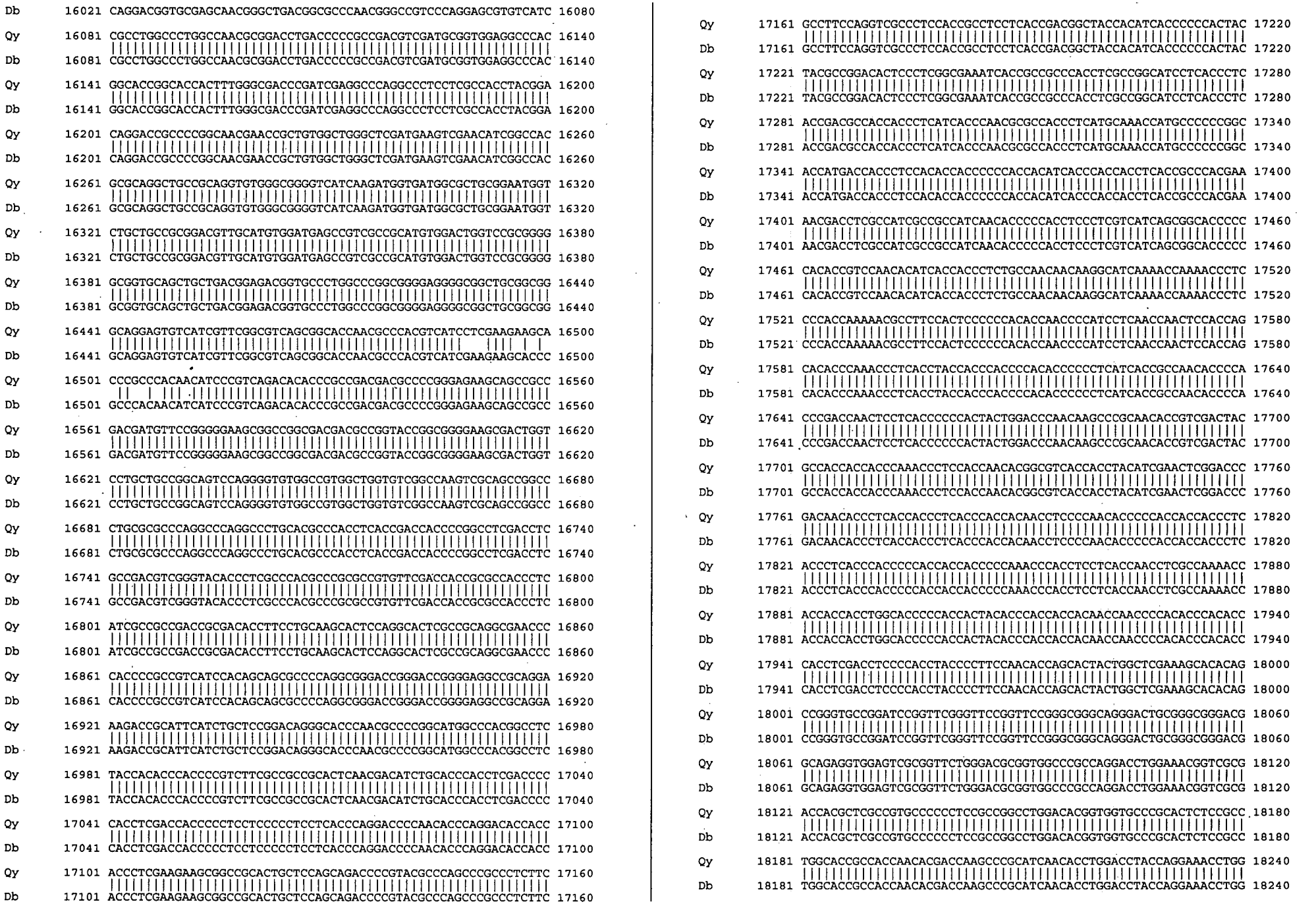
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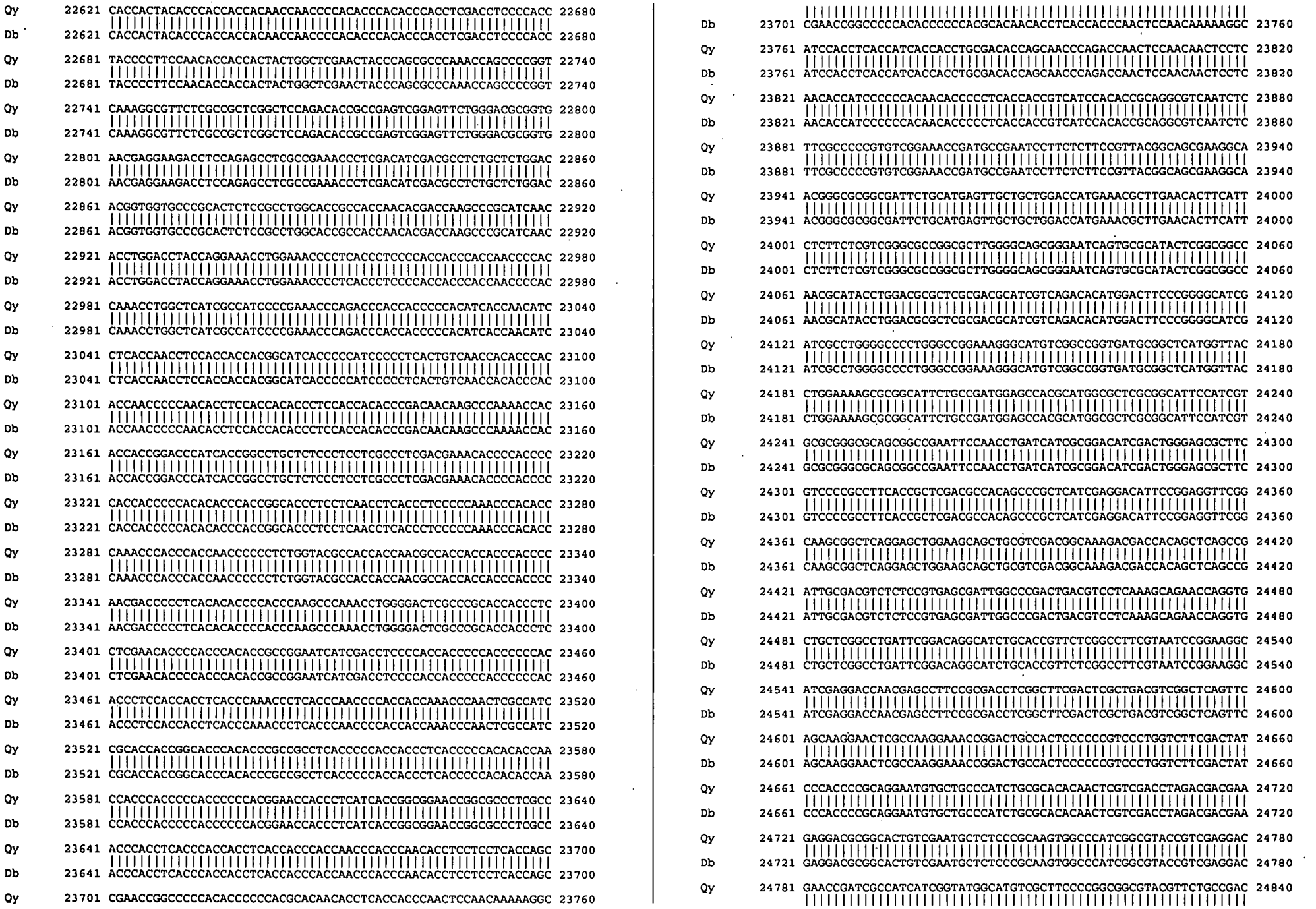
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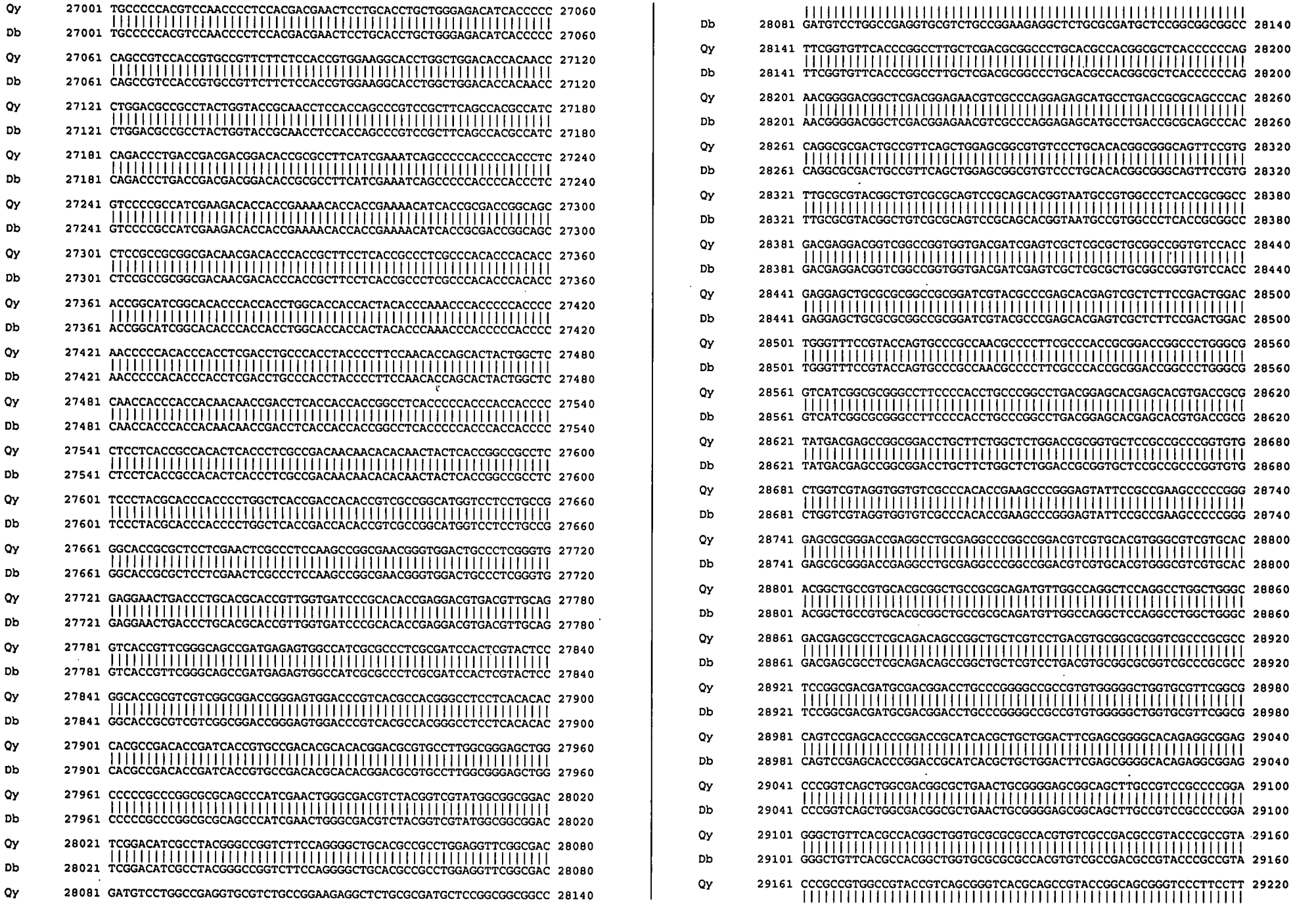
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Db      30361 CAGCTCTCCGGCGGCAGCGAGGAGGACGTACGCAGCCTCCTGACGTCCATTCCGATCGGC 30420

Qy      30421 AGGCTGCGGGACGCGGGGCTCCTCGGGCCCCTGCTCACGCTCGCGGACACGGGCCGCGGC 30480
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Qy      30481 GCCTCGGGCGCCGCCGCAGGTCCGGAGGACGCGCCGCCCTCCGGCCAGGACACACCGGCT 30540
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Db      30481 GCCTCGGGCGCCGCCGCAGGTCCGGAGGACGCGCCGCCCTCCGGCCAGGACACACCGGCT 30540

Qy      30541 CCCGTCTCGATCGACGAGATGGACATCGACGACCTGATGGATCTGGCGCACGGGCATGGC 30600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30541 CCCGTCTCGATCGACGAGATGGACATCGACGACCTGATGGATCTGGCGCACGGGCATGGC 30600

Qy      30601 ACCGCACCCGCCCGTGAGCCCGCCGACGCAGAGGACTCGTCGTCATCACGAAACCGGACA 30660
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Qy      30661 CACCACACACACGAAGGTGAGACAGCGTGA 30690
              ||||||||||||||||||||||||||||||
Db      30661 CACCACACACACGAAGGTGAGACAGCGTGA 30690
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RESULT 3
AAH79279
ID AAH79279 standard; DNA; 11916 BP.
XX
AC AAH79279;
XX
DT 04-DEC-2001 (first entry)
XX
DE Streptomyces avermitilis coding sequence derivative SEQ ID NO: 3.
XX
KW Avermectin aglycone synthase; AAS; avermectin derivative;
KW drug production; vetinary drug; pesticide; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..11916
FT /*tag= a
FT /product= "AAG65268"
FT /partial
XX
PN WO200162939-A1.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-JP01381.
XX
PR 24-FEB-2000; 2000JP-0047405.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (KITA) KITASATO INST.
XX
PI Endo H, Yamaguchi H, Kanda Y, Hashimoto S, Omura S, Ikeda H;
XX
DR WPI; 2001-582053/65.
DR P-PSDB; AAG65268.
XX
PT New modified avermectin aglycone synthase derived from Streptomyces
PT avermectilis used in production of 22,23-dihydroavermectin B1a used in
PT drugs and pesticides -
XX
PS Claim 10; Page 149-167; 257pp; Japanese.
XX

CC The present invention relates to the production of modified derivatives
CC of avermectin aglycone synthase (AAS) derived from Streptomyces
CC avermitilis. The activity of an acyl carrier protein (ACP),
CC beta-ketoacyl carrier protein synthase (KS), acyltransferase (AT),
CC beta-ketoacyl carrier protein reductase (KR), dehydratase (DH), enoyl
CC reductase (ER) and/or thioesterase (TE) domain may be reduced or
CC suppressed. The process can be used in the production of drugs, vetinary
CC drugs and pesticides. The present sequence is modified version of a
CC fragment of the S. avermitilis genome.
XX
SQ Sequence 11916 BP; 1831 A; 4428 C; 3820 G; 1837 T; 0 other;

Query Match 38.8%; Score 11914.4; DB 22; Length 11916;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 11915; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 GTGCAGAGGATGGACGGCGGGGAAGAACCCCGCCCTGCGGCAGGGGAGGTCCTCGGAGTG 60
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Qy         61 GCCGACGAGGCGGACGGCGGCGTCGTCTTCGTTTTTCCCGGGCAGGGCCCGCAATGGCCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCGACGAGGCGGACGGCGGCGTCGTCTTCGTTTTTCCCGGGCAGGGCCCGCAATGGCCG 120

Qy        121 GGCATGGGAAGGGAACTTCTCGACGCTTCCGACGTCTTCCGGGAGAGCGTCCGCGCCTGC 180
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Db        121 GGCATGGGAAGGGAACTTCTCGACGCTTCCGACGTCTTCCGGGAGAGCGTCCGCGCCTGC 180

Qy        181 GAAGCCGCGTTCGCGCCCTACGTCGACTGGTCGGTGGAGCAGGTGTTGCGGGACTCGCCG 240
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Qy        241 GACGCTCCCGGGCTGGACCGGGTGGACGTCGTCCAGCCGACCCTGTTCGCCGTCATGATC 300
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Qy        301 TCCCTGGCCGCCCTCTGGCGCTCGCAAGGGGTCGAGCCGTGCGCGGTGCTGGGACACAGC 360
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Db        301 TCCCTGGCCGCCCTCTGGCGCTCGCAAGGGGTCGAGCCGTGCGCGGTGCTGGGACACAGC 360

Qy        361 CTGGGCGAGATCGCGGCAGCCCACGTCTCGGGAGGCCTGTCCCTGGCCGACGCCGCACGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        421 GTGGTGACGCTTTGGAGCCAGGCACAGACCACCCTTGCCGGGACCGGCGCGCTCGTCTCC 480
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Qy        481 GTCGCCGCCACGCCGGATGAGCTCCTGCCCCGAATCGCTCCGTGGACCGAGGACAACCCG 540
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Db        481 GTCGCCGCCACGCCGGATGAGCTCCTGCCCCGAATCGCTCCGTGGACCGAGGACAACCCG 540

Qy        541 GCGCGGCTCGCCGTCGCAGCCGTCAACGGACCCCGGAGCACAGTCGTTTCCGGTGCCCGC 600
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Db        541 GCGCGGCTCGCCGTCGCAGCCGTCAACGGACCCCGGAGCACAGTCGTTTCCGGTGCCCGC 600

Qy        601 GAGGCCGTCGCGGACCTGGTGGCCGACCTCACCGCCGCGCAGGTGCGCACGCGCATGATC 660
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Qy        661 CCGGTGGACGTTCCCGCCCACTCCCCCCTGATGTACGCCATCGAGGAACGGGTCGTCAGC 720
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Qy        721 GGCCTGCTGCCCATCACCCCACGCCCCTCCCGCATCCCCTTCCACTCCTCGGTGACCGGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        781 GGCCGCCTCGACACCCGCGAGCTAGACGCGGCGTACTGGTACCGCAACATGTCGAGCACG 840
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Qy        901 ATGAGCCCGCACCCGGTGCTGACCATGGGCCTCCAGGAGCTCGCCCCGGACCTGGGCGAC 960
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Qy        961 ACCACCGGCACCGCCGACACCGTGATCATGGGCACGCTGCGCCGCGGCCAGGGCACCCTG 1020
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Db        961 ACCACCGGCACCGCCGACACCGTGATCATGGGCACGCTGCGCCGCGGCCAGGGCACCCTG 1020

Qy       1021 GACCACTTCCTGACGTCTCTCGCCCAACTACGGGGGCATGGTGAGACGTCGGCGACCACC 1080
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Db       1021 GACCACTTCCTGACGTCTCTCGCCCAACTACGGGGGCATGGTGAGACGTCGGCGACCACC 1080

Qy       1081 GTCCTCTCGGCACGCCTGACCGCGCTGTCCCCCACGCAGCAGCAGTCGCTGCTCCTGGAC 1140
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Qy       1141 CTGGTGCGCGCCCACACCATGGCGGTGCTGAACGACGACGGAAACGAGCGCACCGCGTCG 1200
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Db       1141 CTGGTGCGCGCCCACACCATGGCGGTGCTGAACGACGACGGAAACGAGCGCACCGCGTCG 1200

Qy       1201 GATGCCGGCCCATCGGCGAGTTTCGCCCACCTCGGCTTCGACTCCGTCATGGGTGTCGAA 1260
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Qy       1321 CACACCACGCCGGCCGCGGTCGCCGCGCGCCTTCGGACCGCGGCGCTCGGCCACCTCGAC 1380
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Qy       1381 GAGGACACCGCGCCCGTACCGGACTCACCCAGCGGCCACGGAGGCACGGCAGCGGCGGAC 1440
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Qy       1441 GACCCGATCGCCATCATCGGCATGGCATGCCGTTTCCCGGGCGGAGTCCGGTCCCCGAAG 1500
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Db       1441 GACCCGATCGCCATCATCGGCATGGCATGCCGTTTCCCGGGCGGAGTCCGGTCCCCGAAG 1500

Qy       1501 GACCTGTGGGAGCTGGCCGCCTCGGGCGGAGACGCCATCGGGCCGTTCCCCACCGACCGC 1560
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Qy       1561 GGATGGCCCACGGAACAGCGTCACGCCCAGGACCCCACGCAGCCCGGCACGTTCTATCCG 1620
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Qy       1621 CAGGGAGGCGGGTTCCTTCACGACGCGGCGCACTTCGACGCCGGCTTCTTCGGAATCAGT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CAGGGAGGCGGGTTCCTTCACGACGCGGCGCACTTCGACGCCGGCTTCTTCGGAATCAGT 1680

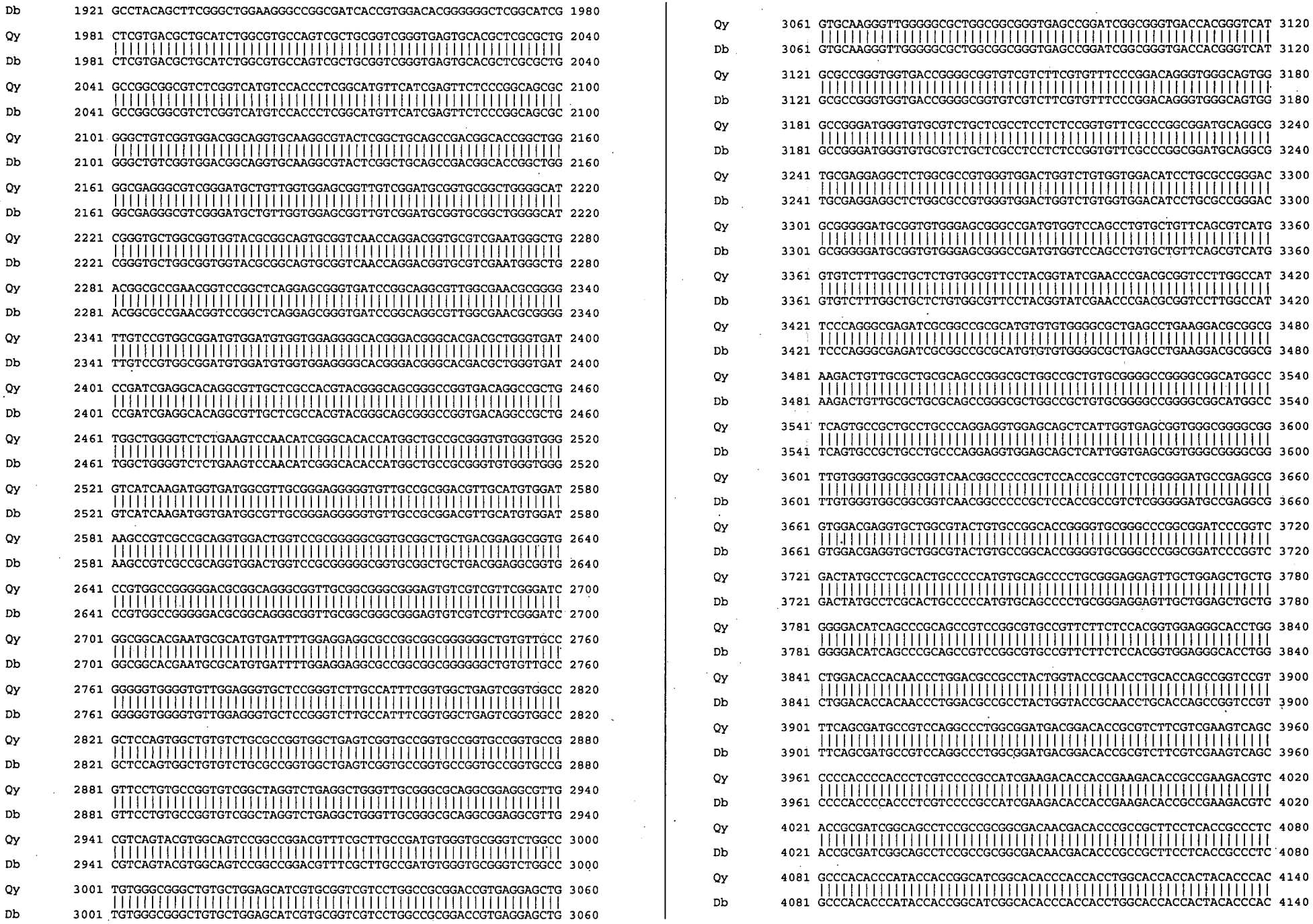
Qy       1681 CCACGTGAGGCACTGGCGATGGATCCGCAGCAGCGGCTGCTGCTGGAGACGTCCTGGGAG 1740
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Qy       1741 GCGTTCGAGCGGGCGGGAATCGATCCGCTGTCGGTACGCGGGTCCCGTACGGGCGTCTTC 1800
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Db       1741 GCGTTCGAGCGGGCGGGAATCGATCCGCTGTCGGTACGCGGGTCCCGTACGGGCGTCTTC 1800

Qy       1801 GCGGGCGCCCTCTCCTTCGACTACGGCCCGCGTATGGACACCGCGTCGTCGGAGGGCGCC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GCGGGCGCCCTCTCCTTCGACTACGGCCCGCGTATGGACACCGCGTCGTCGGAGGGCGCC 1860

Qy       1861 GCGGACGTGGAGGGCCACATCCTCACCGGTACCACGGGCAGCGTCCTGTCGGGCCGTATC 1920
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Db       1861 GCGGACGTGGAGGGCCACATCCTCACCGGTACCACGGGCAGCGTCCTGTCGGGCCGTATC 1920

Qy       1921 GCCTACAGCTTCGGGCTGGAAGGGCCGGCGATCACCGTGGACACGGGGTGCTCGGCATCG 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
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Db 1921 GCCTACAGCTTCGGGCTGGAAGGGCCGGCGATCACCGTGGACACGGGGGGCTCGGCATCG 1980
Qy 1981 CTCGTGACGCTGCATCTGGCGTGCCAGTCGCTGCGGTCGGGTGAGTGCACGCTCGCGCTG 2040
Db 1981 CTCGTGACGCTGCATCTGGCGTGCCAGTCGCTGCGGTCGGGTGAGTGCACGCTCGCGCTG 2040
Qy 2041 GCCGGCGGCGTCTCGGTCATGTCCACCCTCGGCATGTTCATCGAGTTCTCCCGGCAGCGC 2100
Db 2041 GCCGGCGGCGTCTCGGTCATGTCCACCCTCGGCATGTTCATCGAGTTCTCCCGGCAGCGC 2100
Qy 2101 GGGCTGTCGGTGGACGGCAGGTGCAAGGCGTACTCGGCTGCAGCCGACGGCACCGGCTGG 2160
Db 2101 GGGCTGTCGGTGGACGGCAGGTGCAAGGCGTACTCGGCTGCAGCCGACGGCACCGGCTGG 2160
Qy 2161 GGCGAGGGCGTCGGGATGCTGTTGGTGGAGCGGTTGTCGGATGCGGTGCGGCTGGGGCAT 2220
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Qy 2221 CGGGTGCTGGCGGTGGTACGCGGCAGTGCGGTCAACCAGGACGGTGCGTCGAATGGGCTG 2280
Db 2221 CGGGTGCTGGCGGTGGTACGCGGCAGTGCGGTCAACCAGGACGGTGCGTCGAATGGGCTG 2280
Qy 2281 ACGGCGCCGAACGGTCCGGCTCAGGAGCGGGTGATCCGGCAGGCGTTGGCGAACGCGGGG 2340
Db 2281 ACGGCGCCGAACGGTCCGGCTCAGGAGCGGGTGATCCGGCAGGCGTTGGCGAACGCGGGG 2340
Qy 2341 TTGTCCGTGGCGGATGTGGATGTGGTGGAGGGGCACGGGACGGGCACGACGCTGGGTGAT 2400
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Db 2521 GTCATCAAGATGGTGATGGCGTTGCGGGAGGGGGTGTTGCCGCGGACGTTGCATGTGGAT 2580
Qy 2581 AAGCCGTCGCCGCAGGTGGACTGGTCCGCGGGGGCGGTGCGGCTGCTGACGGAGGCGGTG 2640
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Qy 2641 CCGTGGCCGGGGGACGCGGCAGGGCGGTTGCGGCGGGCGGGAGTGTCGTCGTTCGGGATC 2700
Db 2641 CCGTGGCCGGGGGACGCGGCAGGGCGGTTGCGGCGGGCGGGAGTGTCGTCGTTCGGGATC 2700
Qy 2701 GGCGGCACGAATGCGCATGTGATTTTGGAGGAGGCGCCGGCGGCGGGGGGCTGTGTTGCC 2760
Db 2701 GGCGGCACGAATGCGCATGTGATTTTGGAGGAGGCGCCGGCGGCGGGGGGCTGTGTTGCC 2760
Qy 2761 GGGGGTGGGGTGTTGGAGGGTGCTCCGGGTCTTGCCATTTCGGTGGCTGAGTCGGTGGCC 2820
Db 2761 GGGGGTGGGGTGTTGGAGGGTGCTCCGGGTCTTGCCATTTCGGTGGCTGAGTCGGTGGCC 2820
Qy 2821 GCTCCAGTGGCTGTGTCTGCGCCGGTGGCTGAGTCGGTGCCGGTGCCGGTGCCGGTGCCG 2880
Db 2821 GCTCCAGTGGCTGTGTCTGCGCCGGTGGCTGAGTCGGTGCCGGTGCCGGTGCCGGTGCCG 2880
Qy 2881 GTTCCTGTGCCGGTGTCGGCTAGGTCTGAGGCTGGGTTGCGGGCGCAGGCGGAGGCGTTG 2940
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Qy 2941 CGTCAGTACGTGGCAGTCCGGCCGGACGTTTCGCTTGCCGATGTGGGTGCGGGTCTGGCC 3000
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Qy 3001 TGTGGGCGGGCTGTGCTGGAGCATCGTGCGGTCGTCCTGGCCGCGGACCGTGAGGAGCTG 3060
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Qy 3061 GTGCAAGGGTTGGGGGCGCTGGCGGCGGGTGAGCCGGATCGGCGGGTGACCACGGGTCAT 3120
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Qy 3481 AAGACTGTTGCGCTGCGCAGCCGGGCGCTGGCCGCTGTGCGGGGCCGGGGCGGCATGGCC 3540
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Qy      4141 CACCACACCCACCCCCACCCCCACACGCACCTCGACCTGCCCACCTACCCCTTCCAACAC 4200
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Qy      4201 CAGCACTACTGGCTCGAGAGCTCACAGCCGGGTGCCGGATCCGGTTCGGGTGCCGGTGCC 4260
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Qy      4261 GGTTCGGGTGCCGGTTCCGGGCGGGCAGGGACTGCGGGCGGGACGGCAGAGGTGGAGTCG 4320
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Qy      4321 CGGTTCTGGGACGCGGTGGCCCGCCAGGACCTGGAAACGGTCGCGACCACACTCGCCGTG 4380
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 CACCCCCACATCACCAACATCCTCACCAACCTCCACCACCACGGCATCACCCCCATCCCC 4620

Qy      4621 CTCACCCTCAACCACACCCACACCAACCCCCAACACCTCCACCACACCCTCCACCACACC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4621 CTCACCCTCAACCACACCCACACCAACCCCCAACACCTCCACCACACCCTCCACCACACC 4680

Qy      4681 CGACAACAAGCCCAAAACCACACCACCGGAGCCATCACCGGCCTGCTCTCCCTCCTCGCC 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4681 CGACAACAAGCCCAAAACCACACCACCGGAGCCATCACCGGCCTGCTCTCCCTCCTCGCC 4740

Qy      4741 CTCGACGAAACACCCCACCCCCACCACCCCCACACACCCACCGGCACCCTCCTCAACCTC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4741 CTCGACGAAACACCCCACCCCCACCACCCCCACACACCCACCGGCACCCTCCTCAACCTC 4800

Qy      4801 ACCCTCACCCAAACCCACACCCAAACCCACCCACCAACCCCCCCTCTGGTACGCCACCACC 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4801 ACCCTCACCCAAACCCACACCCAAACCCACCCACCAACCCCCCTCTGGTACGCCACCACC 4860

Qy      4861 AACGCCACCACCACCCACCCCAACGACCCCCTCACACACCCCACCCAAGCCCAAACCTGG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4861 AACGCCACCACCACCCACCCCAACGACCCCCTCACACACCCCACCCAAGCCCAAACCTGG 4920

Qy      4921 GGACTCGCCCGCACCACCCTCCTCGAACACCCCACCCACACCGCCGGAATCATCGACCTC 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4921 GGACTCGCCCGCACCACCCTCCTCGAACACCCCACCCACACCGCCGGAATCATCGACCTC 4980

Qy      4981 CCCACCACCCCCACCCCCCACACCCTCCAGCACCTCACCCAAACCCTCACCCAACCCCAC 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4981 CCCACCACCCCCACCCCCCACACCCTCCAGCACCTCACCCAAACCCTCACCCAACCCCAC 5040

Qy      5041 CACCAAACCCAACTCGCCATCCGCACCACCGGCACCCACACCCGCCGCCTCACCCCCACC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 CACCAAACCCAACTCGCCATCCGCACCACCGGCACCCACACCCGCCGCCTCACCCCCACC 5100

Qy      5101 ACCCTCACCCCCACACACCAACCACCCACCCCCACCCCCCACGGAACCACCCTCATCACC 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5101 ACCCTCACCCCCACACACCAACCACCCACCCCCACCCCCCACGGAACCACCCTCATCACC 5160

Qy      5161 GGCGGAACCGGCGCCCTCGCCACCCACCTCACCCACCACCTCACCACCCACCAACCCACC 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5161 GGCGGAACCGGCGCCCTCGCCACCCACCTCACCCACCACCTCACCACCCACCAACCCACC 5220

Qy      5221 CAACACCTCCTCCTCACCAGCCGAACCGGCCCCCACACCCCCCACGCACAACACCTCACC 5280
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 CAACACCTCCTCCTCACCAGCCGAACCGGCCCCCACACCCCCCACGCACAACACCTCACC 5280

Qy      5281 ACCCAACTCCAACAAAAAGGCATCCACCTCACCATCACCACCTGCGACACCAGCAACCCA 5340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5281 ACCCAACTCCAACAAAAAGGCATCCACCTCACCATCACCACCTGCGACACCAGCAACCCA 5340

Qy      5341 GACCAACTCCAACAACTCCTCAACACCATCCCCCCACAACACCCCCTCACCACCGTCATC 5400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341 GACCAACTCCAACAACTCCTCAACACCATCCCCCCACAACACCCCCTCACCACCGTCATC 5400

Qy      5401 CACACCGCAGGCATCCTCGACGACGCCCACCCTCACCAACCTCACCCCCACCCAACTCAAC 5460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401 CACACCGCAGGCATCCTCGACGACGCCCACCCTCACCAACCTCACCCCCACCCAACTCAAC 5460

Qy      5461 AACGTCCTCCGCGCCAAAGCCCACAGCGCCCACCTCCTCCACCAACTCACCCAACACACC 5520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 AACGTCCTCCGCGCCAAAGCCCACAGCGCCCACCTCCTCCACCAACTCACCCAACACACC 5520

Qy      5521 CCCCTCACCGCCTTCGTCCTCTACTCCTCCGCCGCCGCCACCTTCGGCGCACCCGGCCAA 5580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 CCCCTCACCGCCTTCGTCCTCTACTCCTCCGCCGCCGCCACCTTCGGCGCACCCGGCCAA 5580

Qy      5581 GCCAACTACGCCGCAGCCAACGCCTACCTCGACGCCCTCGCCCACCACCGCCACACCCAC 5640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 GCCAACTACGCCGCAGCCAACGCCTACCTCGACGCCCTCGCCCACCACCGCCACACCCAC 5640

Qy      5641 CACCTCCCCGCCACCAGCATCGCCTGGGGCACCTGGCAAGGAAACGGACTCGCTGATTCG 5700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5641 CACCTCCCCGCCACCAGCATCGCCTGGGGCACCTGGCAAGGAAACGGACTCGCTGATTCG 5700

Qy      5701 GACAAGGCCCGCGCATATCTCGACCGCCGCGGGTTTCGACCCATGTCACCCGAGTTGGCC 5760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5701 GACAAGGCCCGCGCATATCTCGACCGCCGCGGGTTTCGACCCATGTCACCCGAGTTGGCC 5760

Qy      5761 ACGGCAGCGGTCACGCAGGCGATCGCGGACACCGAACGGCCGTATGTCGTCATCGCCGAC 5820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5761 ACGGCAGCGGTCACGCAGGCGATCGCGGACACCGAACGGCCGTATGTCGTCATCGCCGAC 5820

Qy      5821 ATCGACTGGAGCAAGATCGAACACACCTCTCAGACCAGCGACCTGGTGAGCGCGGCCCGG 5880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5821 ATCGACTGGAGCAAGATCGAACACACCTCTCAGACCAGCGACCTGGTGAGCGCGGCCCGG 5880

Qy      5881 GAAAGGGAGCCAGCTGTCCAGCGCCCCACTCCACCGGCGGAGTTGCACAAAACGCTGGCC 5940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5881 GAAAGGGAGCCAGCTGTCCAGCGCCCCACTCCACCGGCGGAGTTGCACAAAACGCTGGCC 5940

Qy      5941 CATCAGACGTCGGCCGACCAACGGGCCGCATTGCTCGAGCTCGTACGAGACCATGTGGCG 6000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5941 CATCAGACGTCGGCCGACCAACGGGCCGCATTGCTCGAGCTCGTACGAGACCATGTGGCG 6000

Qy      6001 GCAGTGCTCCGGCACGCGGACCCGAAAGCCATCGCGCCCGACCAGTCGTTCCGTGCACTC 6060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6001 GCAGTGCTCCGGCACGCGGACCCGAAAGCCATCGCGCCCGACCAGTCGTTCCGTGCACTC 6060

Qy      6061 GGCTTCGATTCACTCACGGCCGTCGAGTTCCGAAACCTGCTGATCAAGGCAACAGGACTC 6120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6061 GGCTTCGATTCACTCACGGCCGTCGAGTTCCGAAACCTGCTGATCAAGGCAACAGGACTC 6120

Qy      6121 CGCCTTCCTGTCTCGCTGGTCTTCGACCACCCGACCCCTGCCAAACTCGCCGTACACCTG 6180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6121 CGCCTTCCTGTCTCGCTGGTCTTCGACCACCCGACCCCTGCCAAACTCGCCGTACACCTG 6180

Qy      6181 CAGAACCAACTGCGGGGCACAGCAGCGGAGTCGGCTCCTTCAGCGGCAGCCGTTACCGCC 6240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6181 CAGAACCAACTGCGGGGCACAGCAGCGGAGTCGGCTCCTTCAGCGGCAGCCGTTACCGCC 6240

Qy      6241 GAGGCTTCTGTCACCGAGCCGATCGCCATCGTTGGCATGGCCTGTCGTTTCCCCGGCGGA 6300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6241 GAGGCTTCTGTCACCGAGCCGATCGCCATCGTTGGCATGGCCTGTCGTTTCCCCGGCGGA 6300

Qy      6301 GTGACCTCGGCGGACGACTTCTGGGATCTGATCTCCTCCGAGCAGGACGCGATCGGCGGA 6360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      6301 GTGACCTCGGCGGACGACTTCTGGGATCTGATCTCCTCCGAGCAGGACGCGATCGGCGGA 6360
Qy      6361 TTCCCCACCGACCGCGGCTGGGACCTGGACACGCTCTACGACCCCGACCCCGACCACCCC 6420
Db      6361 TTCCCCACCGACCGCGGCTGGGACCTGGACACGCTCTACGACCCCGACCCCGACCACCCC 6420
Qy      6421 GGCACCTGCTACACCCGAAACGGCGGATTCCTCTACGACGCAGGCCACTTCGACGCCGAA 6480
Db      6421 GGCACCTGCTACACCCGAAACGGCGGATTCCTCTACGACGCAGGCCACTTCGACGCCGAA 6480
Qy      6481 TTCTTCGGCATCAGCCCCCGCGAAGCCCTCGCCATGGACCCCCAGCAACGACTCCTCCTC 6540
Db      6481 TTCTTCGGCATCAGCCCCCGCGAAGCCCTCGCCATGGACCCCCAGCAACGACTCCTCCTC 6540
Qy      6541 GAAACCGCCTGGGAAACCATCGAACACGCCGGCATCAACCCCCACACCCTCCACGGCACC 6600
Db      6541 GAAACCGCCTGGGAAACCATCGAACACGCCGGCATCAACCCCCACACCCTCCACGGCACC 6600
Qy      6601 CCCACCGGAGTCTTCACCGGCACCAACGGACAGGACTACGCACTTCGCGTGCACAACGCG 6660
Db      6601 CCCACCGGAGTCTTCACCGGCACCAACGGACAGGACTACGCACTTCGCGTGCACAACGCG 6660
Qy      6661 GGCCAGTCAACCGATGGTTTCGCACTGACCGGAACCGCCGGCAGCGTCATCTCCGGTCGT 6720
Db      6661 GGCCAGTCAACCGATGGTTTCGCACTGACCGGAACCGCCGGCAGCGTCATCTCCGGTCGT 6720
Qy      6721 ATCTCGTACACGTTTGGTTTTGAGGGTCCTGCGGTGTCGGTGGACACGGCTTGTTCCTCG 6780
Db      6721 ATCTCGTACACGTTTGGTTTTGAGGGTCCTGCGGTGTCGGTGGACACGGCTTGTTCCTCG 6780
Qy      6781 TCGTTGGTGGCTTTGCATCTGGCCTGTCAGGCGTTGCGTGCGGGTGAGTGCTCGATGGCG 6840
Db      6781 TCGTTGGTGGCTTTGCATCTGGCCTGTCAGGCGTTGCGTGCGGGTGAGTGCTCGATGGCG 6840
Qy      6841 CTTGCCGGGGGTGTGACGGTGATGTCGTCTCCGGGTGCCTTCGTGGAGTTTTCGCGGCAG 6900
Db      6841 CTTGCCGGGGGTGTGACGGTGATGTCGTCTCCGGGTGCCTTCGTGGAGTTTTCGCGGCAG 6900
Qy      6901 CGGGGTCTGGCCGCGGACGGGCATTGCAAGGCGTTCTCGGCGGCGGCGGACGGGACCGGC 6960
Db      6901 CGGGGTCTGGCCGCGGACGGGCATTGCAAGGCGTTCTCGGCGGCGGCGGACGGGACCGGC 6960
Qy      6961 TGGGGTGAGGGTGTGGGGATGCTGCTGGTGGAGCGGCTCTCCGACGCCCATCGCAACGGT 7020
Db      6961 TGGGGTGAGGGTGTGGGGATGCTGCTGGTGGAGCGGCTCTCCGACGCCCATCGCAACGGT 7020
Qy      7021 CACCGTGTCCTGGCCGTGGTGCGTGGCAGTGCGGTCAACCAGGACGGTGCGAGCAACGGT 7080
Db      7021 CACCGTGTCCTGGCCGTGGTGCGTGGCAGTGCGGTCAACCAGGACGGTGCGAGCAACGGT 7080
Qy      7081 CTGACCGCGCCCAACGGGCCGTCCCAGCAGCGTGTCATCCGCCAGGCCCTCGCCAACGCC 7140
Db      7081 CTGACCGCGCCCAACGGGCCGTCCCAGCAGCGTGTCATCCGCCAGGCCCTCGCCAACGCC 7140
Qy      7141 GGCTTGTCGGCCGGTGATGTCGACGCGGTGGAGGCCCACGGCACCGGCACCACTTTGGGC 7200
Db      7141 GGCTTGTCGGCCGGTGATGTCGACGCGGTGGAGGCCCACGGCACCGGCACCACTTTGGGC 7200
Qy      7201 GACCCGATCGAGGCCCAGGCCCTCCTCGCGACCTACGGACAGGACCGTGCCGGCGAGGGG 7260
Db      7201 GACCCGATCGAGGCCCAGGCCCTCCTCGCGACCTACGGACAGGACCGTGCCGGCGAGGGG 7260
Qy      7261 CCGCTGTGGCTGGGCTCGGTCAAGTCCAATGTCGGTCACACACAGGCTGCCGCGGGCGTC 7320
Db      7261 CCGCTGTGGCTGGGCTCGGTCAAGTCCAATGTCGGTCACACACAGGCTGCCGCGGGCGTC 7320
Qy      7321 GCCGGGGGTGATCAAGATGGTGATGGCGCTGCGGCATGGTCTGCTGCCGCGGACGTTGCAT 7380
Db      7321 GCCGGGGGTGATCAAGATGGTGATGGCGCTGCGGCATGGTCTGCTGCCGCGGACGTTGCAT 7380
Qy      7381 GTGGATGAGCCGTCGCCGCATGTGGACTGGTCCGCGGGTGCGGTGCAGCTGCTGACGGAG 7440
Db      7381 GTGGATGAGCCGTCGCCGCATGTGGACTGGTCCGCGGGTGCGGTGCAGCTGCTGACGGAG 7440
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Qy      7441 ACGGTGCCCTGGCCCGGCGGGGAGGGGCGGCTACGGCGGGCAGGAGTGTCATCATTCGGC 7500
Db      7441 ACGGTGCCCTGGCCCGGCGGGGAGGGGCGGCTACGGCGGGCAGGAGTGTCATCATTCGGC 7500
Qy      7501 GTCAGCGGCACCAACGCCCACGTCATCCTCGAAGAAGCACCCGCCGACGACGTTCCGGGG 7560
Db      7501 GTCAGCGGCACCAACGCCCACGTCATCCTCGAAGAAGCACCCGCCGACGACGTTCCGGGG 7560
Qy      7561 GGACCACCCGCCGGCGAGGGTGACGCGGGCAGCGACGATGAGGCTGCTGCCGGCAGTCCT 7620
Db      7561 GGACCACCCGCCGGCGAGGGTGACGCGGGCAGCGACGATGAGGCTGCTGCCGGCAGTCCT 7620
Qy      7621 GGGGTGTGGCCGTGGCTGGTGTCGGCCAAGTCGCAGCCGGCCCTGCGCGCCCAGGCCCAG 7680
Db      7621 GGGGTGTGGCCGTGGCTGGTGTCGGCCAAGTCGCAGCCGGCCCTGCGCGCCCAGGCCCAG 7680
Qy      7681 GCCCTGCACGCCCACCTCACCGACCACCCCGGCCTCGACCTCGCGGATGTCGGATACACC 7740
Db      7681 GCCCTGCACGCCCACCTCACCGACCACCCCGGCCTCGACCTCGCGGATGTCGGATACACC 7740
Qy      7741 CTCGCCCACGCCCGCGCCGTGTTCGACCACCGCGCCACCCTCATCGCCGCGGACCGCGAC 7800
Db      7741 CTCGCCCACGCCCGCGCCGTGTTCGACCACCGCGCCACCCTCATCGCCGCGGACCGCGAC 7800
Qy      7801 ACGTTCCTGCAAGCACTCCAGGCACTCGCCGCAGGCGAGCCCCACCCCGCCGTCATCCAC 7860
Db      7801 ACGTTCCTGCAAGCACTCCAGGCACTCGCCGCAGGCGAGCCCCACCCCGCCGTCATCCAC 7860
Qy      7861 AGCAGCGCCCCGGGCGGGACCGGGACCGGGGAGGCCGCAGGAAAGACCGCATTCATCTGC 7920
Db      7861 AGCAGCGCCCCGGGCGGGACCGGGACCGGGGAGGCCGCAGGAAAGACCGCATTCATCTGC 7920
Qy      7921 TCCGGACAGGGCACCCAACGCCCCGGCATGGCCCACGGCCTCTACCACACCCACCCCGTC 7980
Db      7921 TCCGGACAGGGCACCCAACGCCCCGGCATGGCCCACGGCCTCTACCACACCCACCCCGTC 7980
Qy      7981 TTCGCCGCCGCACTCAACGACATCTGCACCCACCTCGACCCCCACCTCGACCACCCCCTC 8040
Db      7981 TTCGCCGCCGCACTCAACGACATCTGCACCCACCTCGACCCCCACCTCGACCACCCCCTC 8040
Qy      8041 CTCCCCCTCCTCACCCAAAACGACAACGACAACGAGGACGCGGCCGCACTGCTCCAGCAG 8100
Db      8041 CTCCCCCTCCTCACCCAAAACGACAACGACAACGAGGACGCGGCCGCACTGCTCCAGCAG 8100
Qy      8101 ACCCGCTACGCCCAGCCCGCCCTCTTCGCCTTCCAGGTCGCCCTCCACCGCCTCCTCACC 8160
Db      8101 ACCCGCTACGCCCAGCCCGCCCTCTTCGCCTTCCAGGTCGCCCTCCACCGCCTCCTCACC 8160
Qy      8161 GACGGCTACCACATCACCCCCCACTACTACGCCGGACACTCCCTCGGCGAAATCACCGCC 8220
Db      8161 GACGGCTACCACATCACCCCCCACTACTACGCCGGACACTCCCTCGGCGAAATCACCGCC 8220
Qy      8221 GCCCACCTCGCCGGCATCCTCACCCTCACCGACGCCACCACCCTCATCACCCAACGCGCC 8280
Db      8221 GCCCACCTCGCCGGCATCCTCACCCTCACCGACGCCACCACCCTCATCACCCAACGCGCC 8280
Qy      8281 ACCCTCATGCAAACCATGCCCCCCGGCACCATGACCACCCTCCACACCACCCCCCACCAC 8340
Db      8281 ACCCTCATGCAAACCATGCCCCCCGGCACCATGACCACCCTCCACACCACCCCCCACCAC 8340
Qy      8341 ATCACCCACCACCTCACCGCCCACGAAAACGACCTCGCCATCGCCGCCATCAACACCCCC 8400
Db      8341 ATCACCCACCACCTCACCGCCCACGAAAACGACCTCGCCATCGCCGCCATCAACACCCCC 8400
Qy      8401 ACCTCCCTCGTCATCAGCGGCACCCCCCACACCGTCCAACACATCACCACCCTCTGCCAA 8460
Db      8401 ACCTCCCTCGTCATCAGCGGCACCCCCCACACCGTCCAACACATCACCACCCTCTGCCAA 8460
Qy      8461 CAACAAGGCATCAAAACCAAAACCCTCCCCACCAACCACGCCTTCCACTCCCCCCACACC 8520
Db      8461 CAACAAGGCATCAAAACCAAAACCCTCCCCACCAACCACGCCTTCCACTCCCCCCACACC 8520
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Db      10681 GGGGTGCGGGATCTGCTGTTGGTGAGCCGGCGTGGTCCGGATGCTCCGGGTGCGGAGGGT 10740

Qy      10741 CTGCGGGCGGAGCTGGCCGCGTTGGGGGCGGAGGTGCGGATTGTTGCGTGTGATGTGGGG 10800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10741 CTGCGGGCGGAGCTGGCCGCGTTGGGGGCGGAGGTGCGGATTGTTGCGTGTGATGTGGGG 10800

Qy      10801 GAGCGGCGGGAGGTGGTCCGGCTGCTGGAGGGTGTTCCTGCCGGGTGTCCGCTGACGGGT 10860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10801 GAGCGGCGGGAGGTGGTCCGGCTGCTGGAGGGTGTTCCTGCCGGGTGTCCGCTGACGGGT 10860

Qy      10861 GTCGTGCATGCGGCTGGTGTGCTGGACGATGCGACGATCGCCTCTCTCACGCCCGAGCGG 10920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10861 GTCGTGCATGCGGCTGGTGTGCTGGACGATGCGACGATCGCCTCTCTCACGCCCGAGCGG 10920

Qy      10921 CTGGGCACGGTGTTCGCGGCCAAGGTGGATGCCGCTCTTTTGCTGGATGAGCTGACGCGG 10980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10921 CTGGGCACGGTGTTCGCGGCCAAGGTGGATGCCGCTCTTTTGCTGGATGAGCTGACGCGG 10980

Qy      10981 GGTATGGAGCTGTCGGCGTTCGTGCTGTTCTCCTCGGCCGCGGGGATCCTGGGGTCGGCC 11040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10981 GGTATGGAGCTGTCGGCGTTCGTGCTGTTCTCCTCGGCCGCGGGGATCCTGGGGTCGGCC 11040

Qy      11041 GGGCAGGGCAACTACGCCGCGGCCAATGCCGCTCTGGACGCGCTGGCGTACCGGCGGCGG 11100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11041 GGGCAGGGCAACTACGCCGCGGCCAATGCCGCTCTGGACGCGCTGGCGTACCGGCGGCGG 11100

Qy      11101 GCGGCGGGTCTGCCGGGGGGTGTCGCTGGCGTGGGGGCTGTGGGAAGAGGCCAGCGGGATG 11160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11101 GCGGCGGGTCTGCCGGGGGGTGTCGCTGGCGTGGGGGCTGTGGGAAGAGGCCAGCGGGATG 11160

Qy      11161 ACCGGGCACCTGGCCGGCACCGACCACCGGCGCATCATCCGTTCCGGTCTGCATCCCATG 11220
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Db      11161 ACCGGGCACCTGGCCGGCACCGACCACCGGCGCATCATCCGTTCCGGTCTGCATCCCATG 11220

Qy      11221 TCGACCCCGGACGCACTGGCCCTCTTCGATGCGGCCCTGGCTCTGGACCGGCCGGTCCTG 11280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11221 TCGACCCCGGACGCACTGGCCCTCTTCGATGCGGCCCTGGCTCTGGACCGGCCGGTCCTG 11280

Qy      11281 CTGCCCGCCGACCTGCGTCCCGCCCCGCCCCTGCCGCCCCTGCTGCAGGACCTCCTGCCC 11340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11281 CTGCCCGCCGACCTGCGTCCCGCCCCGCCCCTGCCGCCCCTGCTGCAGGACCTCCTGCCC 11340

Qy      11341 GCCACCCGCCGCCGCACCACCCGCACCACCACTACCGGTGGTGCGGACAACGGCGCCCAG 11400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11341 GCCACCCGCCGCCGCACCACCCGCACCACCACTACCGGTGGTGCGGACAACGGCGCCCAG 11400

Qy      11401 CTGCACGCCCGGCTGGCCGGCCAGACACACGAACAACAGCACACCACCCTCCTCGCCCTG 11460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11401 CTGCACGCCCGGCTGGCCGGCCAGACACACGAACAACAGCACACCACCCTCCTCGCCCTG 11460

Qy      11461 GTCCGCTCCCACATCGCCACCGTCCTGGGCCACACCACCCCCGACACCATCCCCCCCGAC 11520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11461 GTCCGCTCCCACATCGCCACCGTCCTGGGCCACACCACCCCCGACACCATCCCCCCCGAC 11520

Qy      11521 CGCGCGTTCCGCGACCTCGGCTTCGACTCCCTCACCGCCGTCGAACTACGCAACCGGCTC 11580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11521 CGCGCGTTCCGCGACCTCGGCTTCGACTCCCTCACCGCCGTCGAACTACGCAACCGGCTC 11580

Qy      11581 TCCCGCACCACCGGACTCCGCCTCCCCACCACCCTCGCCTTCGACCACCCCAACCCCACC 11640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11581 TCCCGCACCACCGGACTCCGCCTCCCCACCACCCTCGCCTTCGACCACCCCAACCCCACC 11640

Qy      11641 ACCCTCACCCACCACCTCCACACACAACTCCAGCCACAACCGGACAACGCTGTCGCCCCC 11700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11641 ACCCTCACCCACCACCTCCACACACAACTCCAGCCACAACCGGACAACGCTGTCGCCCCC 11700

Qy      11701 GTGTTGGCGGAGCTCGACAAACTCGAATCCGCCCTCTCCGCCCTCGACAAAACCGACAGC 11760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11701 GTGTTGGCGGAGCTCGACAAACTCGAATCCGCCCTCTCCGCCCTCGACAAAACCGACAGC 11760

Qy      11761 GCCAGCGAAAGAGTCACCCTGCGGCTGAAGTCACTCATGTTGAGGTGGAACGCACCCCAG 11820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11761 GCCAGCGAAAGAGTCACCCTGCGGCTGAAGTCACTCATGTTGAGGTGGAACGCACCCCAG 11820

Qy      11821 CATCCGACAGCCGAAAGCGCTGATGACGACGAGAAGTTCACATCGGCAACAGAGGCTGAG 11880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11821 CATCCGACAGCCGAAAGCGCTGATGACGACGAGAAGTTCACATCGGCAACAGAGGCTGAG 11880

Qy      11881 ATTTTCAAATTCATTGACAACGACCTCGGCCTGTCC 11916
              |||||||||||||||||||||||||||||||||||
Db      11881 ATTTTCAAATTCATTGACAACGACCTCGGCCTGTCC 11916
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RESULT 4
AAZ58381
ID AAZ58381 standard; DNA; 12381 BP.
XX
AC AAZ58381;
XX
DT 23-MAY-2000 (first entry)
XX
DE Streptomyces avermitilis avermectin polyketide synthase modules 1+2.
XX
KW Polyketide synthase; avermectin; insecticide; ss.
XX
OS Streptomyces avermitilis.
XX
PN WO200001827-A2.
XX
PD 13-JAN-2000.
XX
PF 06-JUL-1999; 99WO-GB02158.
XX
PR 06-JUL-1998; 98GB-0014622.
XX
PA (BIOT-) BIOTICA TECHNOLOGY LTD.
PA (PFIZ) PFIZER INC.
XX
PI Kellenberger JL, Leadlay PF, Staunton J, Stutzman-Engwall KJ;
PI McArthur HAI;
XX
DR WPI; 2000-182117/16.
XX
PT Mutated Type I polyketide synthase containing a polylinker site in an
PT extension module for replacement of a reductive loop sequence, for
PT producing polyketides, e.g. B1 avermectin -
XX
PS Disclosure; Fig 7a-f; 75pp; English.
XX
CC The present sequence is that of DNA encoding the first 2 modules
CC of the avermectin polyketide synthase (PKS) of Streptomyces
CC avermitilis. The invention relates to nucleic acids encoding a
CC Type I PKS such as avermectin in which a polylinker with multiple
CC restriction sites replaces or 1 more PKS genes encoding enzymes
CC associated with reduction. Novel PKS are provided in which in
CC which the reductive loop in a selected module of the Type I PKS is
CC replaced with the equivalent segment from the same or different
CC PKS gene cluster or by a mutated or synthetic segment. Vectors and
CC host cells, and methods for producing novel polyketides by
CC culturing host cells are claimed. The polyketides obtained are
CC useful as antibiotics and insecticides. Fermentation products
CC containing C22-C23 dihydroavermectin, ivermectin and B1
CC avermectins are claimed.
XX
SQ Sequence 12381 BP; 1884 A; 4561 C; 4005 G; 1931 T; 0 other;

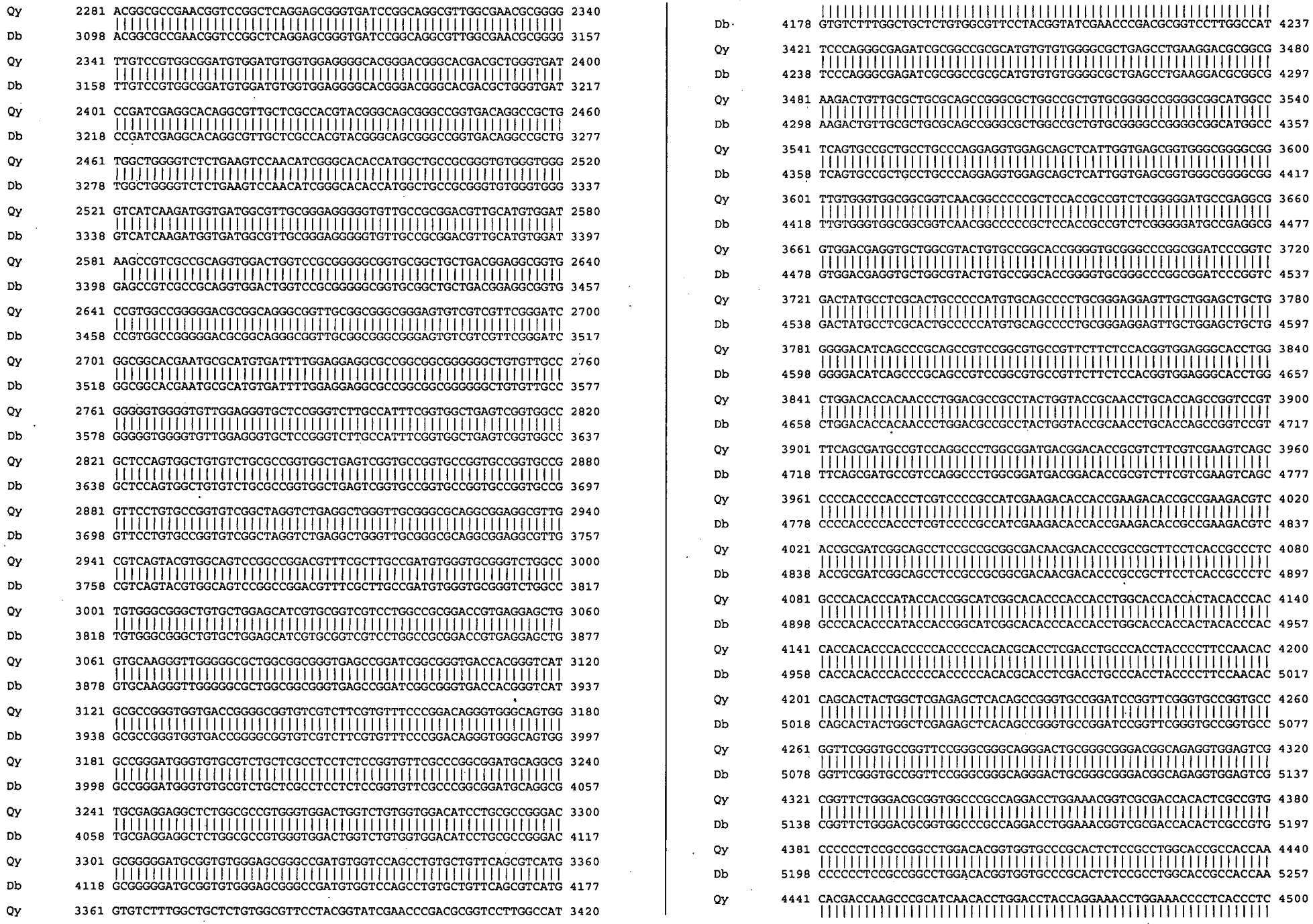
 Query Match 37.6%; Score 11548; DB 21; Length 12381;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 11554; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy          1 GTGCAGAGGATGGACGGCGGGGAAGAACCCCGCCCTGCGGCAGGGGAGGTCCTCGGAGTG 60
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Db        818 GTGCAGAGGATGGACGGCGGGGAAGAACCCCGCCCTGCGGCAGGGGAGGTCCTCGGAGTG 877

Qy         61 GCCGACGAGGCGGACGGCGGCGTCGTCTTCGTTTTTCCCGGGCAGGGCCCGCAATGGCCG 120
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Db        878 GCCGACGAGGCGGACGGCGGCGTCGTCTTCGTTTTTCCCGGGCAGGGCCCGCAATGGCCG 937
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Db        938 GGCATGGGAAGGGAACTTCTCGACGCTTCCGACGTCTTCCGGGAGAGCGTCCGCGCCTGC 997
Qy        181 GAAGCCGCGTTCGCGCCCTACGTCGACTGGTCGGTGGAGCAGGTGTTGCGGGACTCGCCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 GACGCTCCCGGGCTGGACCGGGTGGACGTCGTCCAGCCGACCCTGTTCGCCGTCATGATC 300
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Qy        301 TCCCTGGCCGCCCTCTGGCGCTCGCAAGGGGTCGAGCCGTGCGCGGTGCTGGGACACAGC 360
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Qy        361 CTGGGCGAGATCGCGGCAGCCCACGTCTCGGGAGGCCTGTCCCTGGCCGACGCCGCACGC 420
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Qy        601 GAGGCCGTCGCGGACCTGGTGGCCGACCTCACCGCCGCGCAGGTGCGCACGCGCATGATC 660
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Db       1418 GAGGCCGTCGCGGACCTGGTGGCCGACCTCACCGCCGCGCAGGTGCGCACGCGCATGATC 1477
Qy        661 CCGGTGGACGTTCCCGCCCACTCCCCCCTGATGTACGCCATCGAGGAACGGGTCGTCAGC 720
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Qy        721 GGCCTGCTGCCCATCACCCCACGCCCCTCCCGCATCCCCTTCCACTCCTCGGTGACCGGC 780
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Qy        781 GGCCGCCTCGACACCCGCGAGCTAGACGCGGCGTACTGGTACCGCAACATGTCGAGCACG 840
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Qy        841 GTCCGGTTCGAGCCCGCCGCCCGGCTGCTTCTGCAGCAGGGGCCCAAGACGTTCGTCGAG 900
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Db       1658 GTCCGGTTCGAGCCCGCCGCCCGGCTGCTTCTGCAGCAGGGGCCCAAGACGTTCGTCGAG 1717
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Qy        961 ACCACCGGCACCGCCGACACCGTGATCATGGGCACGCTGCGCCGCGGCCAGGGCACCCTG 1020
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Qy       1261 CTGCGCAACCGCCTCAGCAAGGCCACGGGCCTGCGGTTGCCCGTGACGCTCATCTTCGAC 1320
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Qy 3001 TGTGGGCGGGCTGTGCTGGAGCATCGTGCGGTCGTCCTGGCCGCGGACCGTGAGGAGCTG 3060
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Qy       5761 ACGGCAGCGGTCACGCAGGCGATCGCGGACACCGAACGGCCGTATGTCGTCATCGCCGAC 5820
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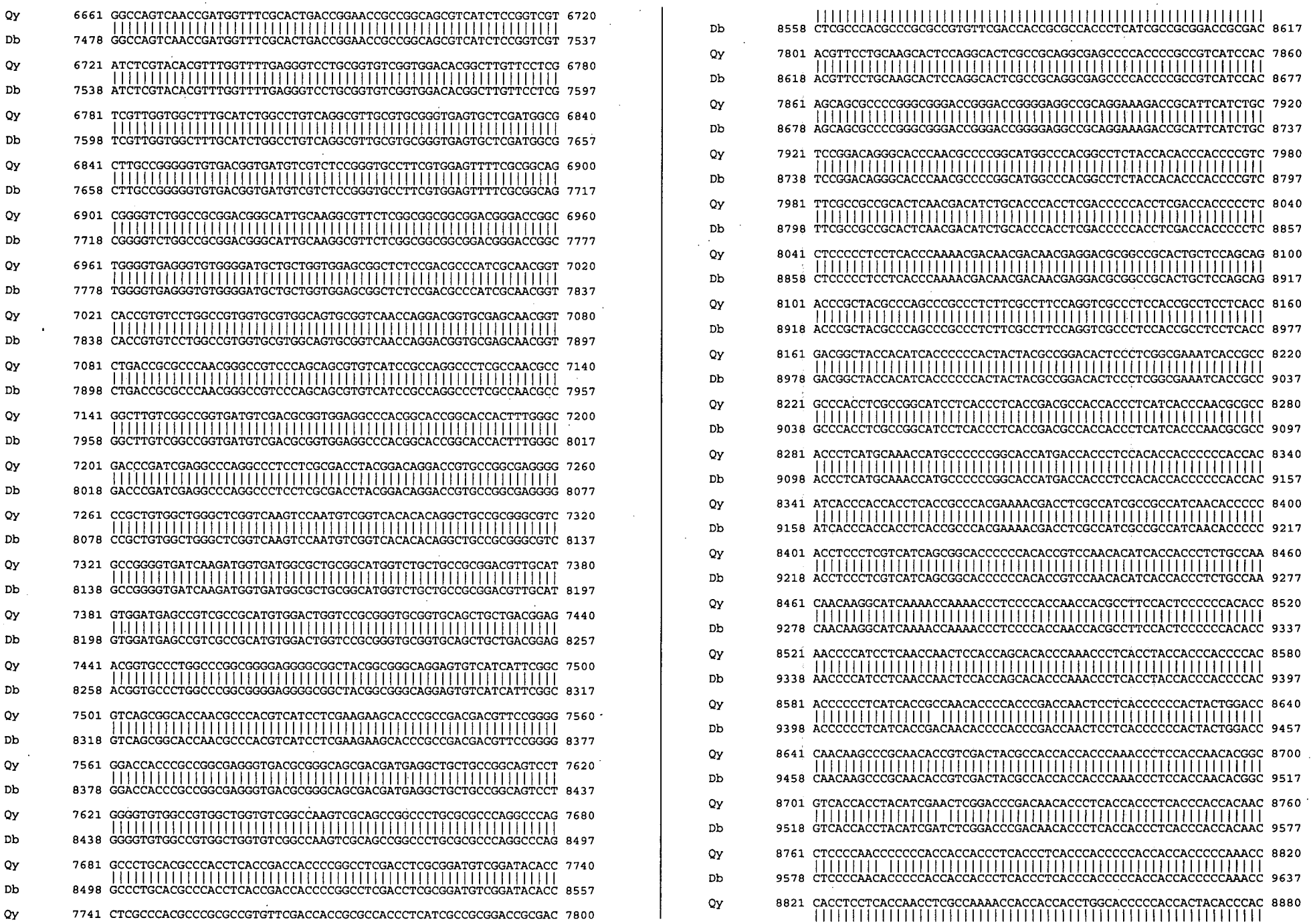
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Qy       6541 GAAACCGCCTGGGAAACCATCGAACACGCCGGCATCAACCCCCACACCCTCCACGGCACC 6600
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Qy       6601 CCCACCGGAGTCTTCACCGGCACCAACGGACAGGACTACGCACTTCGCGTGCACAACGCG 6660
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Db       7418 CCCACCGGAGTCTTCACCGGCACCAACGGACAGGACTACGCACTTCGCGTGCACAACGCG 7477
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Qy      10081 GGTGGCGGTGGCGGTGGTGGCGGTGGTGTGGGTGAGGTTGTTGGTGGGGGTGTTGGGTGTG 10140
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Qy      10201 GGTGCGGTGGTGGCCGGCCCGGAGGACGGCCCGGTGGATGTGGTGGGTGCGTCGGTGTGG 10260
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RESULT 5
AAA92302
ID AAA92302 standard; DNA; 31422 BP.
XX
AC AAA92302;
XX
DT 10-JAN-2001 (first entry)
XX
DE S. avermitilis avermectin aglycon synthase DNA aveAII SEQ ID NO:2.
XX
KW Streptomyces avermitilis; avermectin aglycon synthase; biosynthesis;
KW multifunctional enzyme; polyketide; avermectin; veterinary drug;
KW agrochemical; ds.
XX
OS Streptomyces avermitilis.
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FH Key Location/Qualifiers
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PA (KITA) KITASATO INST.
XX
PI Omura S, Ikeda H;
XX
DR WPI; 2000-565458/52.
DR P-PSDB; AAB23751, AAB23752.
XX
PT Avermectin aglycone synthase DNA and proteins encoded by all or part of
PT it for the production of avermectin and its derivatives for drug and
PT agrochemical use -
XX
PS Claim 2; Page 134-203; 314pp; Japanese.
XX
CC The present sequence represents DNA which encodes avermectin aglycon
CC synthase proteins. Also described are: (1) polypeptides encoded by all
CC or part of the DNA; (2) expression vectors containing the DNA; (3) host
CC cells transformed by the vectors; (4) preparation of the polypeptides
CC by culture of the transformants; (5) preparation of avermectin aglycon
CC or its derivatives by culture of transformed avermectin-producing
CC microorganisms; and (6) oligonucleotides of 5-60 bases in length
CC containing sense or antisense sequences from the avermectin aglycon
CC synthase DNA. The enzymes are useful for the production of modified
CC forms of avermectin and of the intermediates in its biosynthesis, for
CC use as drugs, veterinary drugs and agrochemicals.
XX
SQ Sequence 31422 BP; 4136 A; 10238 C; 11677 G; 5371 T; 0 other;

Query Match 21.0%; Score 6437.2; DB 21; Length 31422;
Best Local Similarity 69.9%; Pred. No. 0;
Matches 9934; Conservative 0; Mismatches 2928; Indels 1350; Gaps 39;

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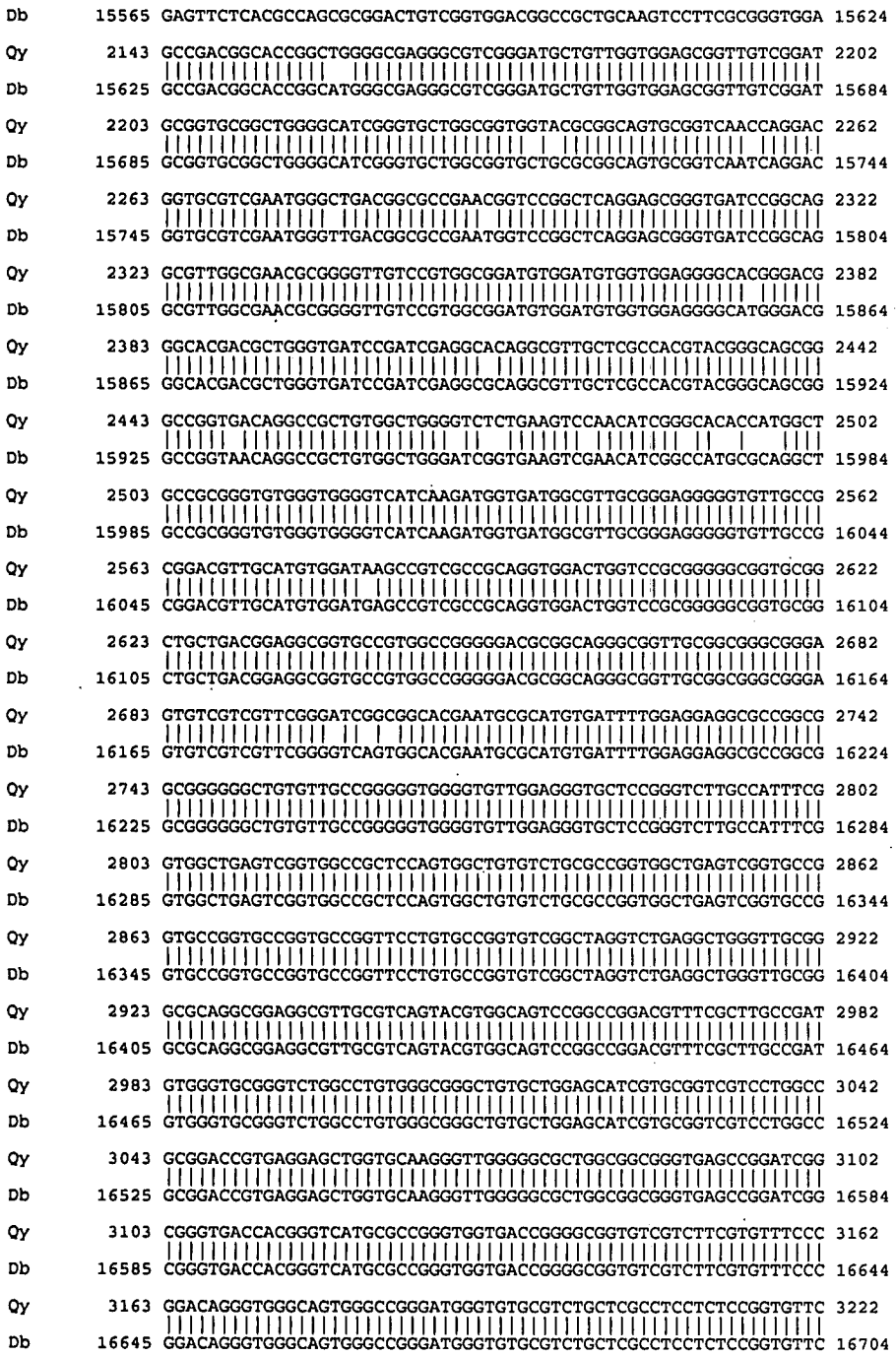
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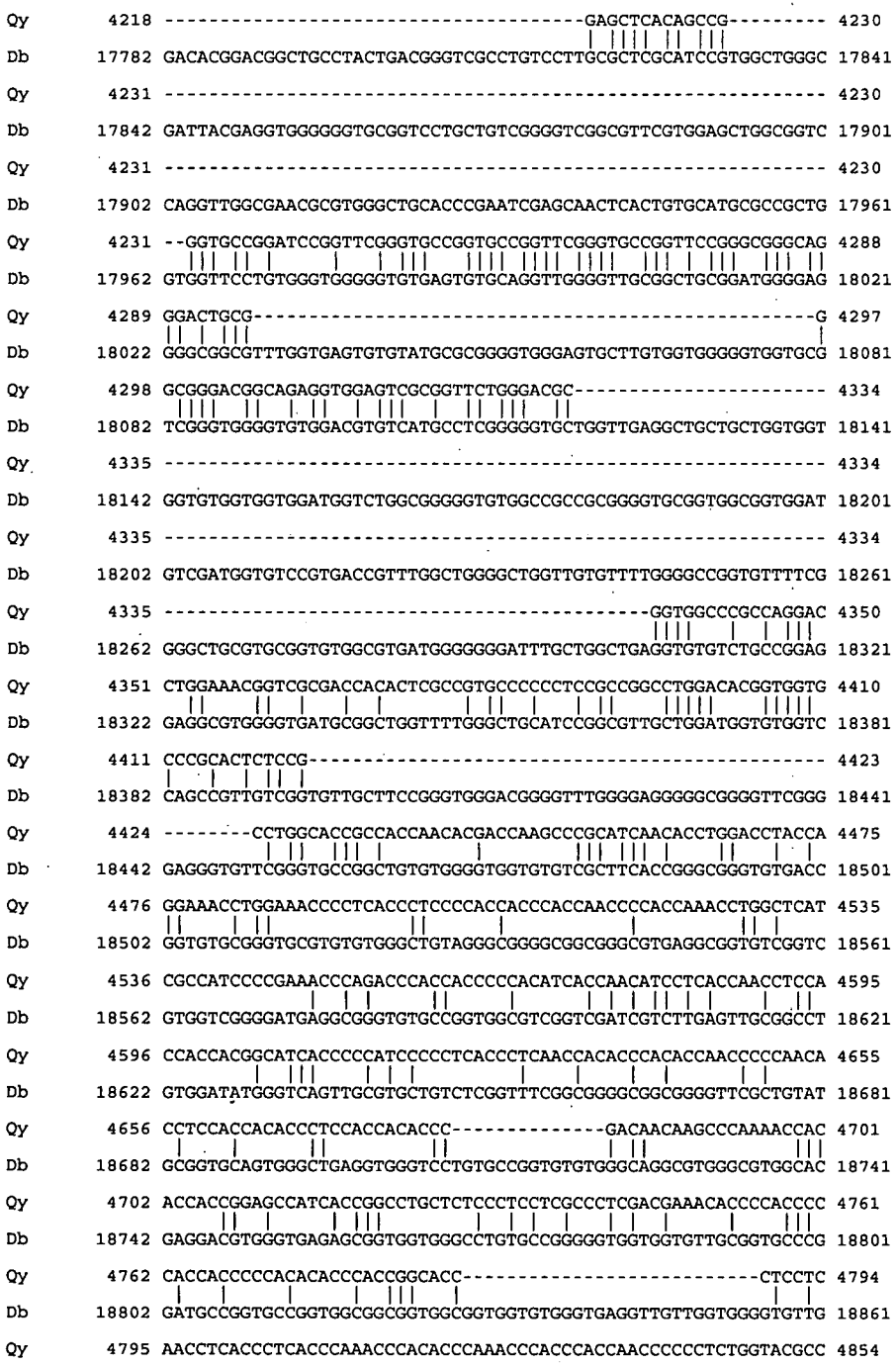
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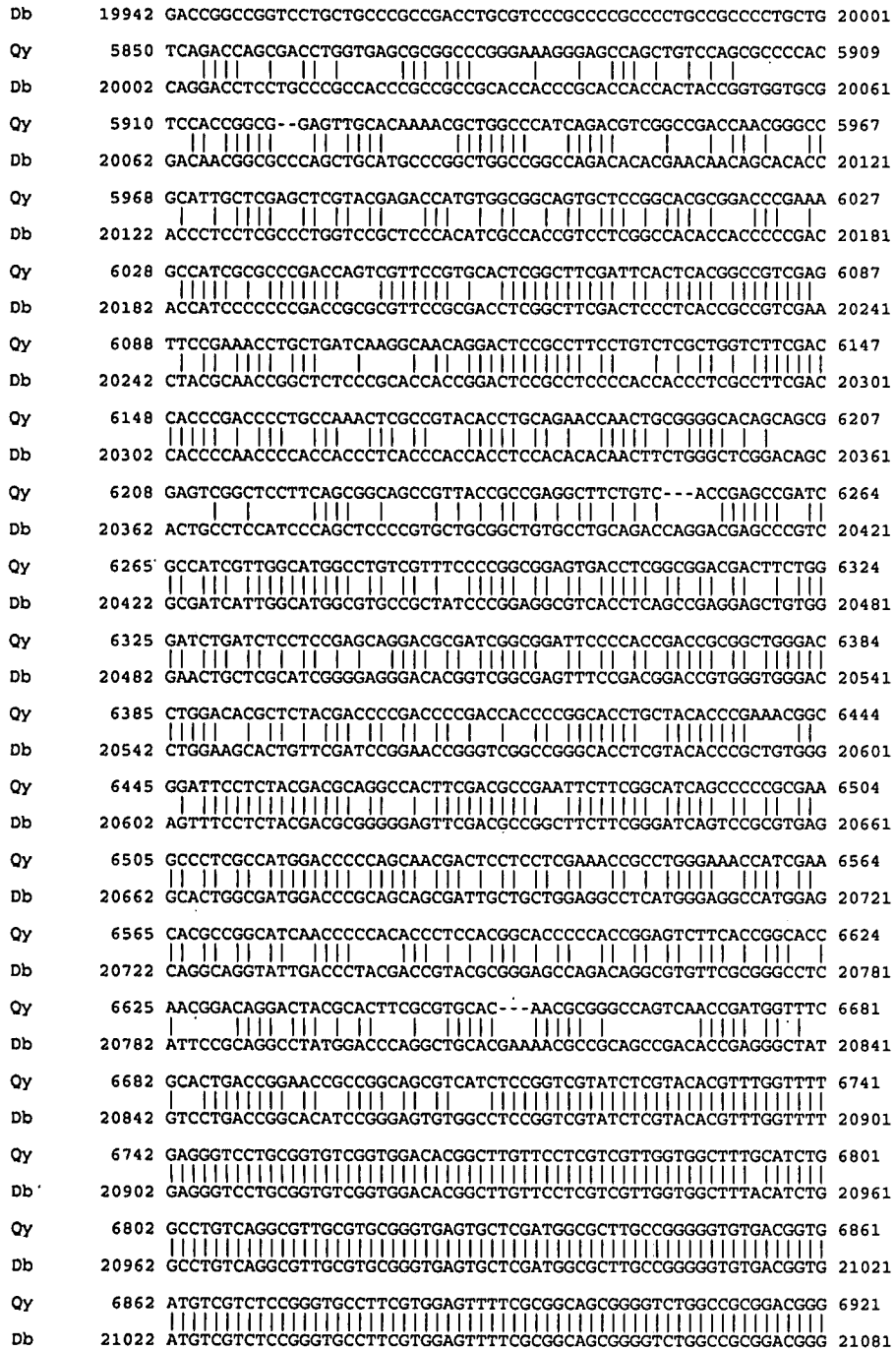
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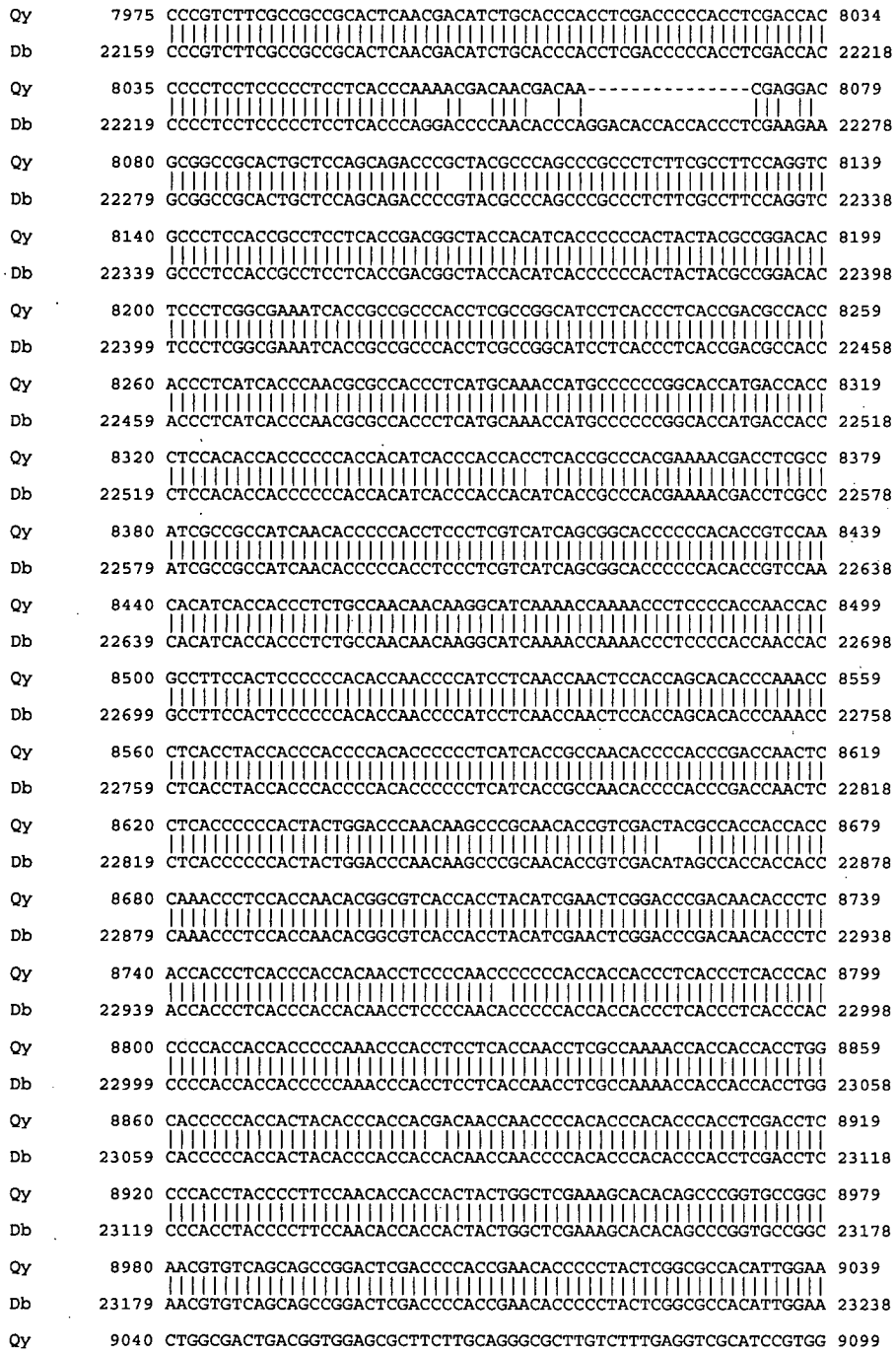
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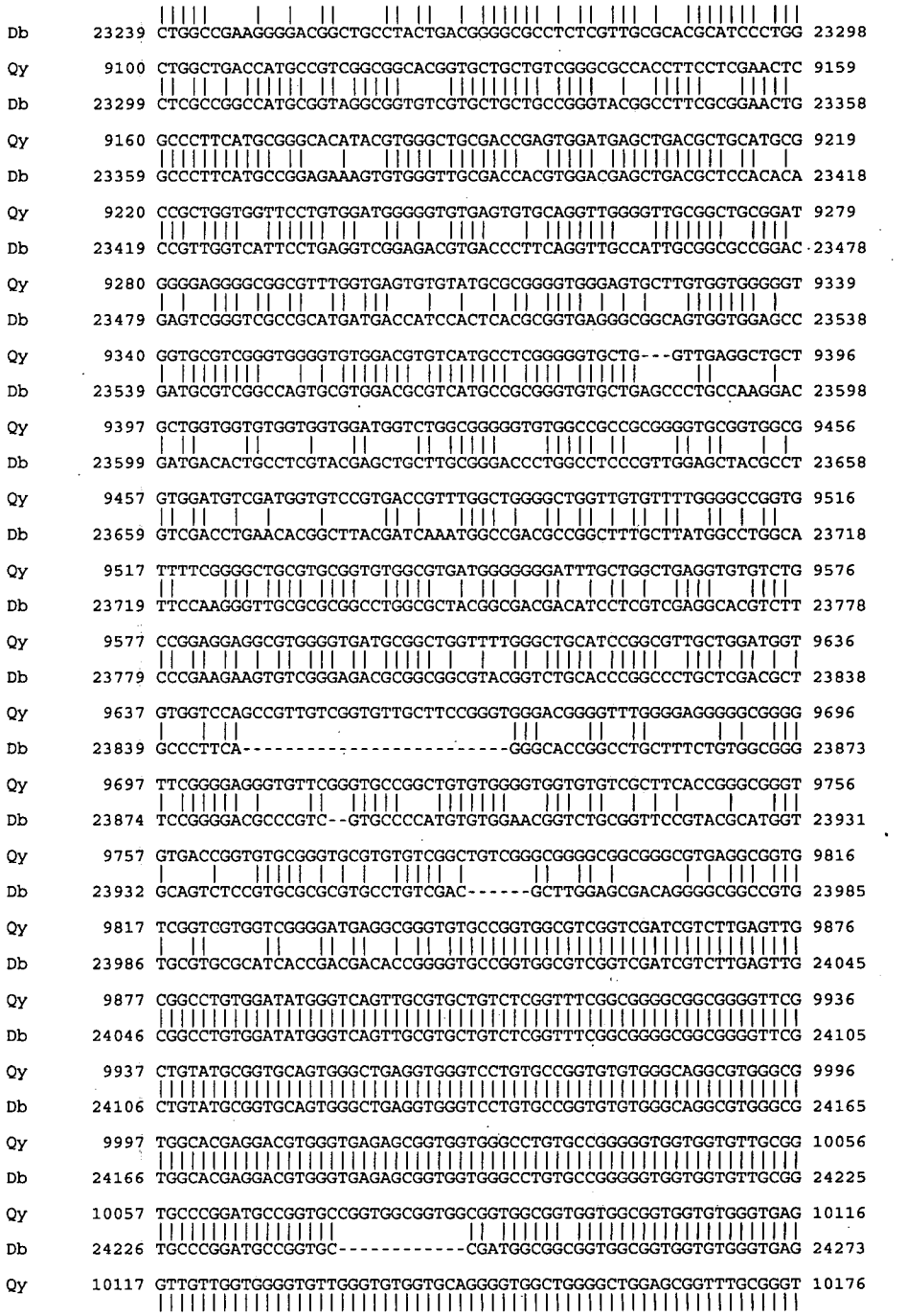
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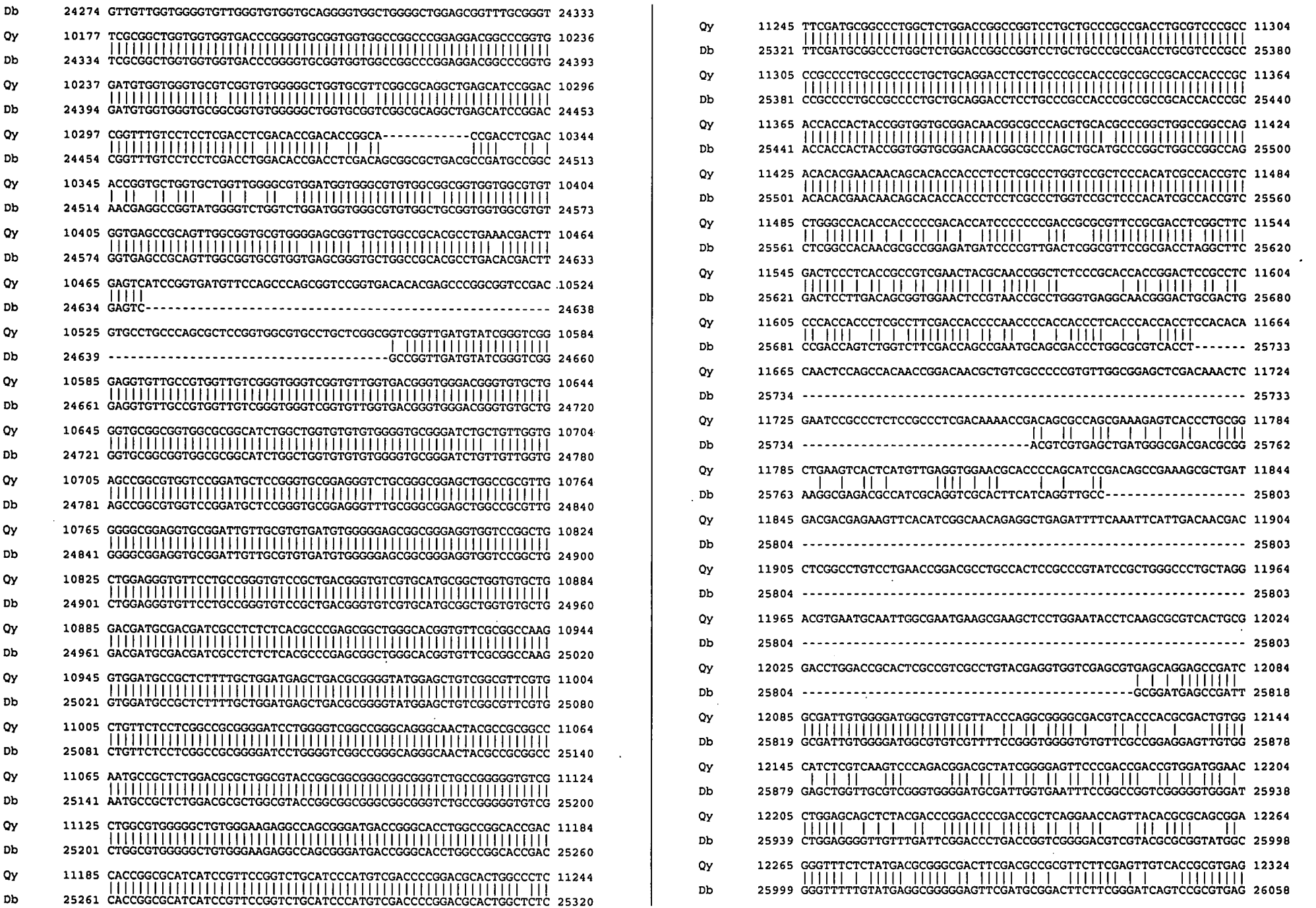

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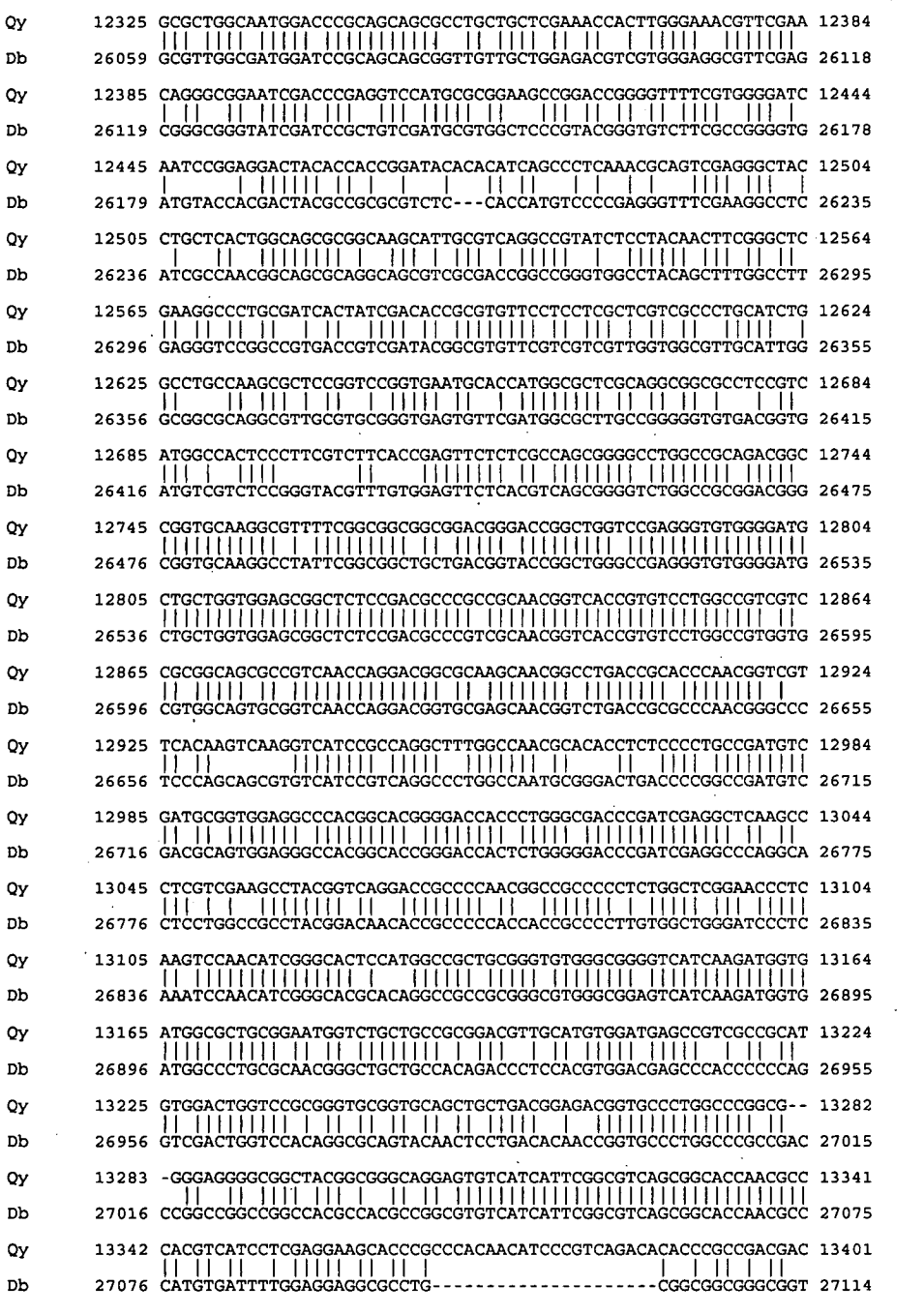

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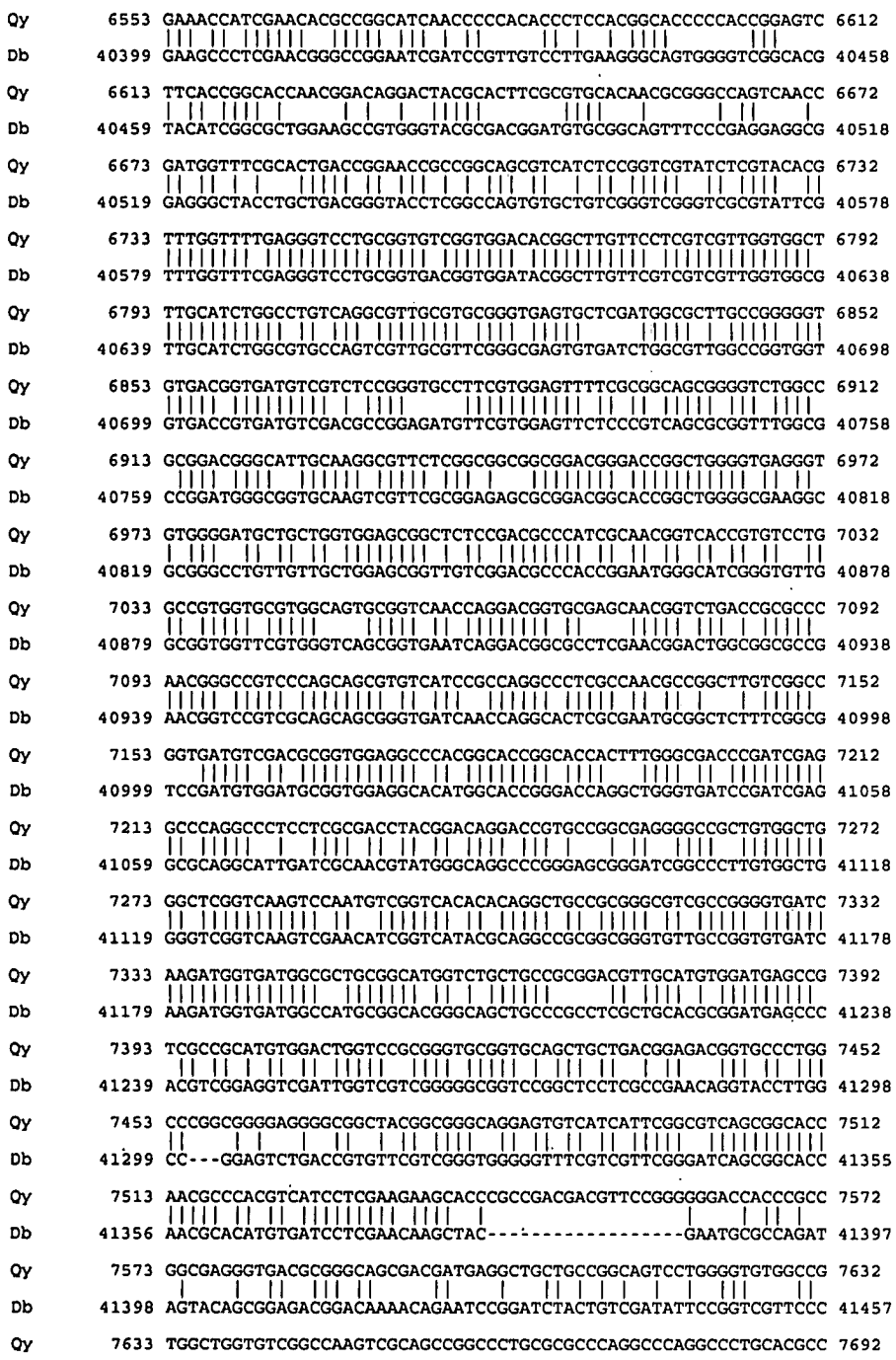

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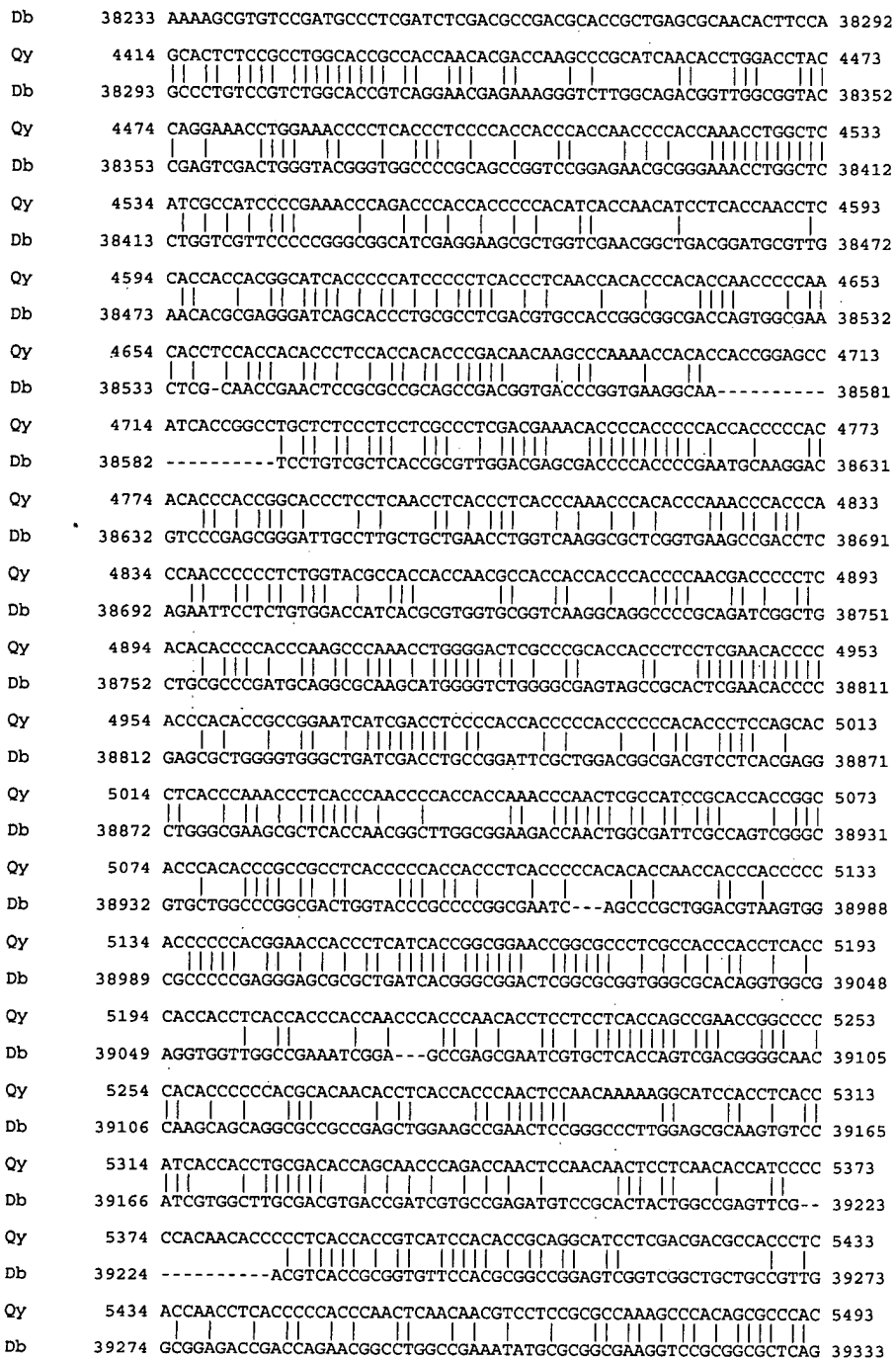

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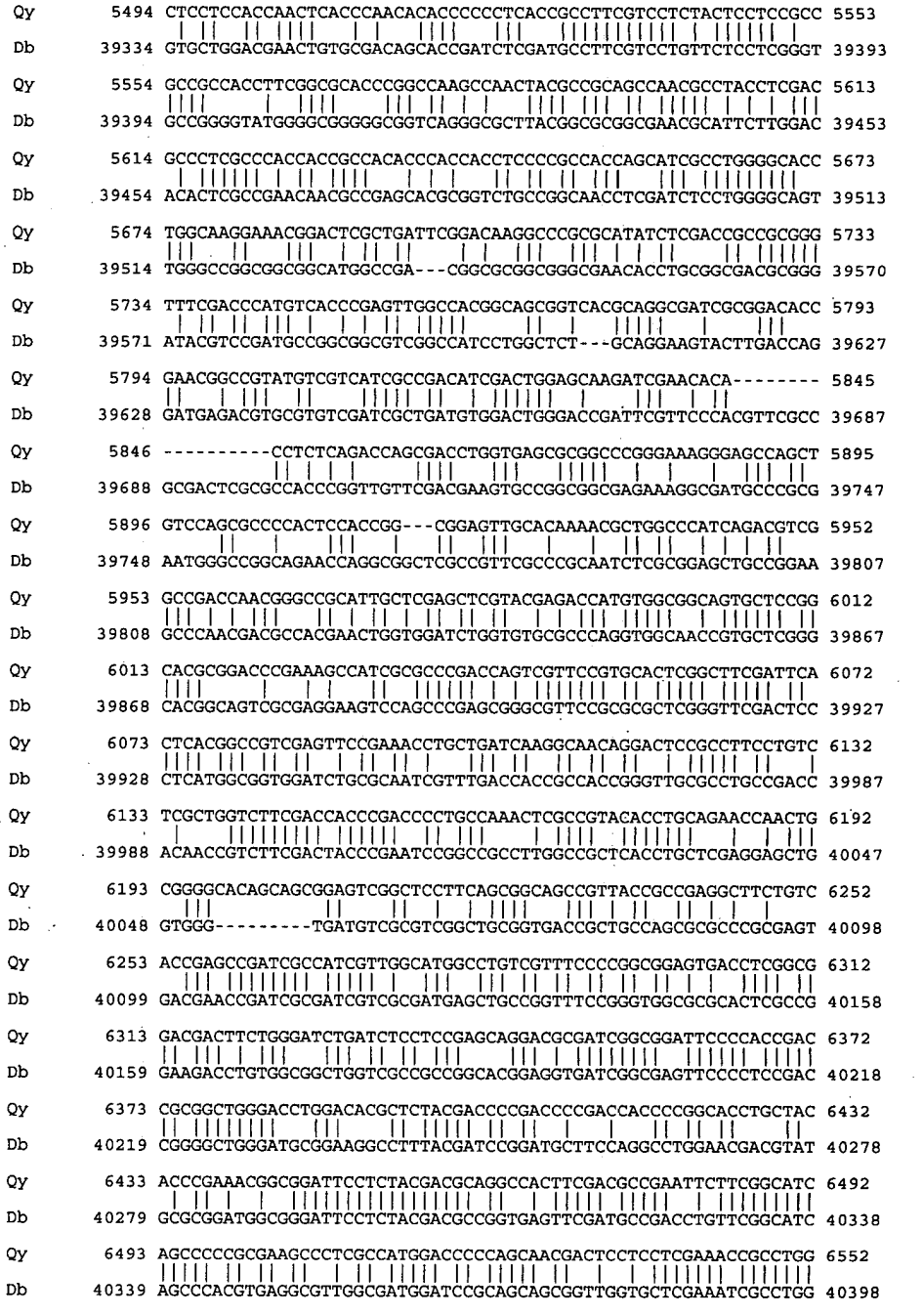

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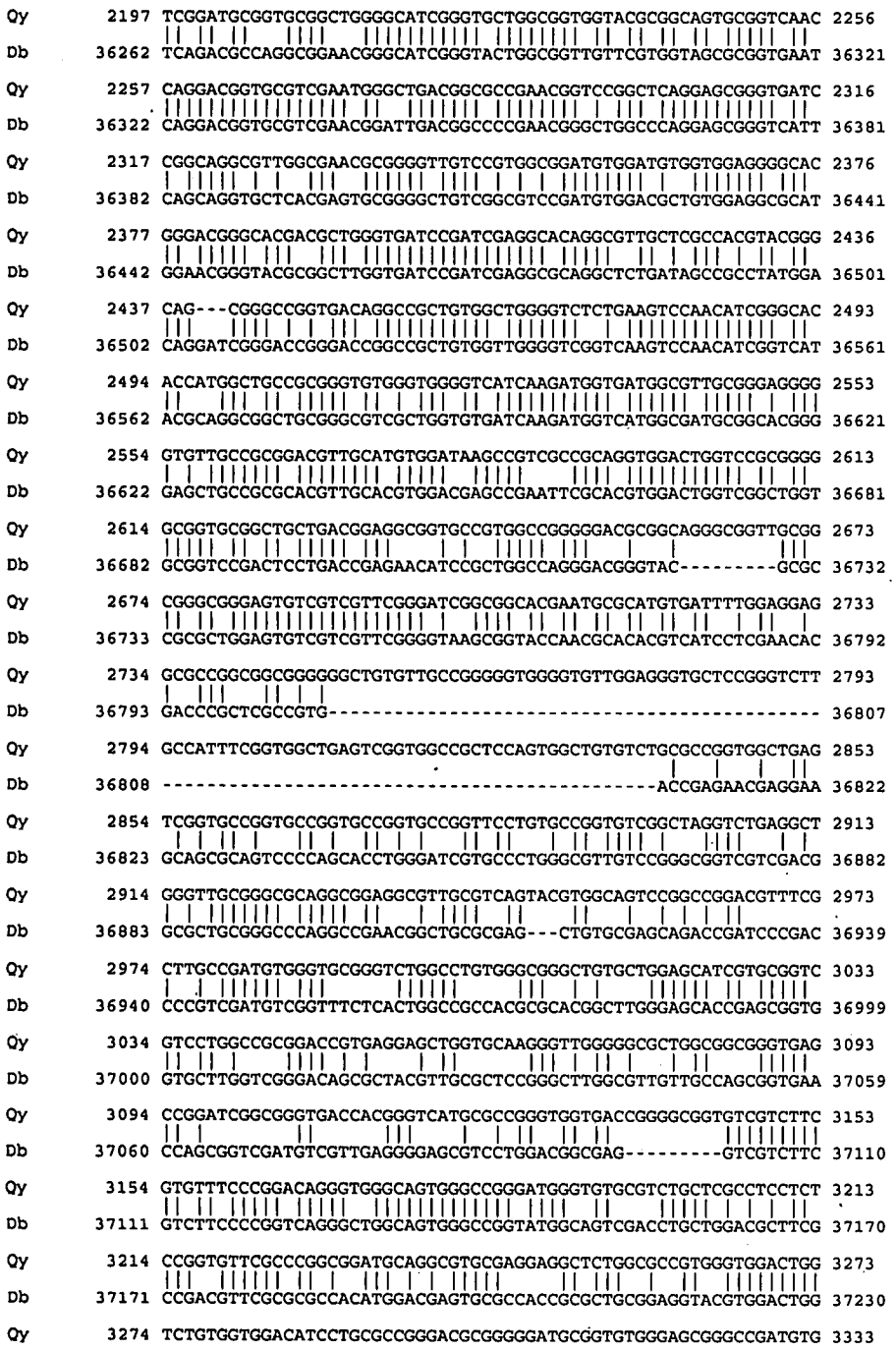


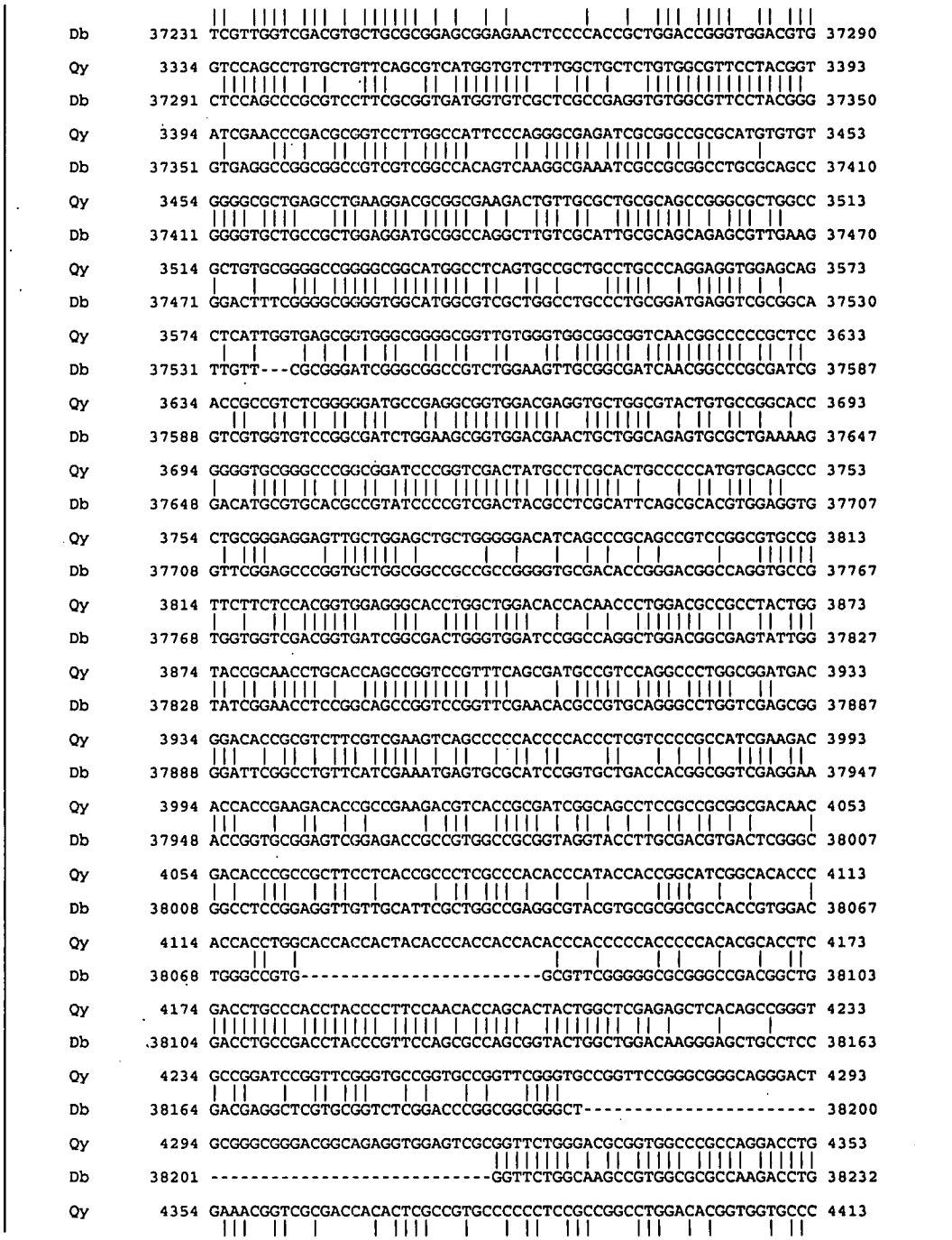

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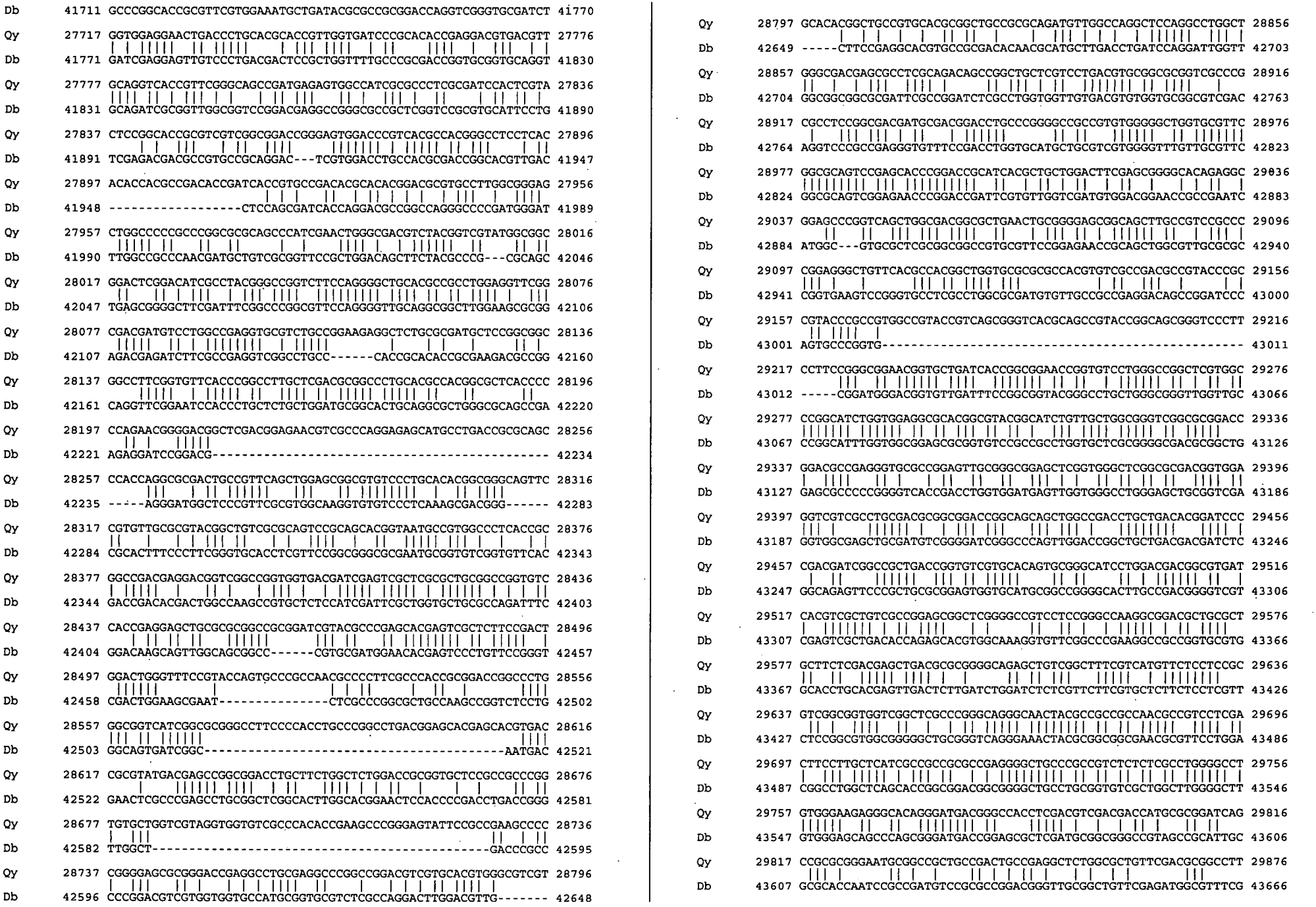
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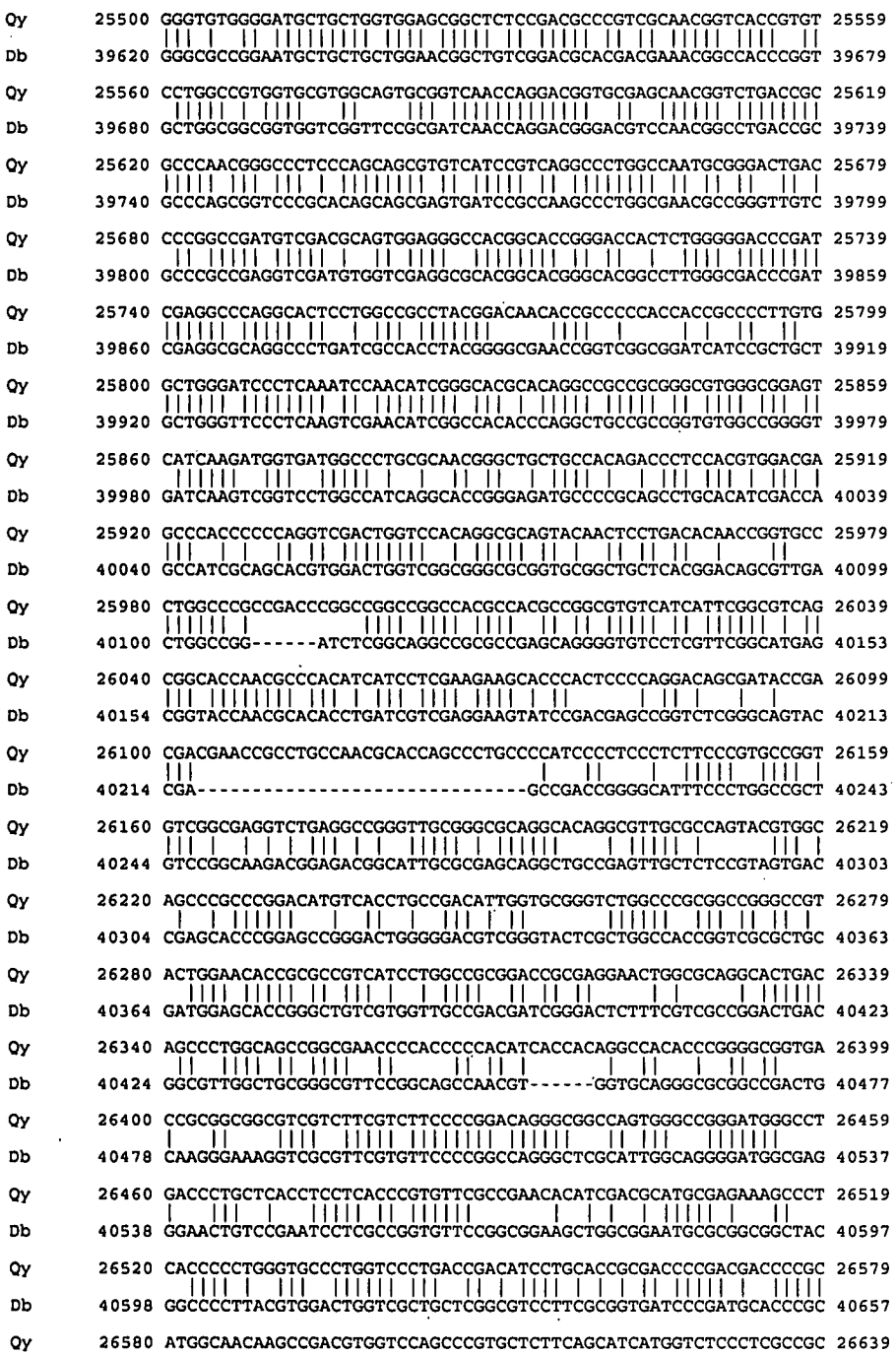
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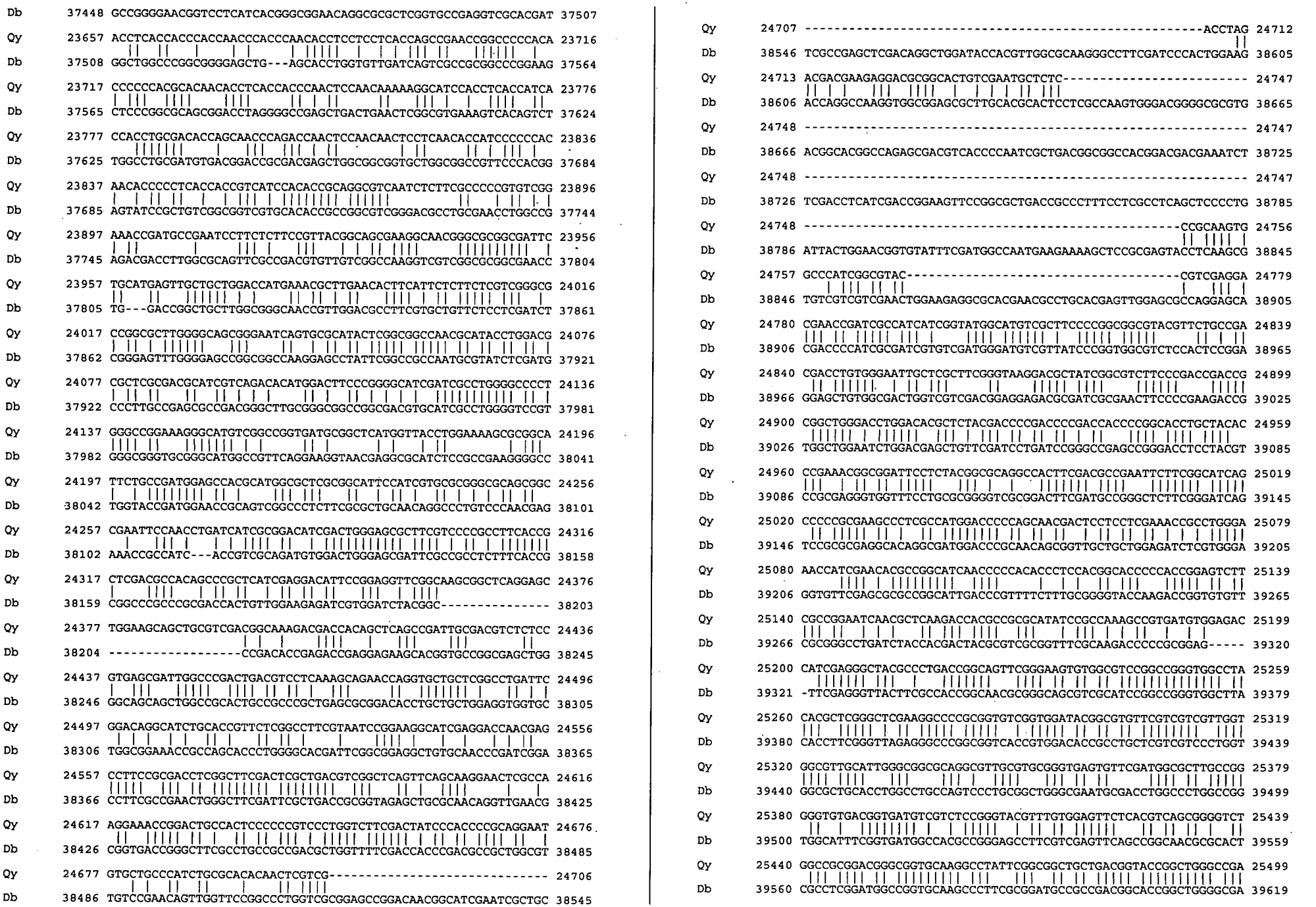
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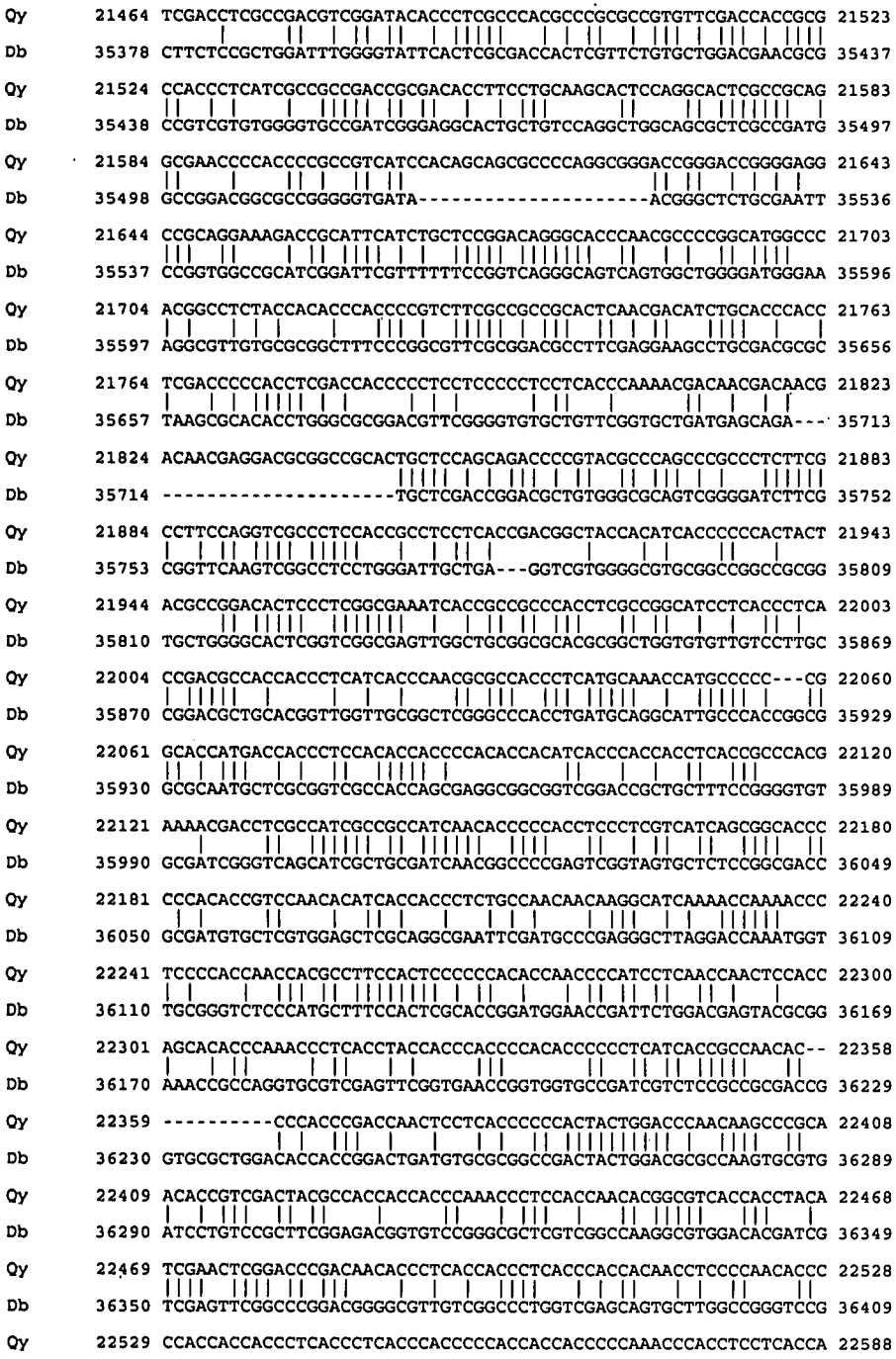
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XX
KW Spinosyn biosynthetic enzyme; open reading frame; ORF; insecticidal
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KW PKS; extender module; initiator module; acyl transferase domain; AT;
KW acyl carrier protein; ACP; beta-ketosynthase domain; KS; KR;
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XX
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XX

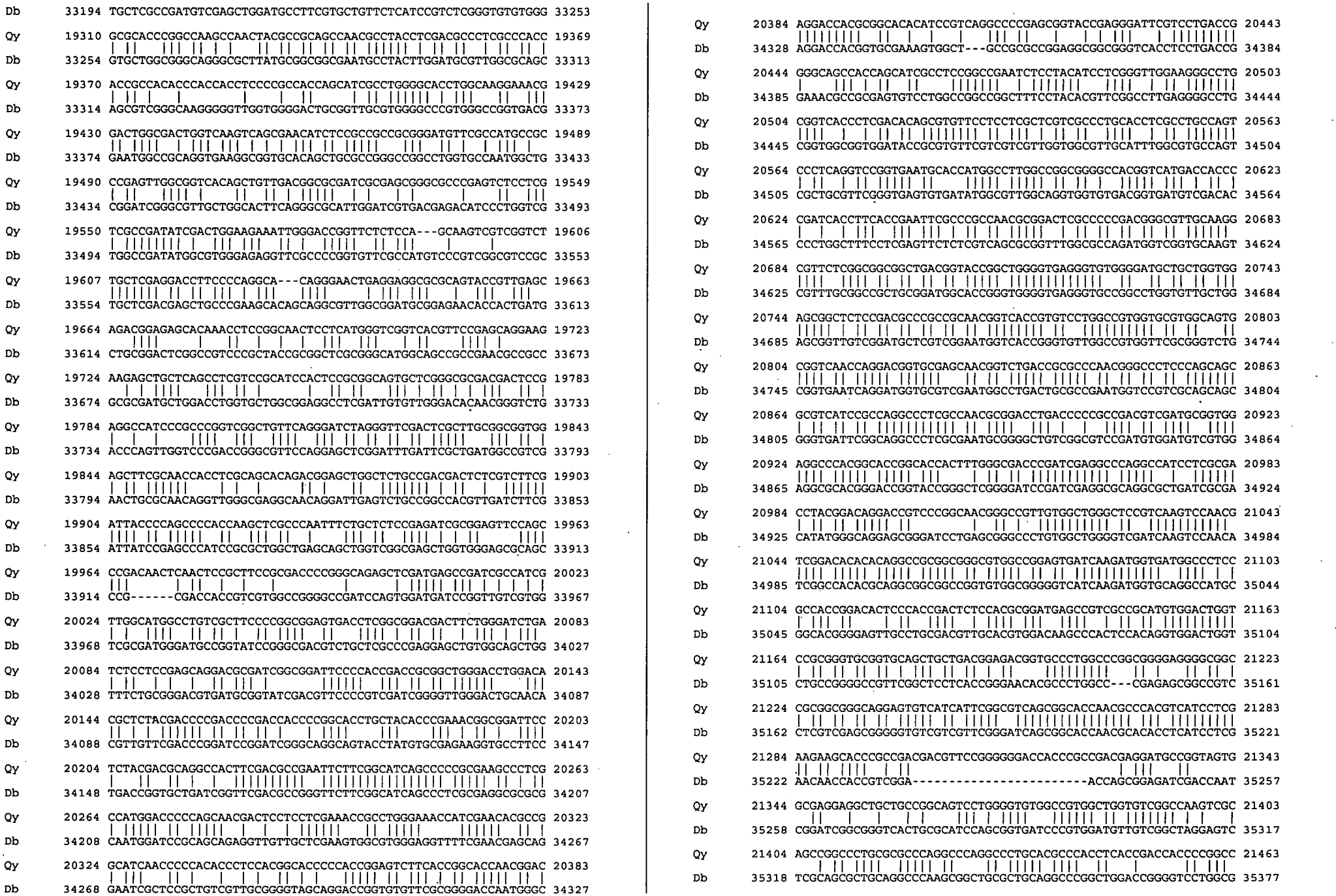
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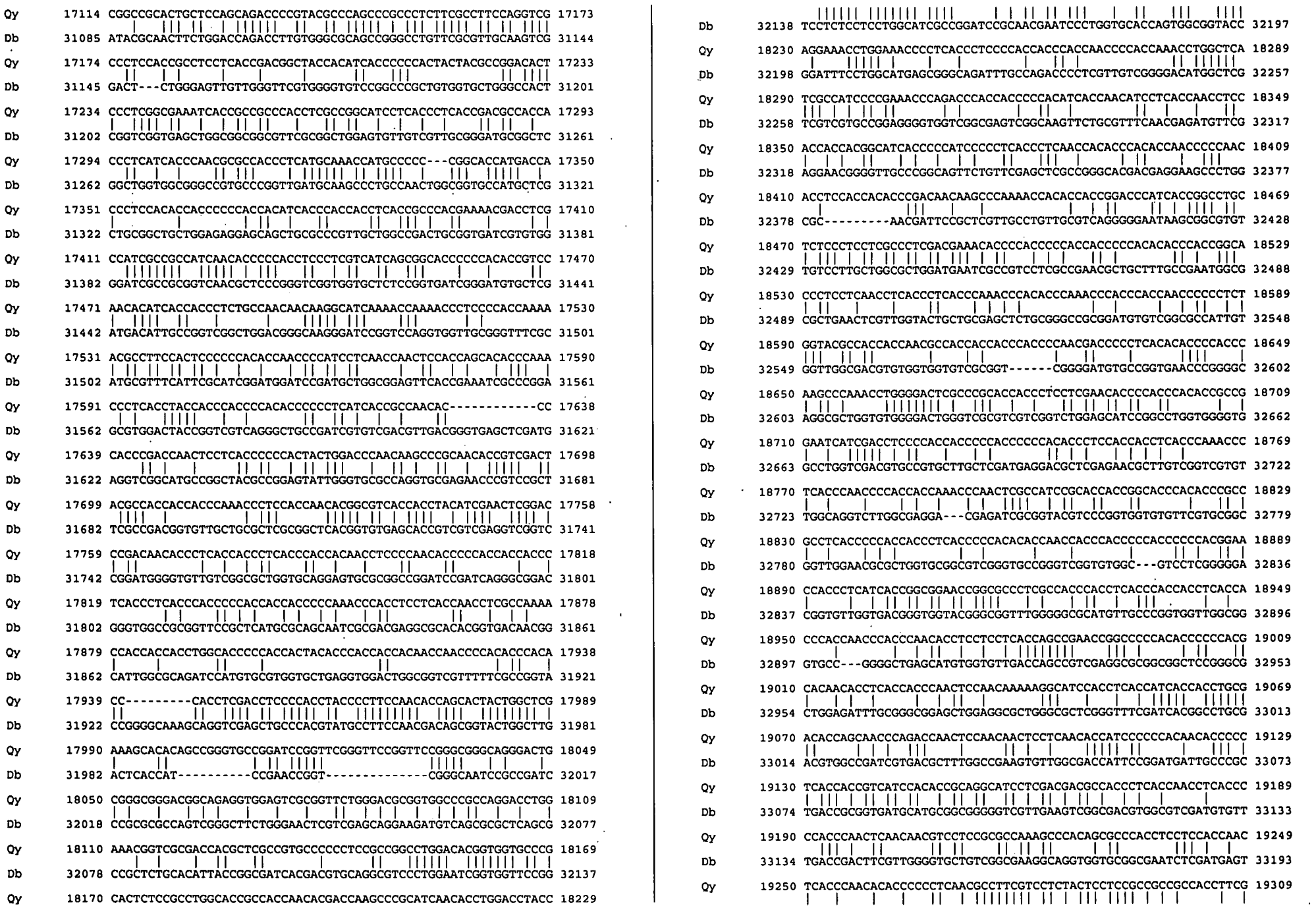


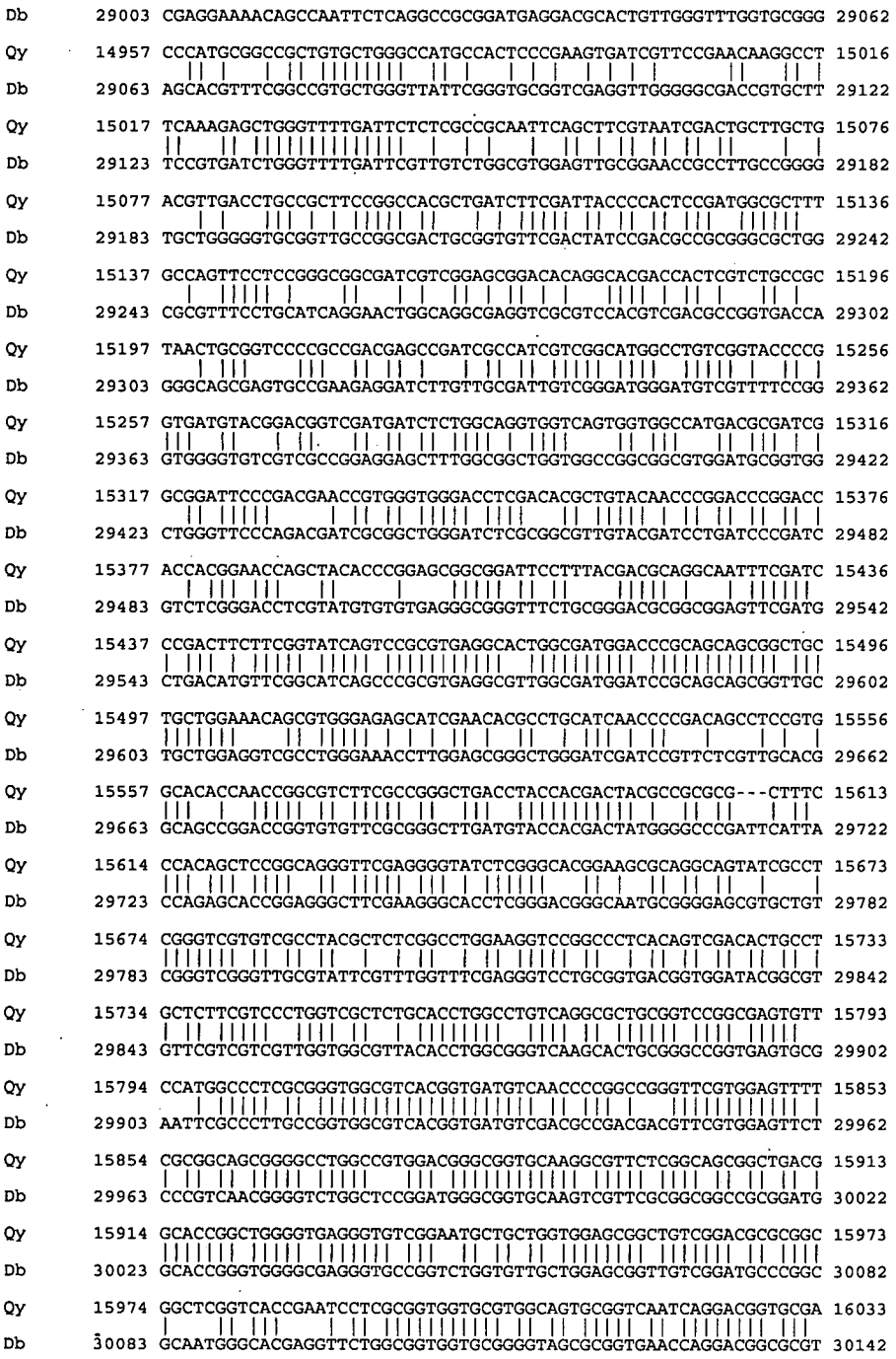

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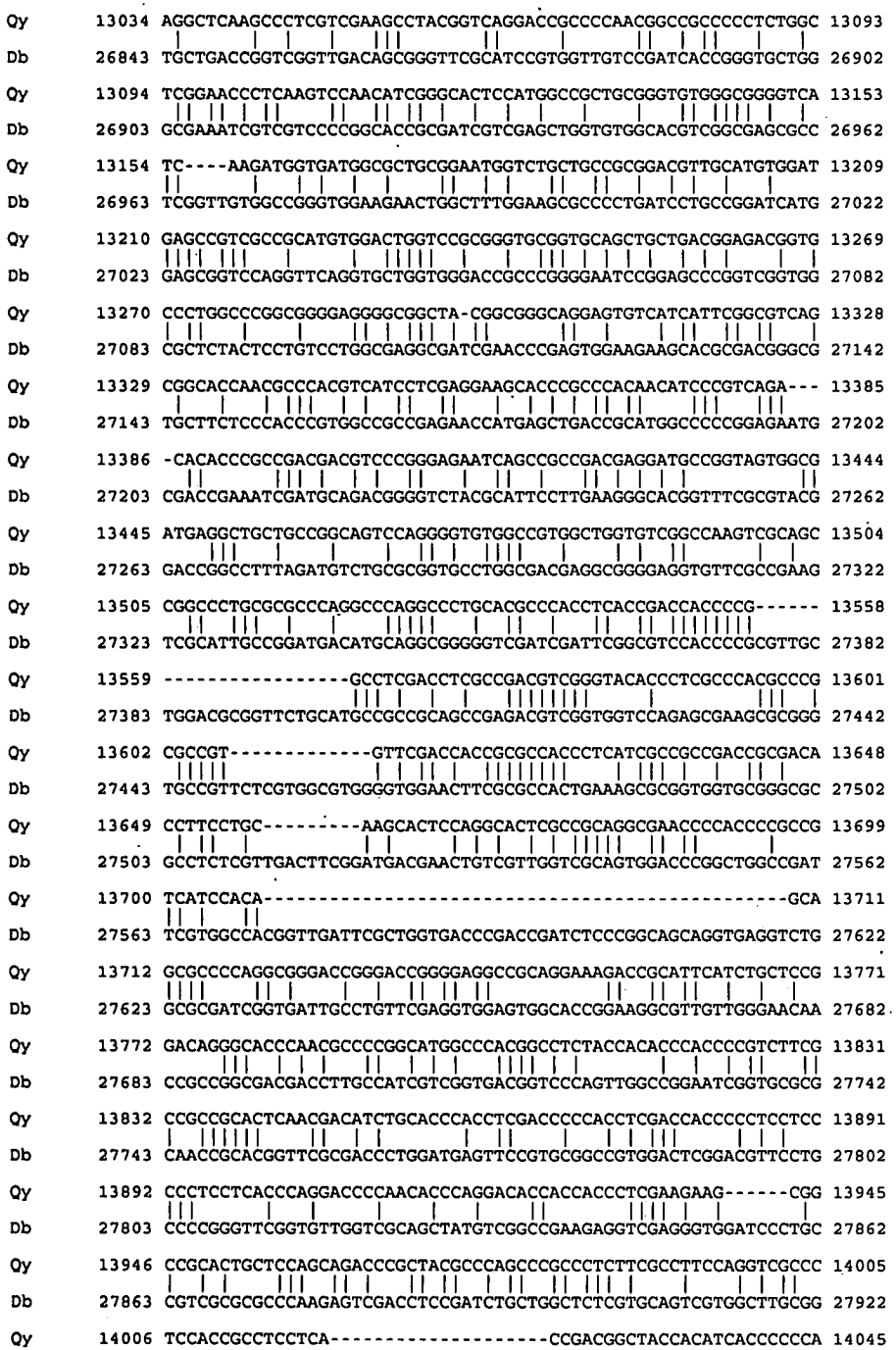


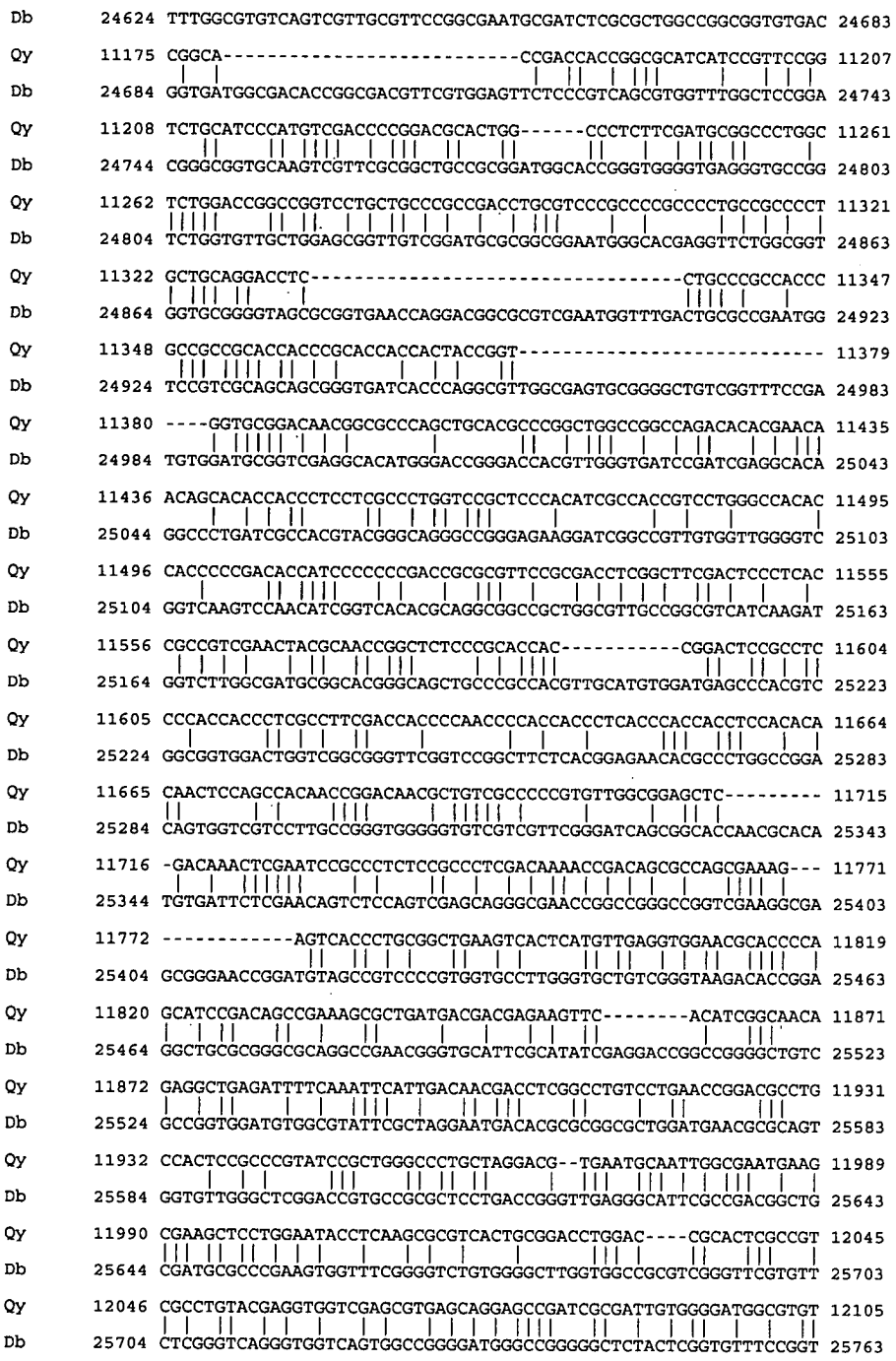

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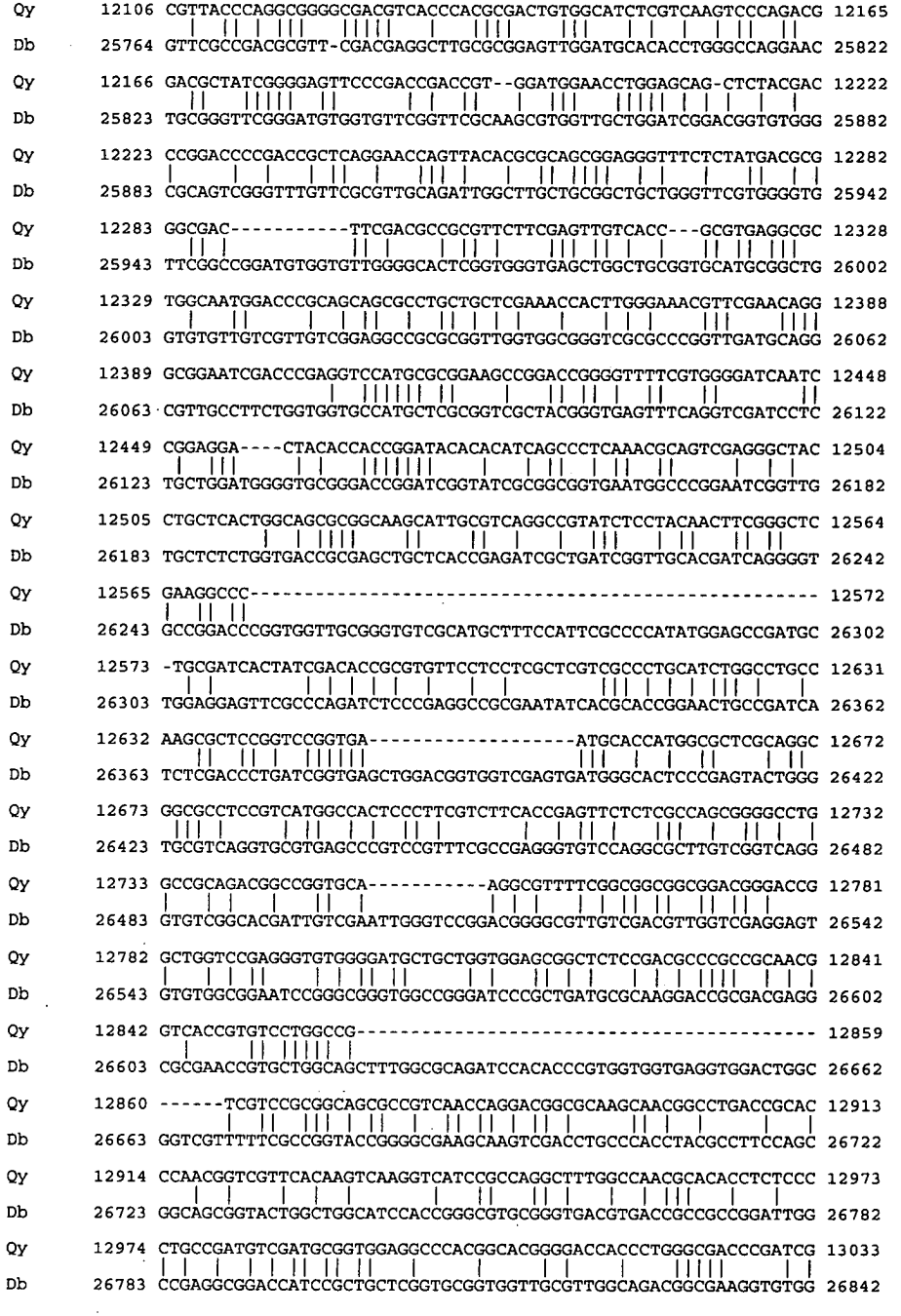


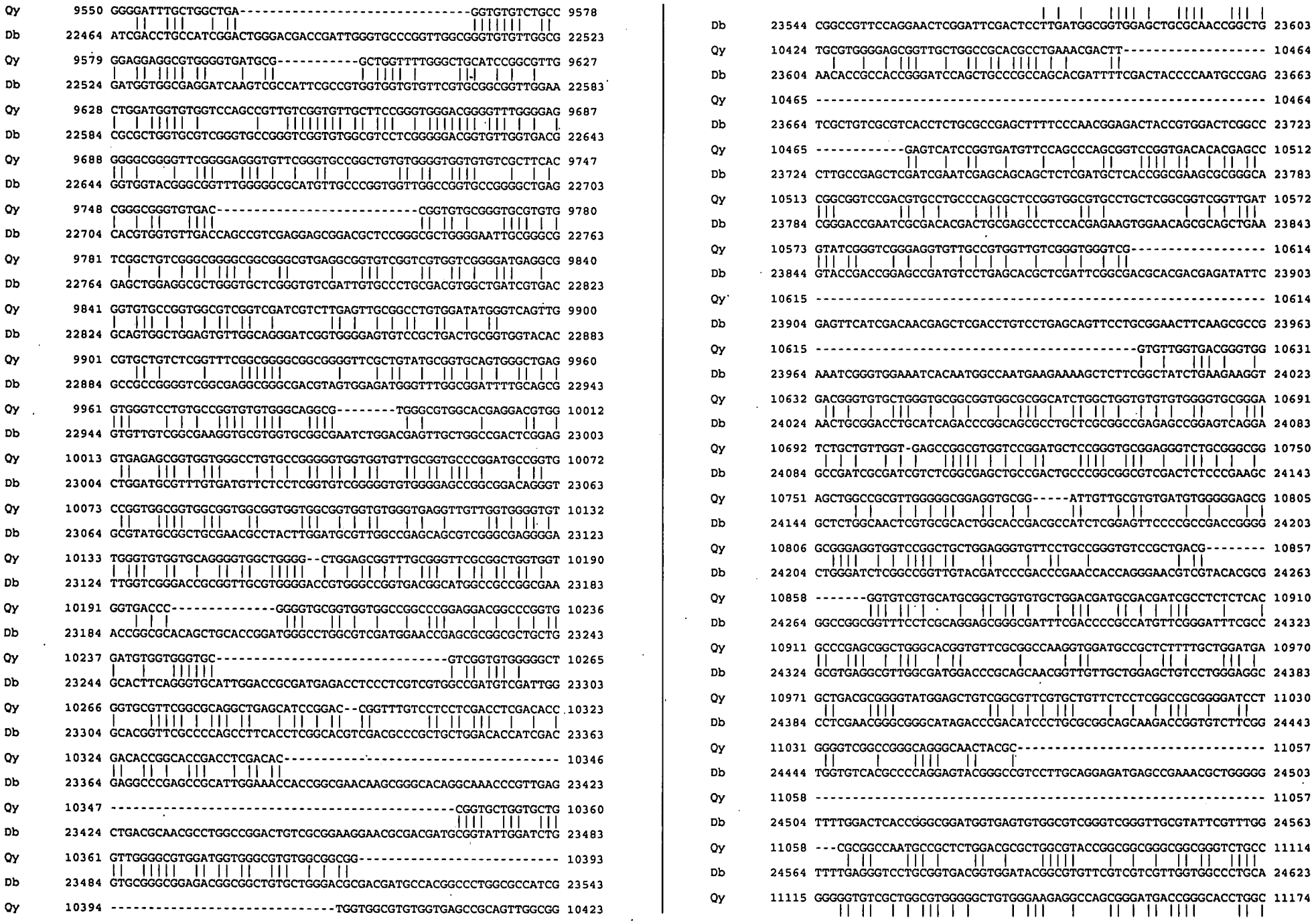


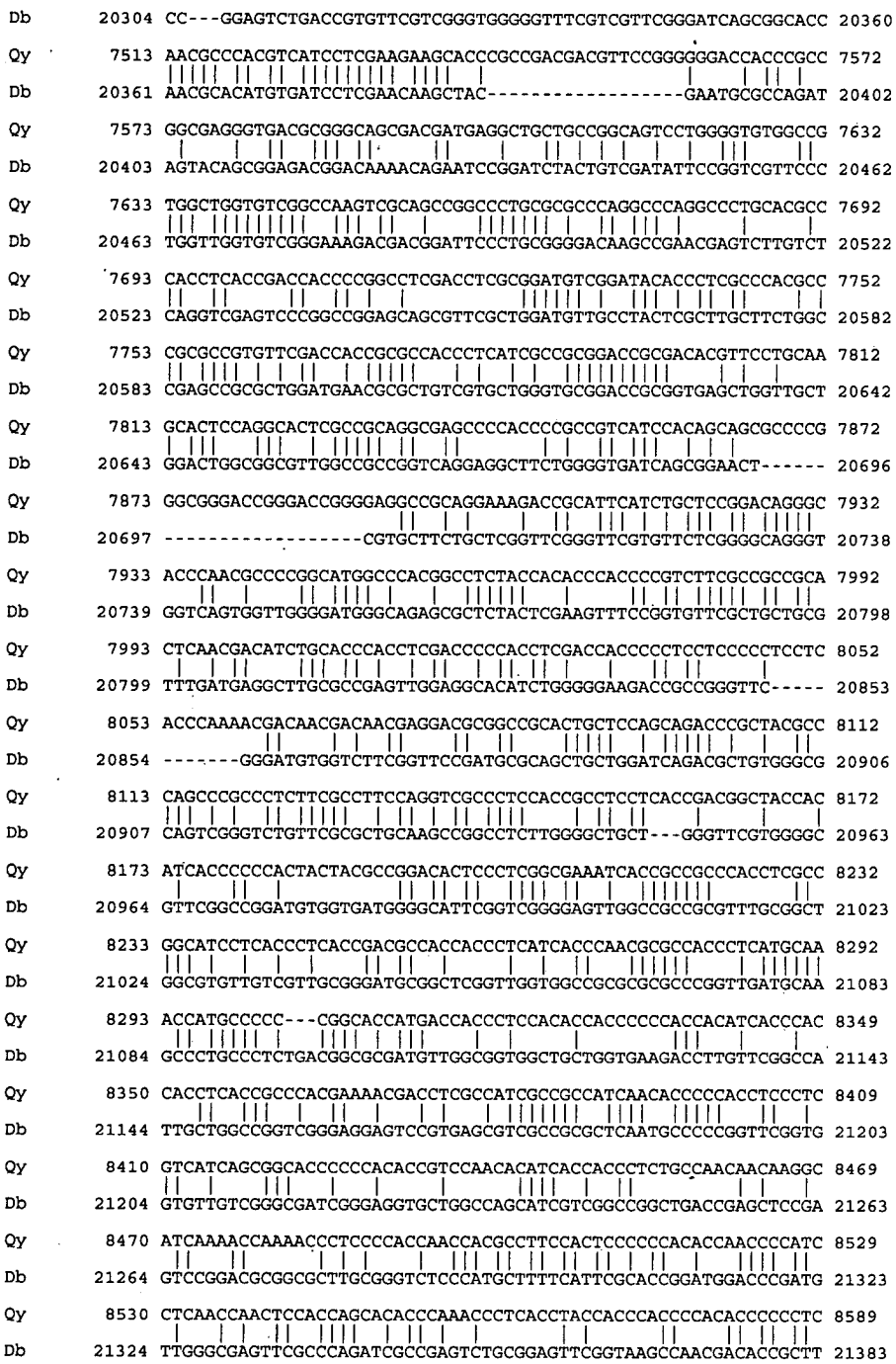

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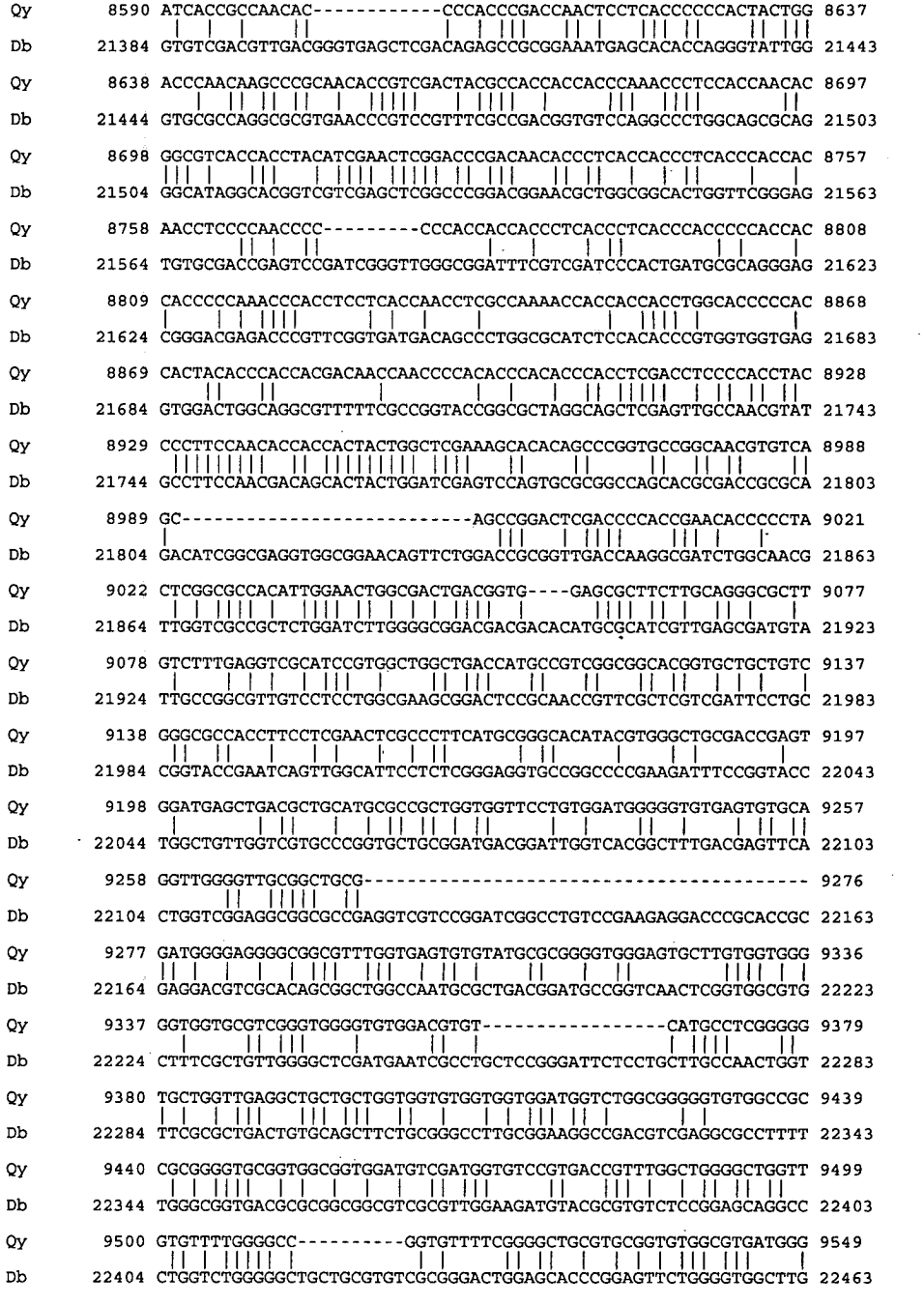

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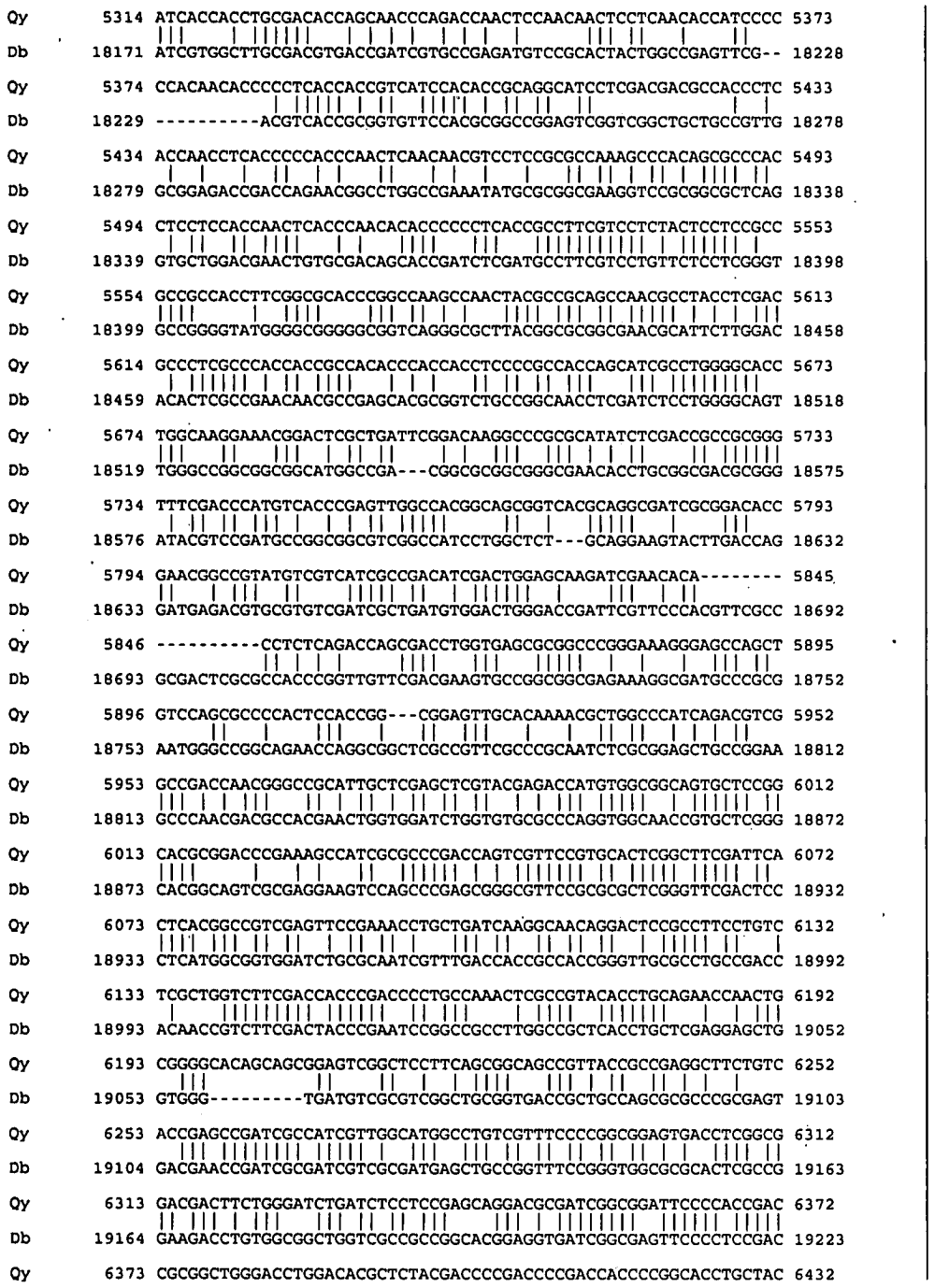


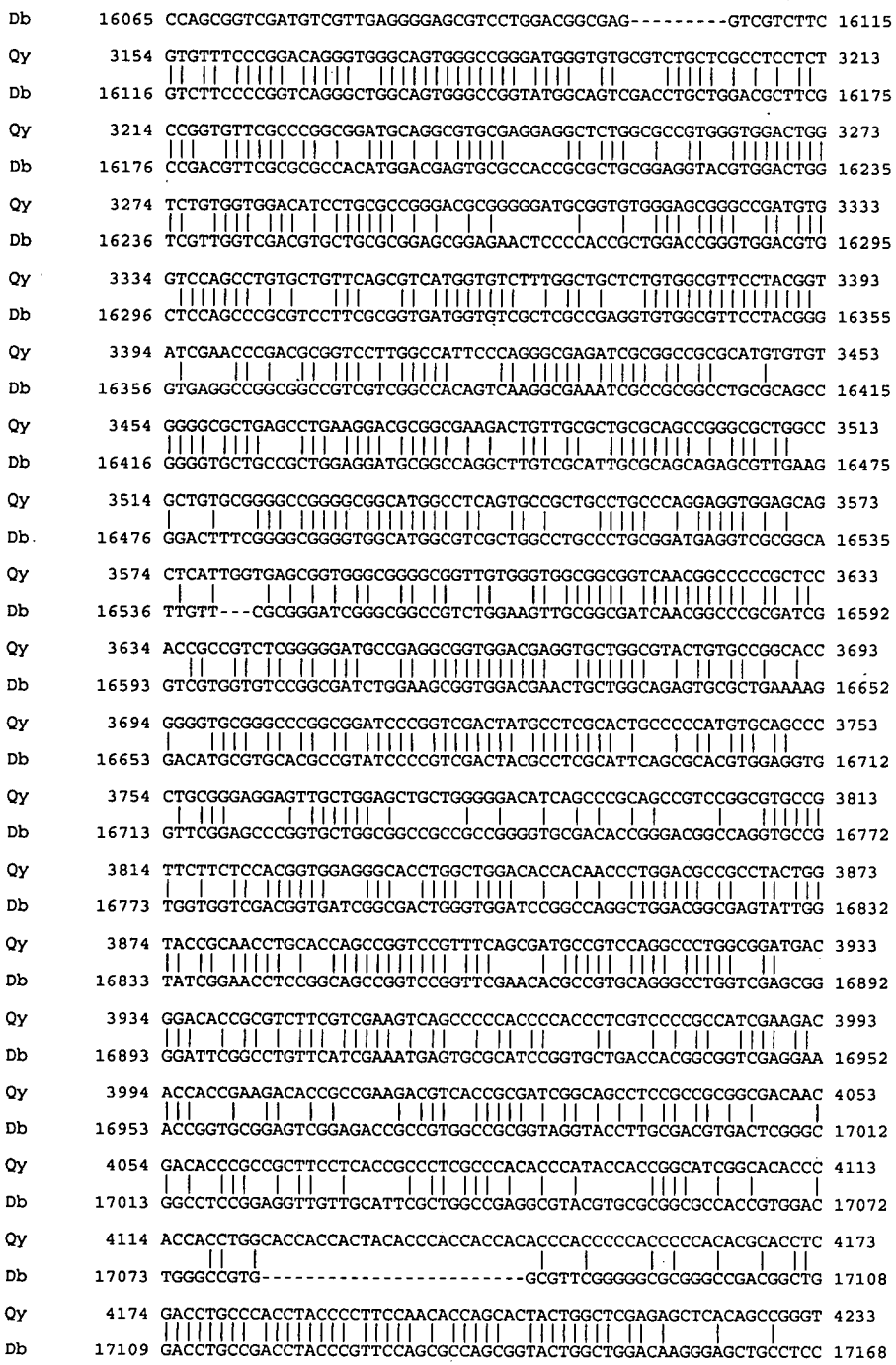











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XX
PT New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for
PT recombinant production of insecticidal spinosyns and their derivatives
PT -
XX
PS Claim 7; Page 74-91; 354pp; German.
XX
CC This invention describes a novel method nucleic acid (I) and its encoded
CC polypeptide (II) containing at least one region that encodes an enzymatic
CC activity involved in biosynthesis of spinosyns. (I) are used (i) to
CC identify, inactivate or modulate genes involved in the biosynthesis of
CC (II); (ii) to generate a library of polyketide synthases; (iii) for
CC adding forosamine or trimethylrhamnose to a spinosyn or polyketide
CC aglycone; and (iv) for recombinant production of the corresponding
CC enzymes, which are used for production of (II), their precursors or
CC derivatives, including production of transgenic plants that express (II)
CC and thus have increased resistance to insects. (I) are also useful as
CC markers for sequencing of the Saccharopolyspora spinosa genome. (II) are
CC macrolides with insecticidal, but not antibacterial, activity, and can
CC also be used to raise specific antibodies, useful for identifying
CC expression clones in a gene bank. Cells transformed with (I) may produce
CC (II) at significantly increased levels or produce new derivatives of
CC (II). This sequence represents a genomic DNA fragment of the S. spinosa
CC genome which contains the coding regions for proteins involved in
CC forosamine and trimethylrhamnose biosynthesis.
XX
SQ Sequence 50000 BP; 6944 A; 14312 C; 19170 G; 9574 T; 0 other;

Query Match 10.2%; Score 3142; DB 22; Length 50000;
Best Local Similarity 49.2%; Pred. No. 0;
Matches 15063; Conservative 0; Mismatches 12830; Indels 2753; Gaps 147;

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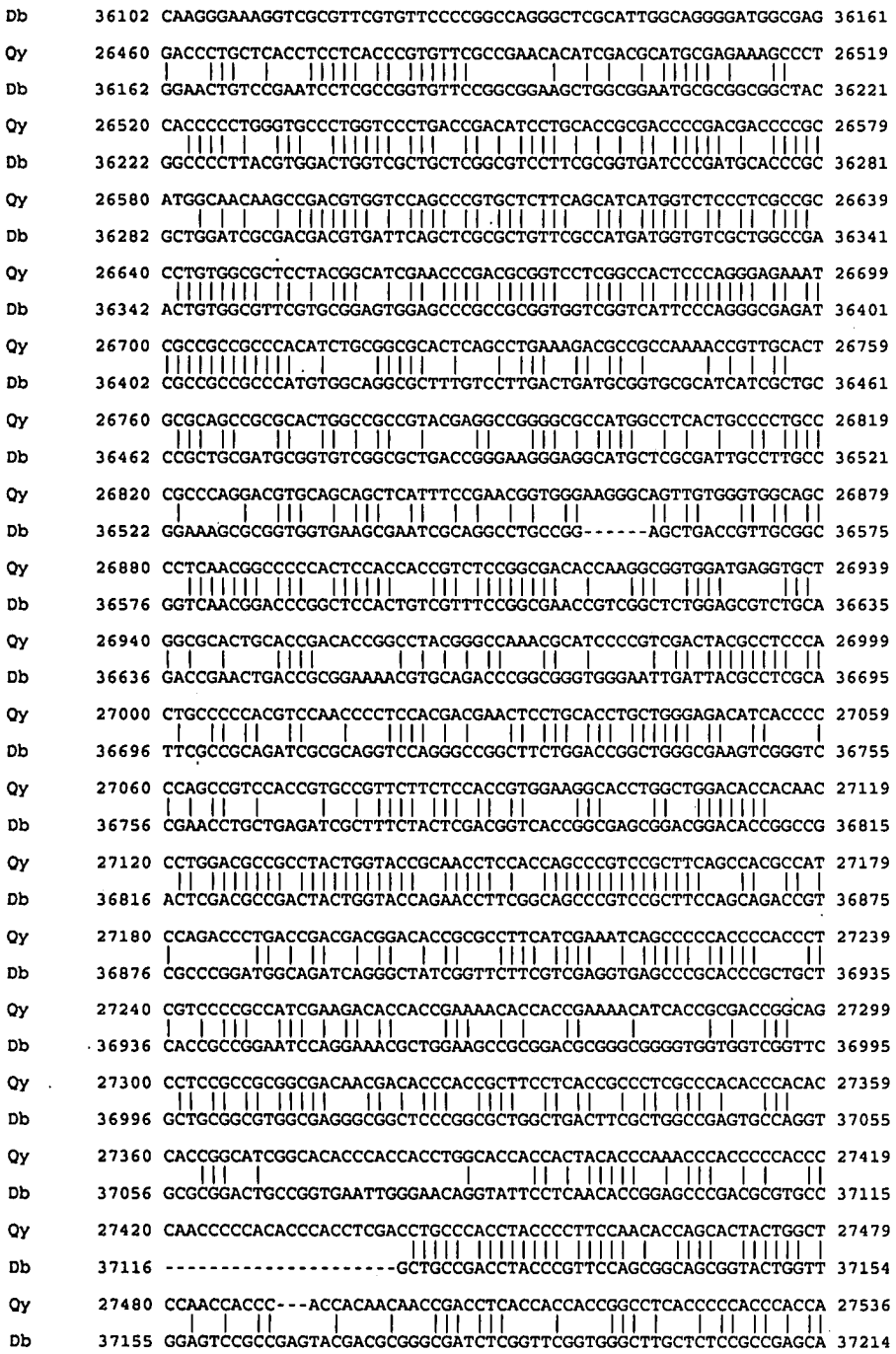
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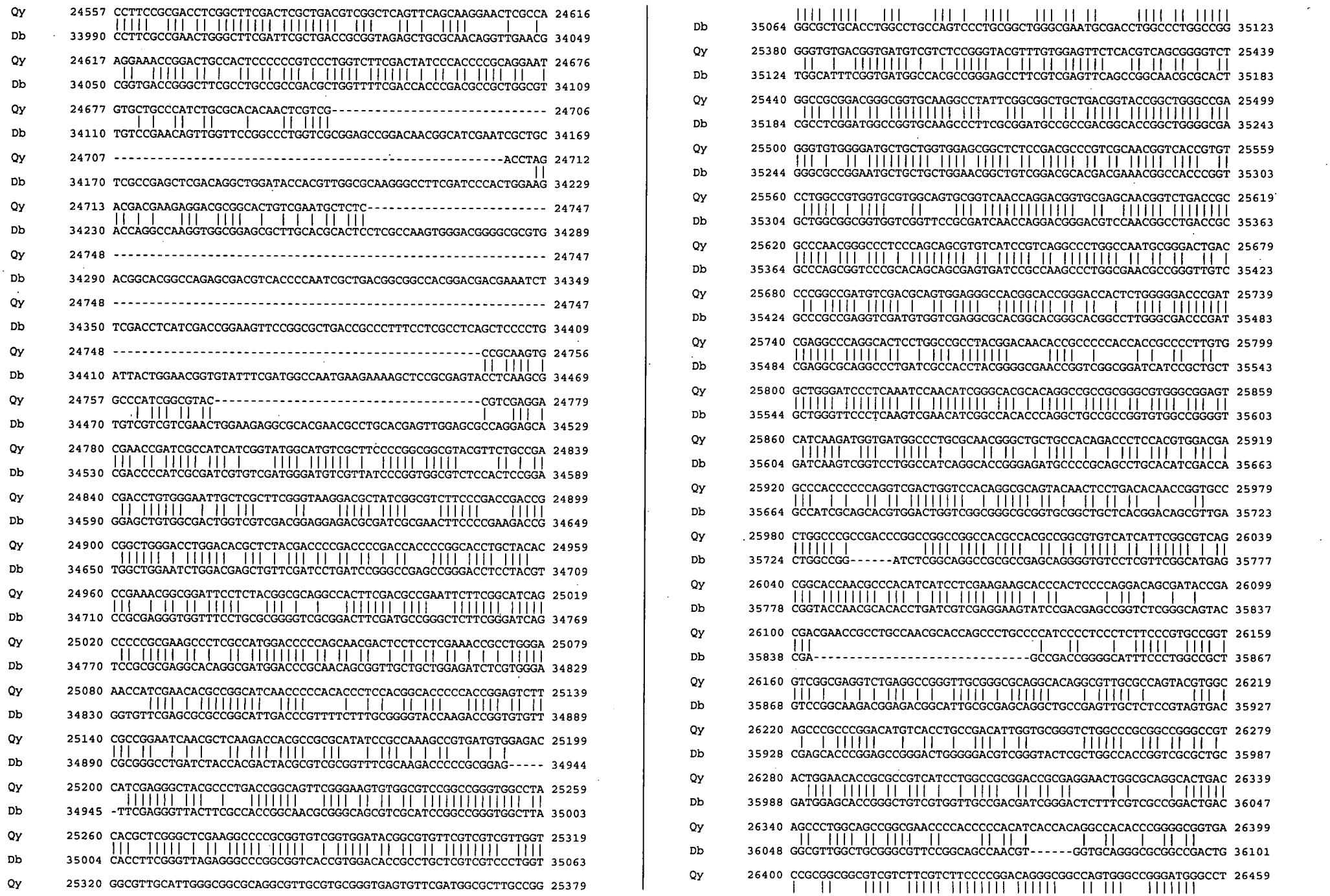
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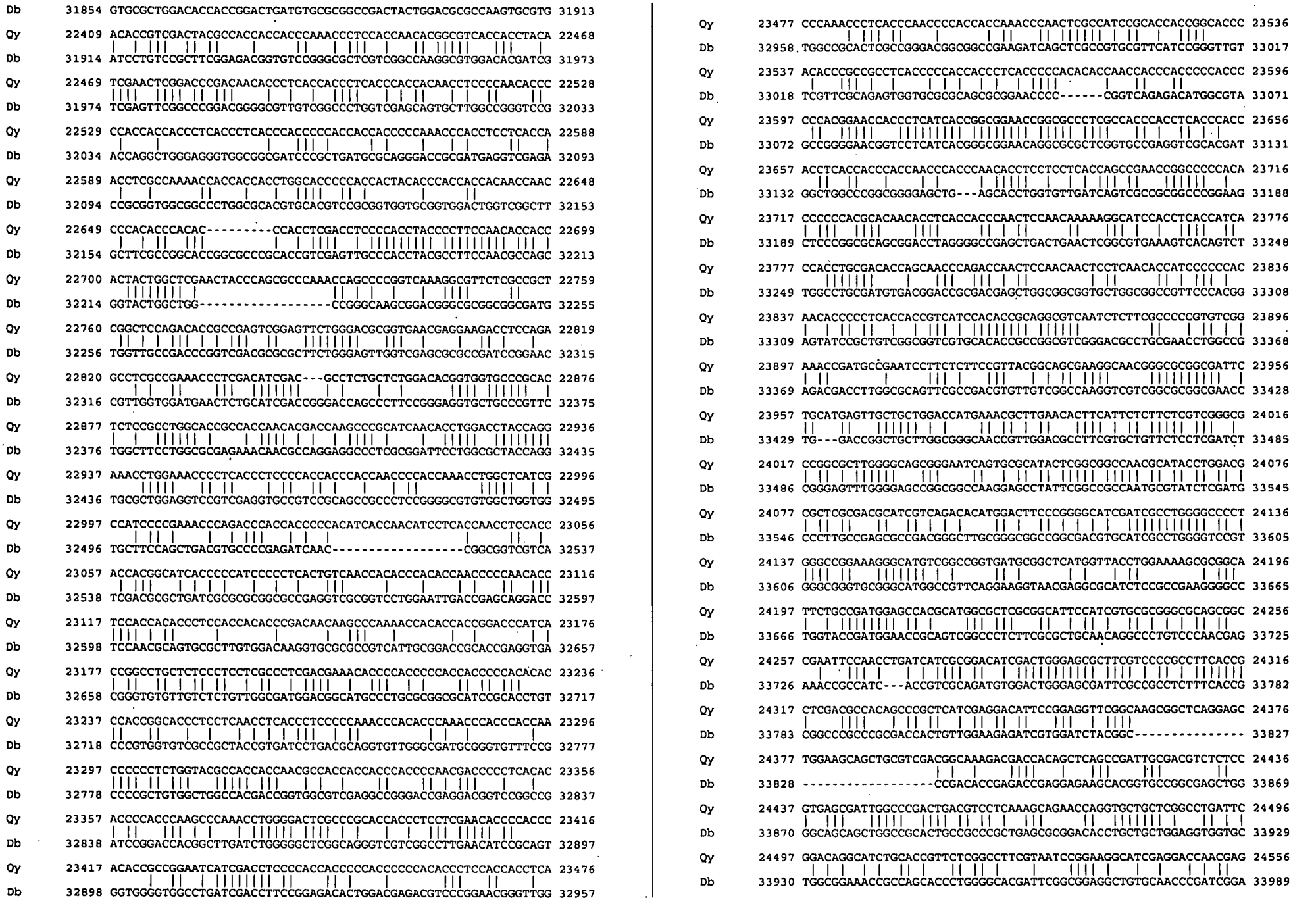
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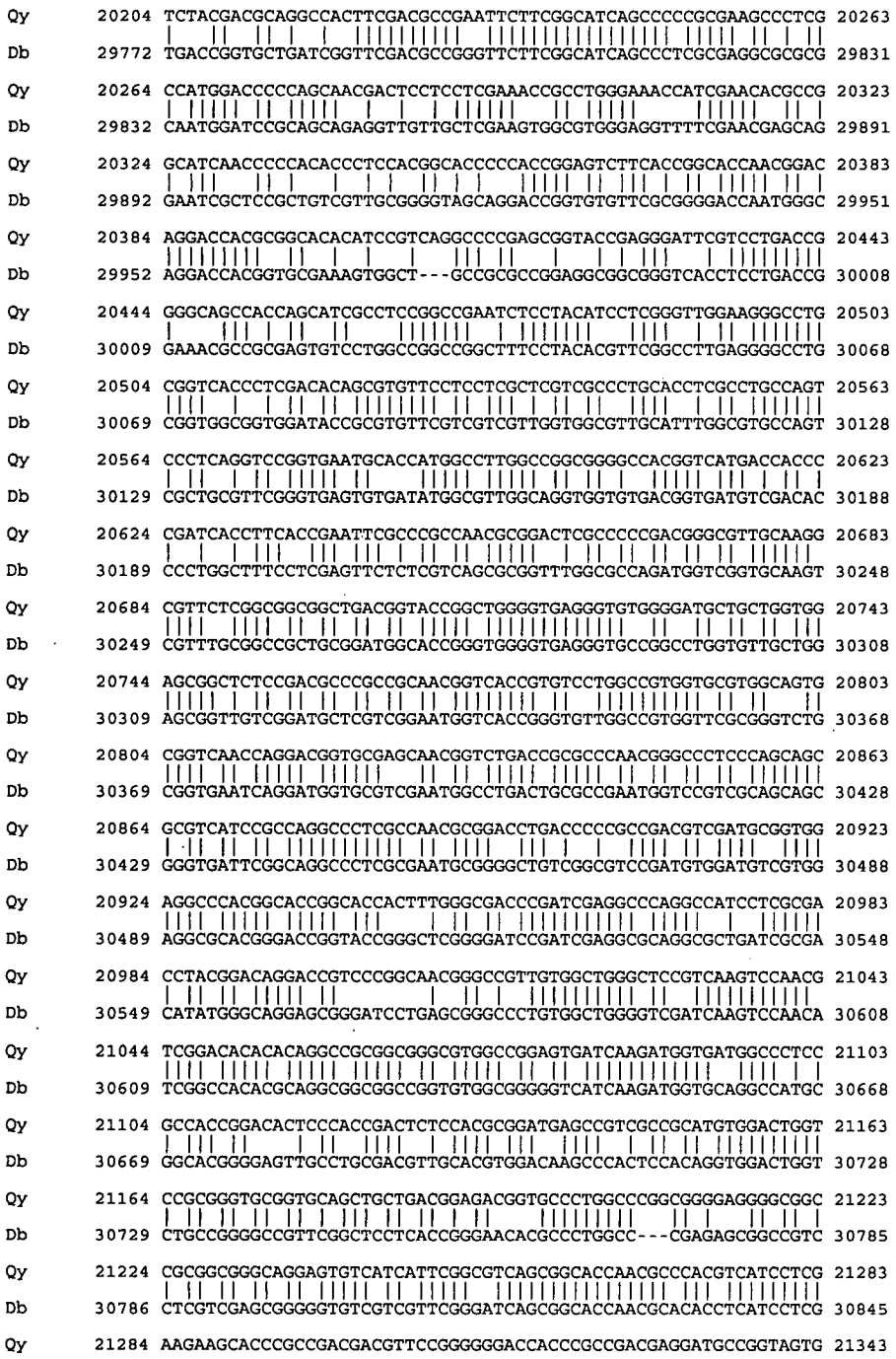
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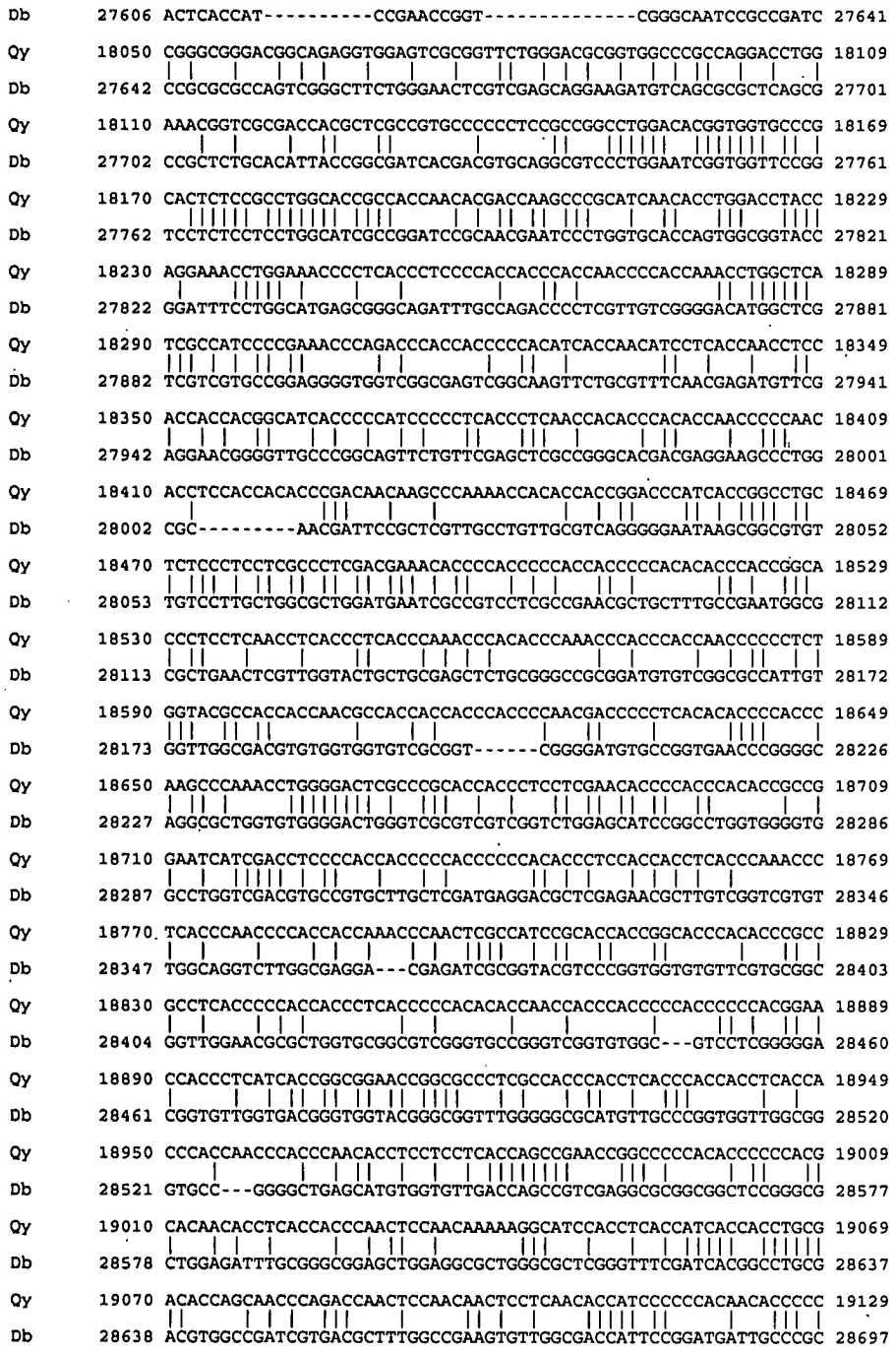
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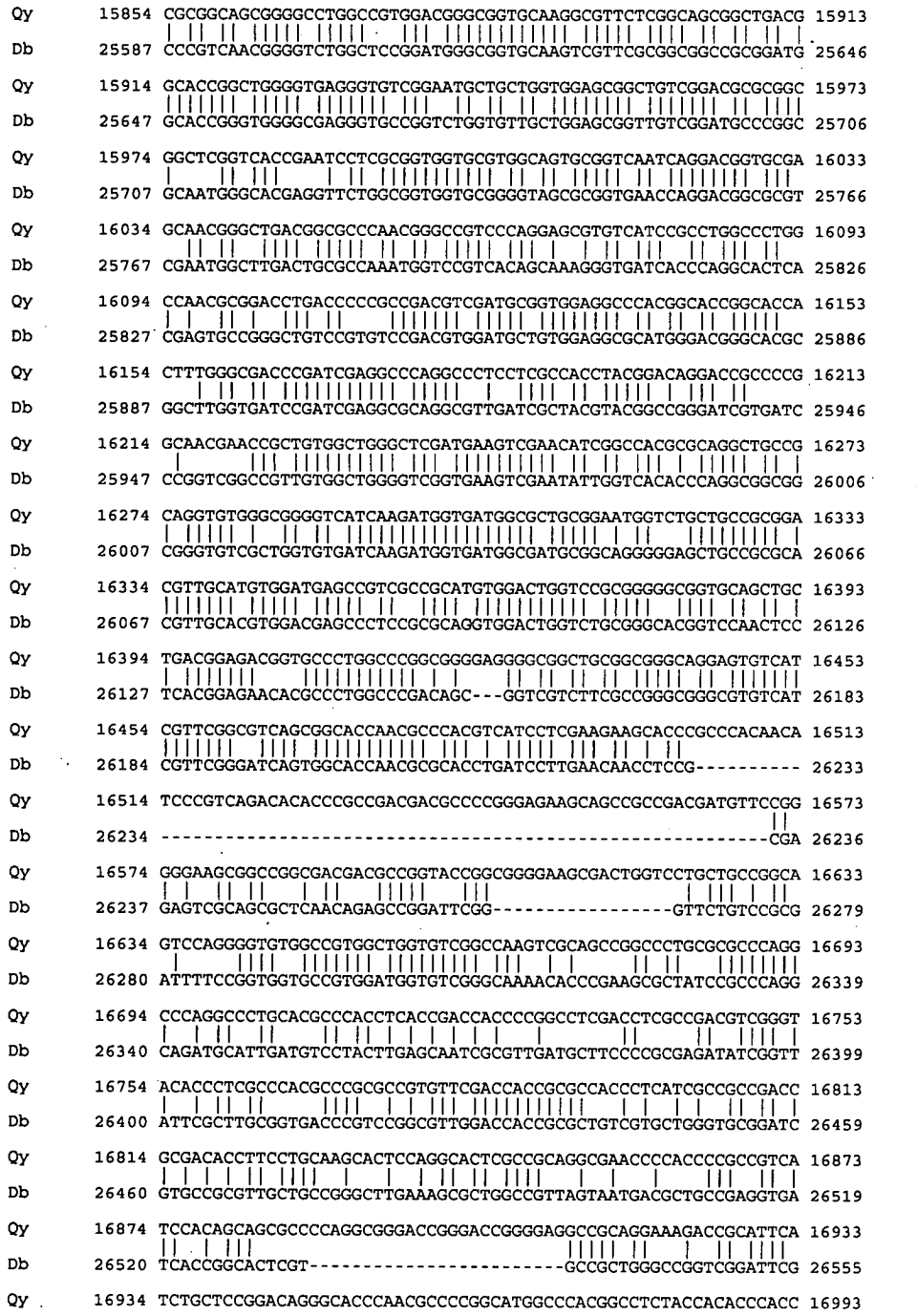

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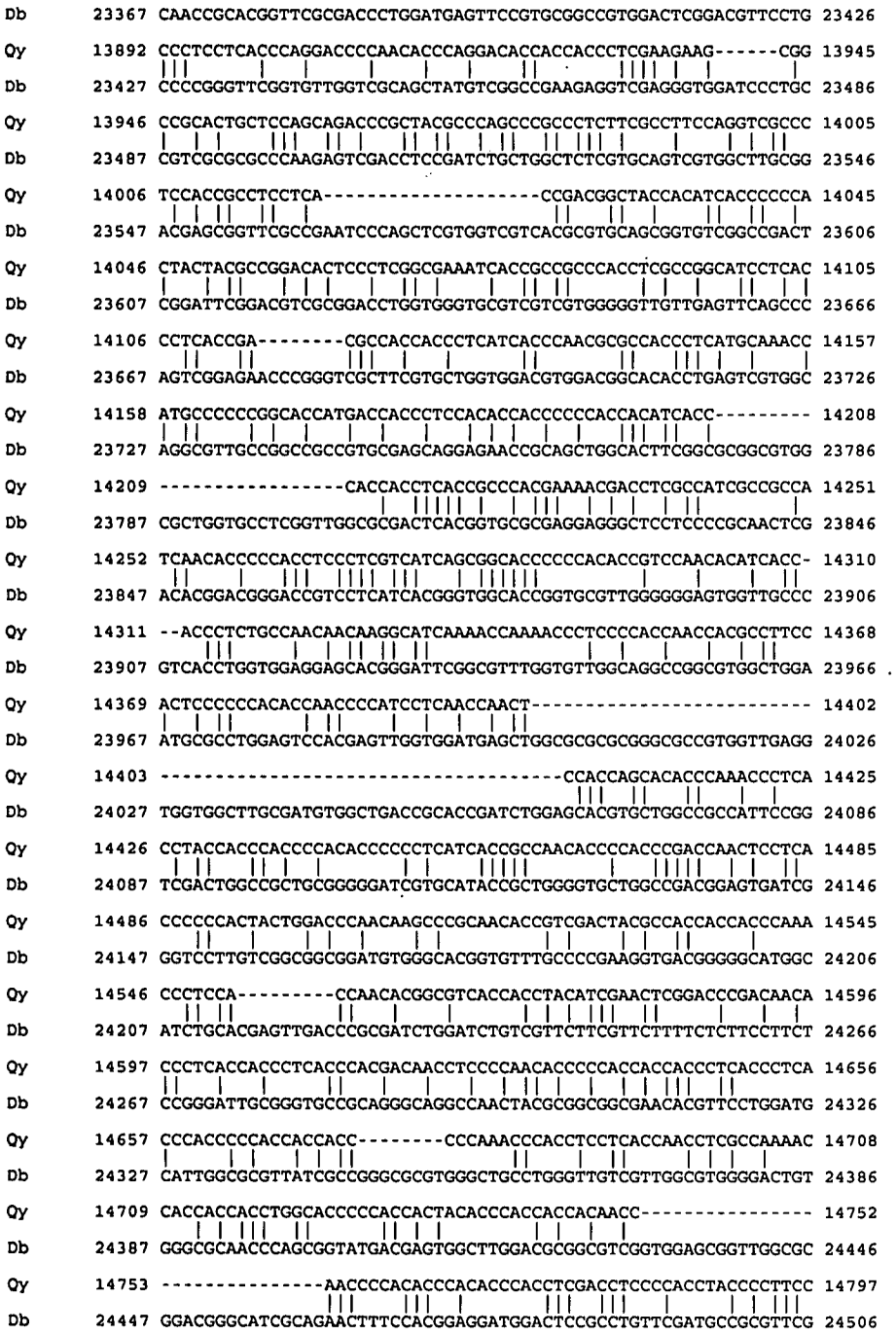


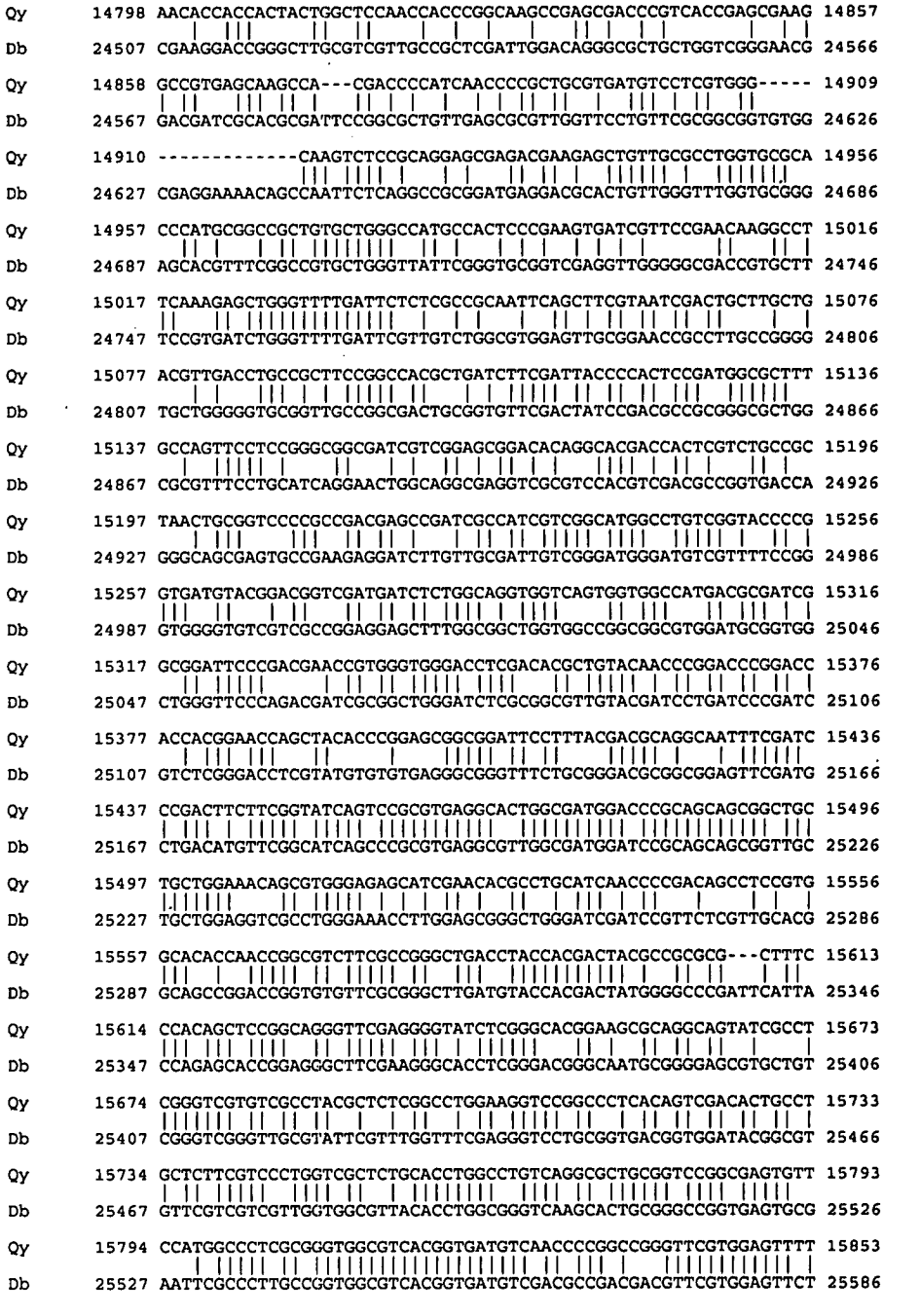


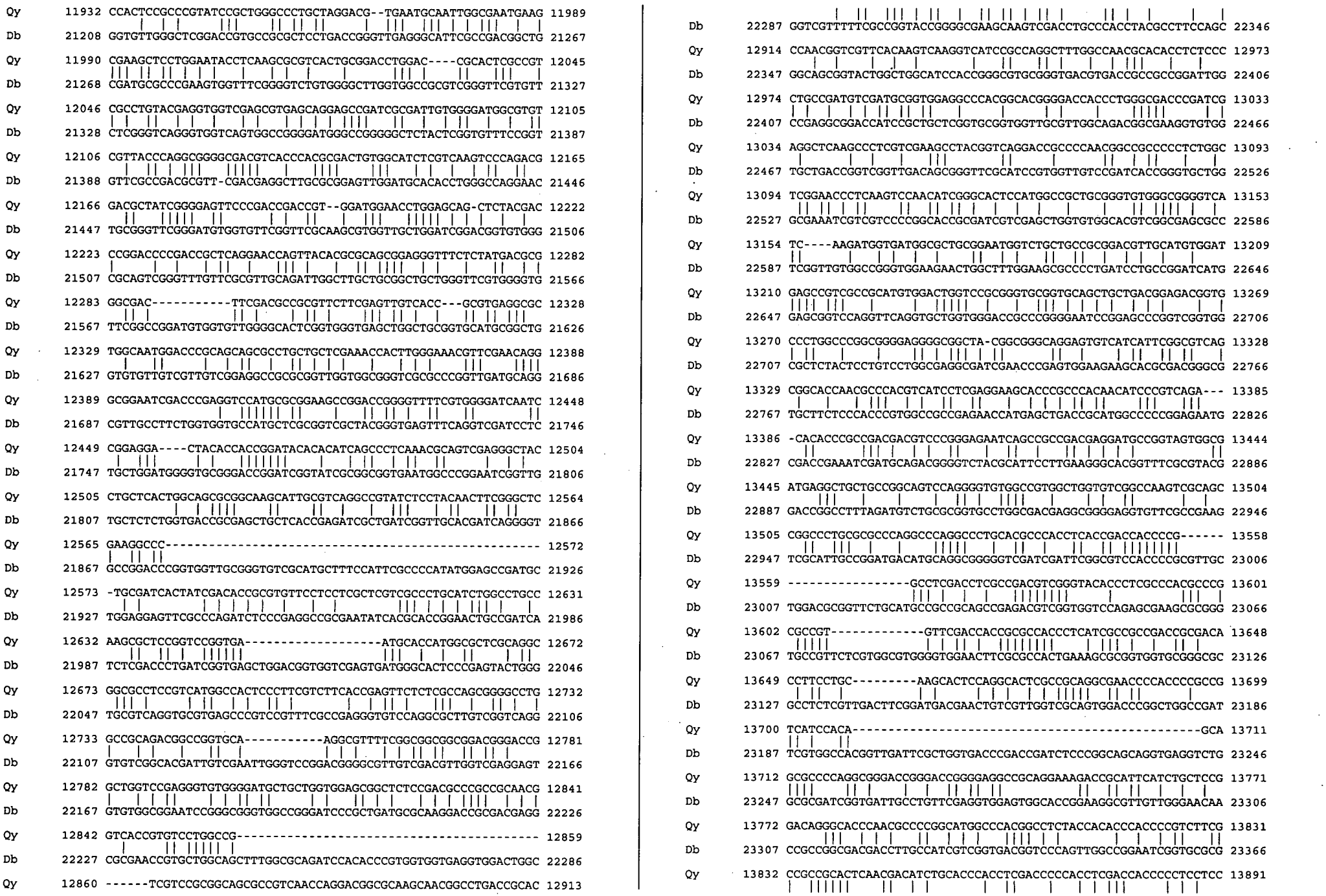


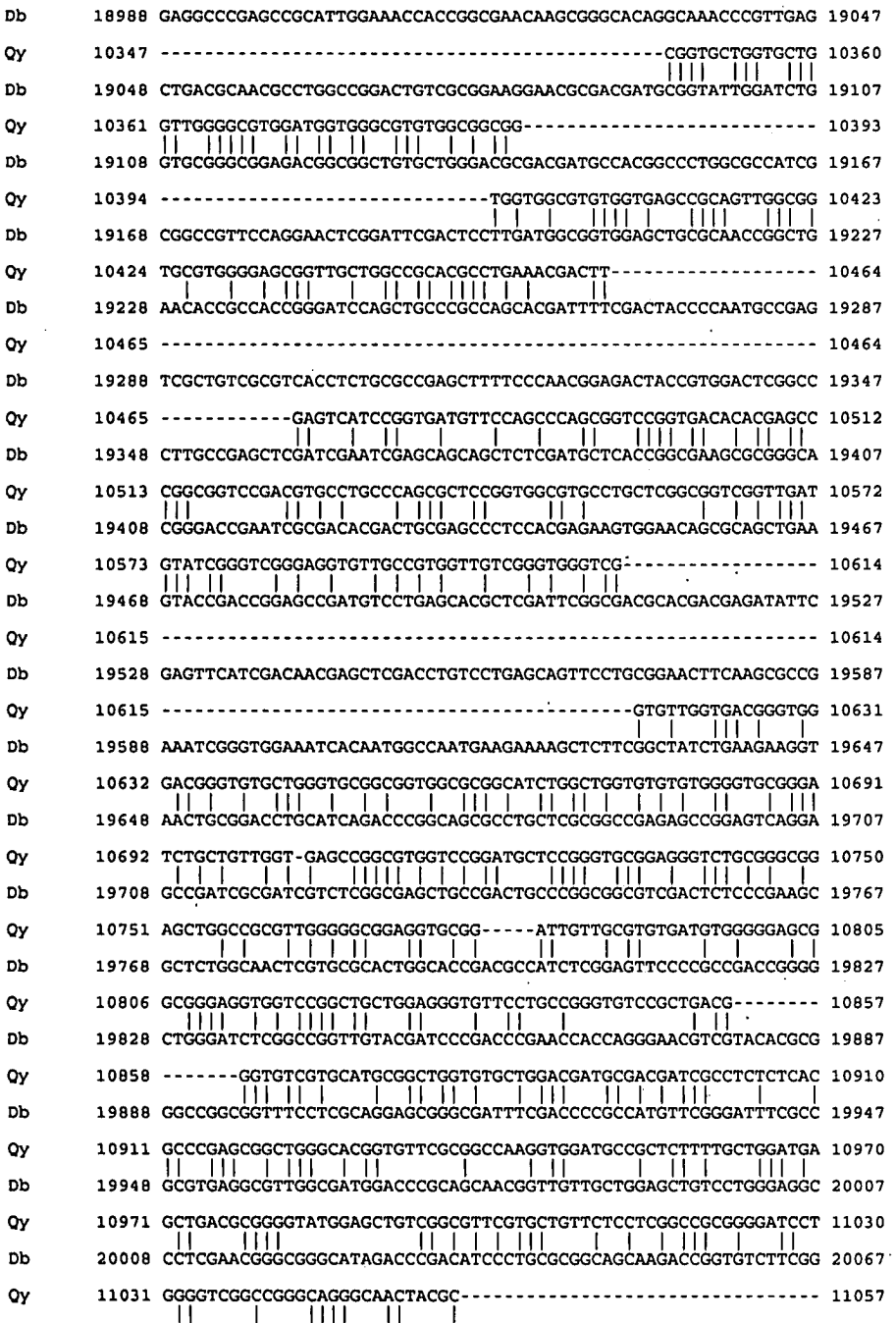

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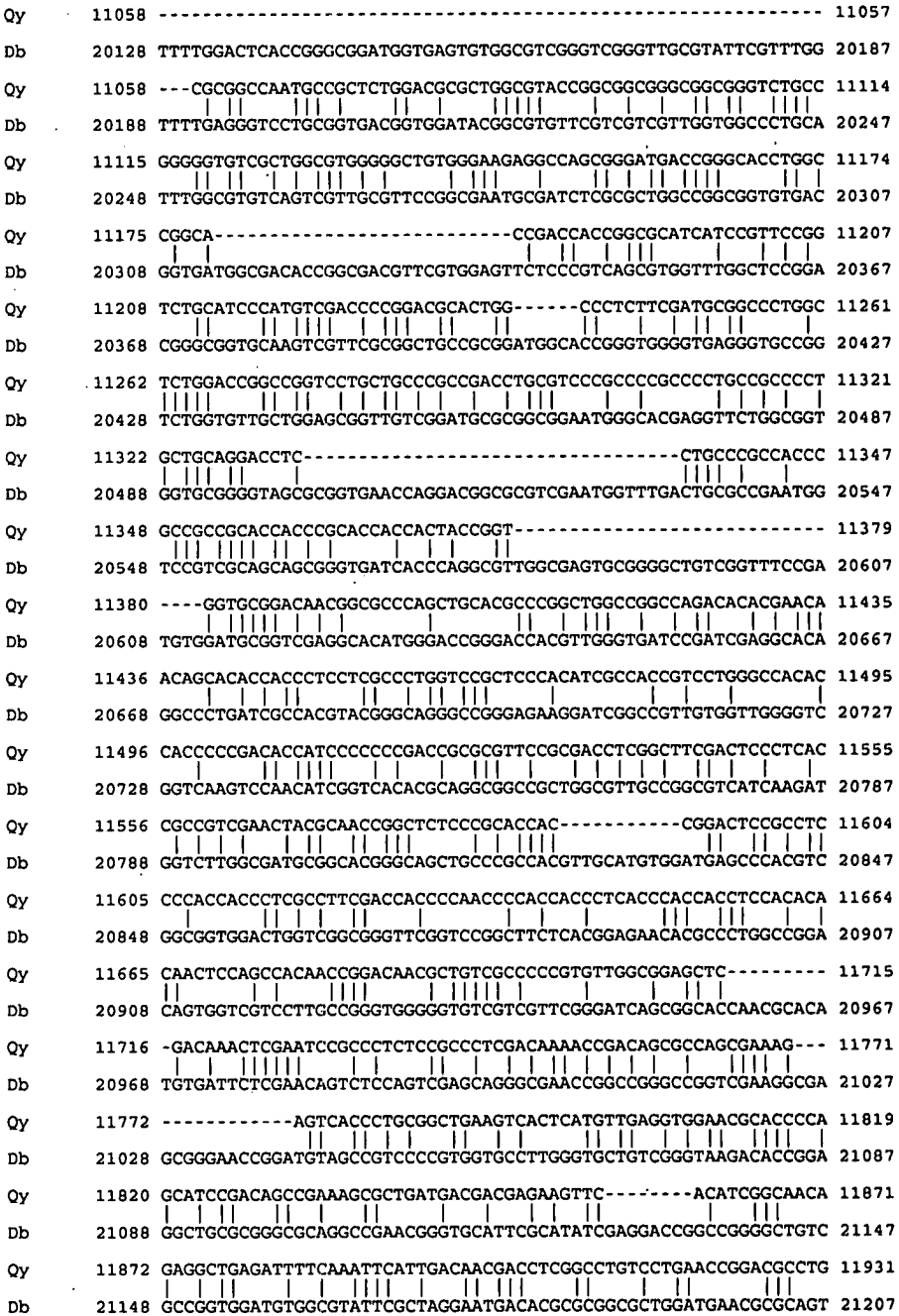

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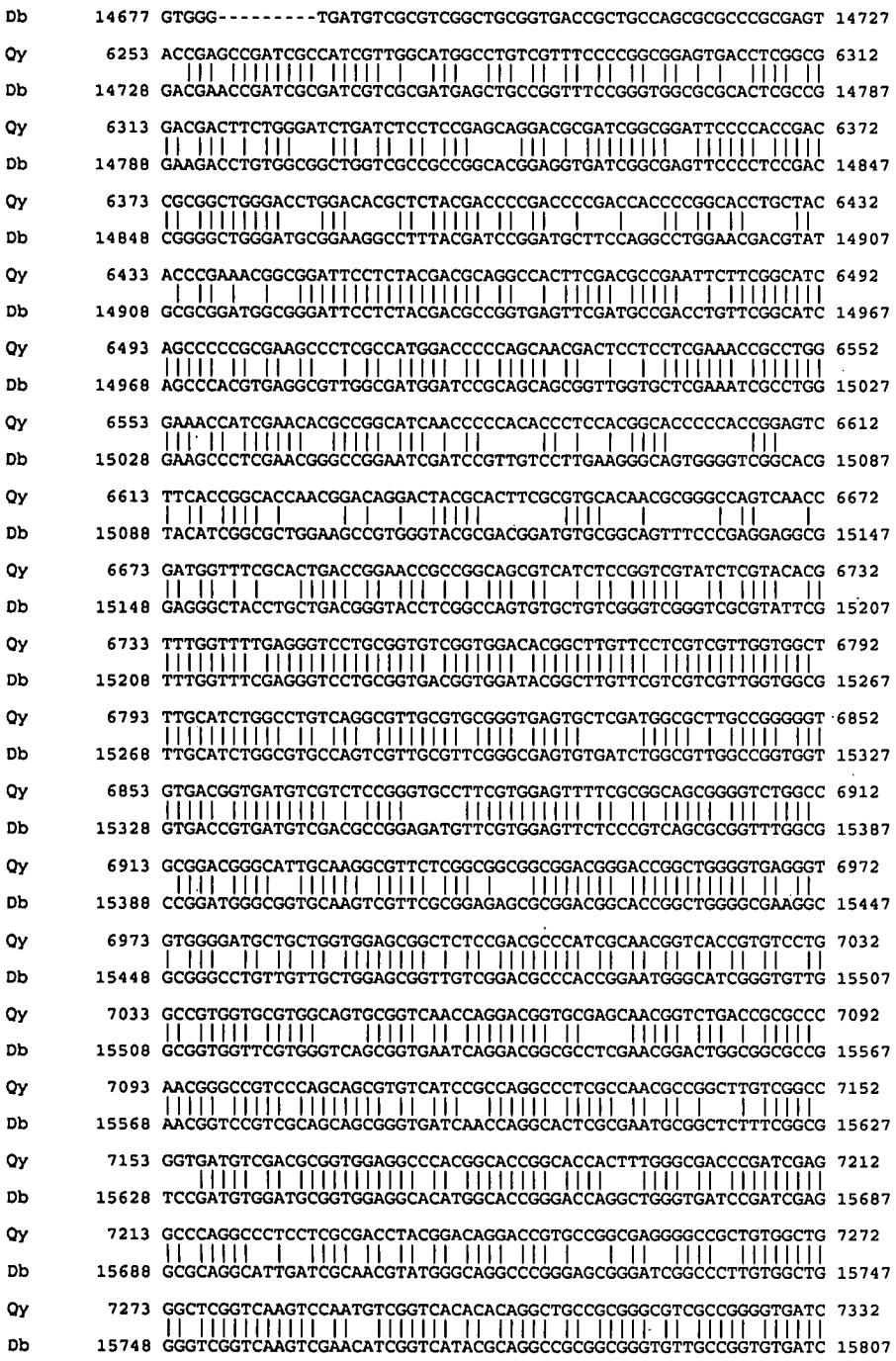


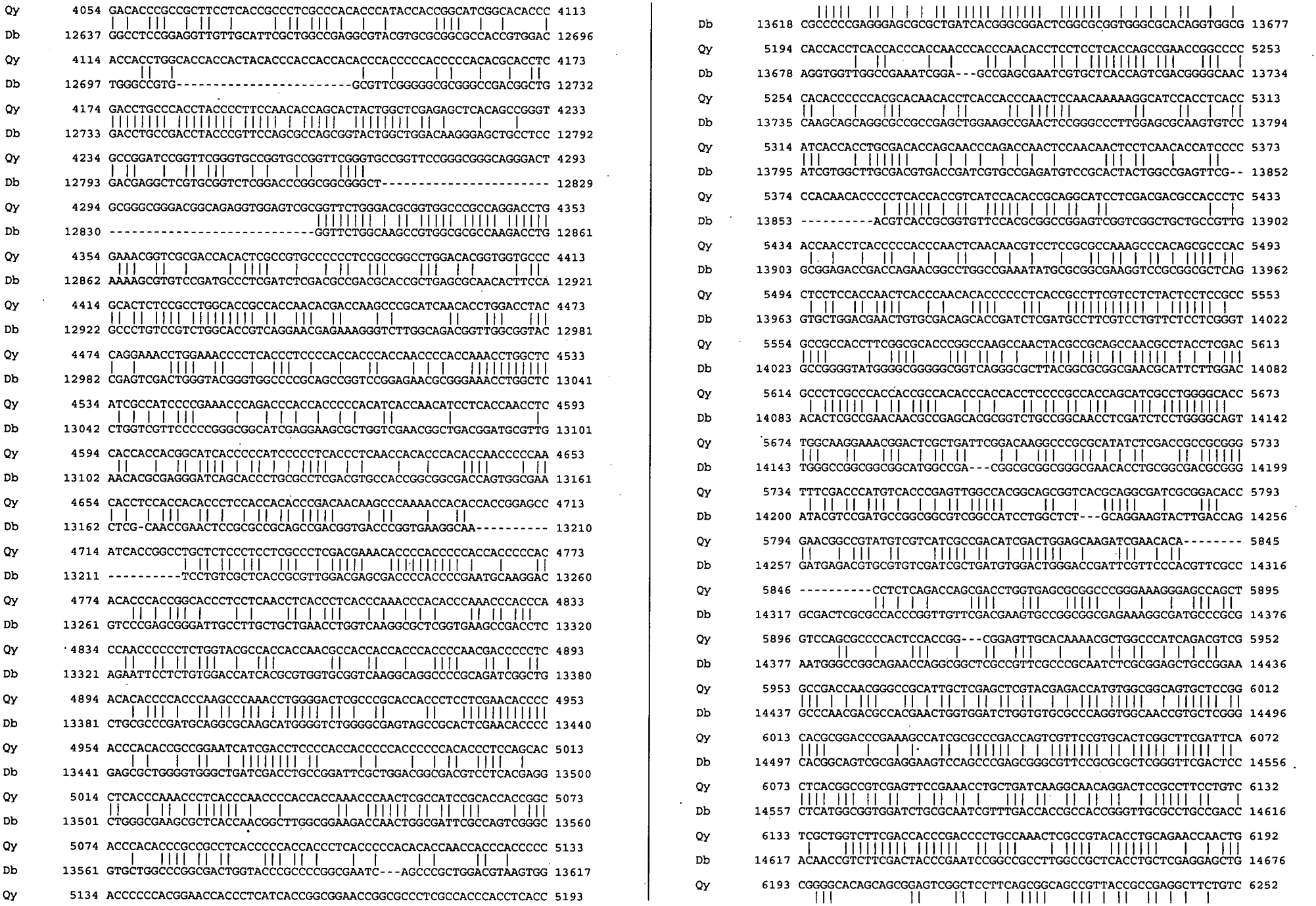


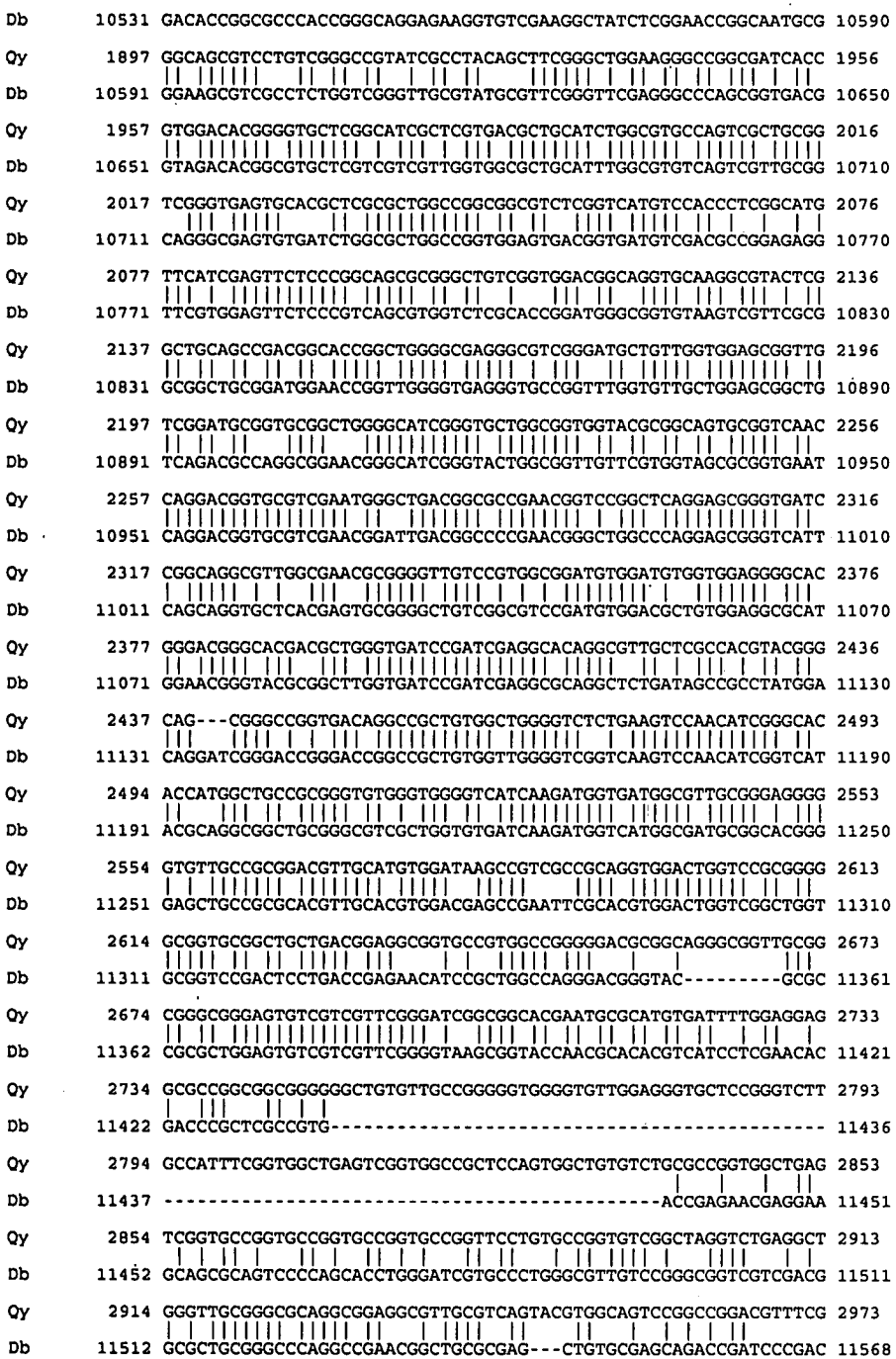


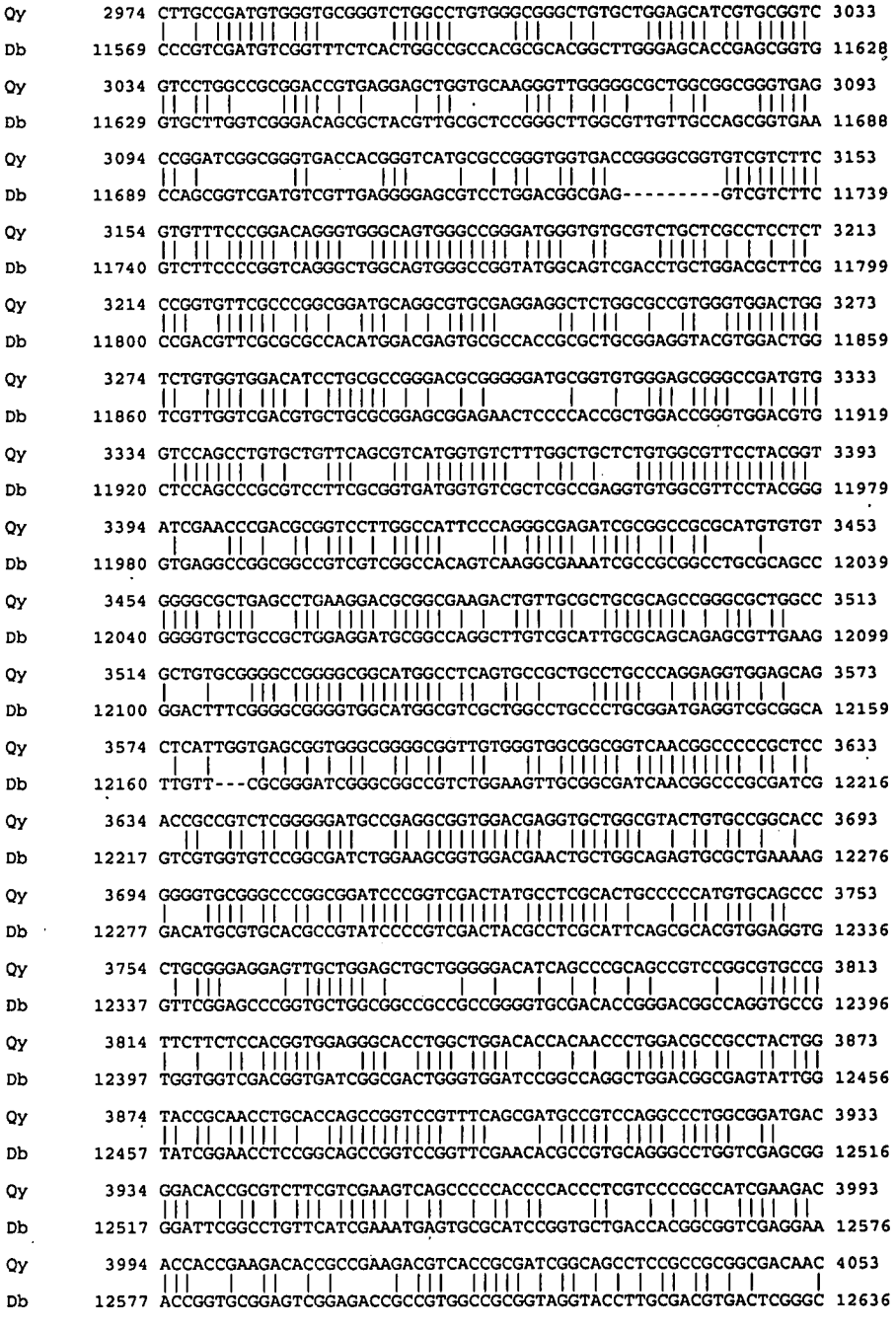





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Db      44977 CTTCGATGCGGCGCTCTTCCGAACCGAGACCGCCCTGGTCCCCGCGCGCTTCGACTTGAG 45036

Qy      29922 GGCCGTACGGTCTGGTGCCGCGTCCGCACCGGTGCCGCCGCTGCTGCAAGGTCTGCTTCA 29981

Db      45037 CGCGCTCAGGGCGAACGCCGGCAGC------GTCCCCCCGTTGTTCCAACGTCTCGTCCG 45090

Qy      29982 GCTGCCTCGGTCCCGCTCGGCCGCCGCGGCCCCCGGCCATGGGGCCCCGGCGGCGGACGA 30041

Db      45091 CGCTCGCACCGTACGCAAGGCCGCCAGCAACACCGCCC----------A 45129

Qy      30042 GGCGGCGGCCTGGCGTGAGCGTCTGGCCCGGCAGAGTGCCGGTGAGCGCAGGCAGGCGCT 30101

Db      45130 GGCCTCGTCGCTTACAGAGCGCCTCTCAGCCCTCCCGCCCGCCGAACGCGAGCGTGCCCT 45189

Qy      30102 GCTGCGCCTGGTGCGGTCGCATGTCGCGGCGGTGCTCGGCCATAGCGGTGCCGACGGAAT 30161

Db      45190 GCTCGATCTCATCCGCACCGAAGCCGCCGCCGTCCTCGGCCTCGCCTCCTTCGAATCGCT 45249

Qy      30162 CGACGCATCGCGGGCGTTCCGCGAGCTGGGGTTCGACTCGCTCACGGCGGTCGAGCTGCG 30221

Db      45250 CGATCCCGATCGCCTCCTCCAAGAGCTTGGCCTCGACTCCATCATCGCGCTCGATCTCCG 45309

Qy      30222 CAACCGTCTCACGGCCGCGACGGGCCTGCGGCTGCGGGCCACGCTGGCCTTCGATTTCCC 30281

Db      45310 AAATCGGCTCGCCGCCGCCACCGGCGTGCGACTCCCAGCCACCCTCCTCTTCGAGCATCC 45369

Qy      30282 GACCCCGGCAGCGCTGGCCG 30301

Db      45370 AACCCCAGCTGCGCTCGCAG 45389


RESULT 12
AAF88313
ID   AAF88313 standard; DNA; 50000 BP.
XX
AC   AAF88313;
XX
DT   28-AUG-2001  (first entry)
XX
DE   S. spinosa DNA fragment SEQ ID 2.
XX
KW   Forosamine; trimethylrhamnose; polyketide synthase; biosynthesis;
KW   spinosyn; polyketide aglycone; transgenic plant; insect resistance;
KW   macrolide; insecticidal; ds.
XX
OS   Saccharopolyspora spinosa.
XX
PN   DE19957268-A1.
XX
PD   08-MAR-2001.
XX
PF   29-NOV-1999;   99DE-1057268.
XX
PR   27-AUG-1999;   99DE-1040596.
XX
PA   (FARB ) BAYER AG.
XX
PI   Eberz G,  Moehrle V,  Froede R,  Velten R,  Salas JA;
XX
DR   WPI; 2001-267102/28.
XX
PT   New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for
PT   recombinant production of insecticidal spinosyns and their derivatives
PT   -
XX
PS   Claim 7; Page 31-49; 354pp; German.
XX
CC   This invention describes a novel method nucleic acid (I) and its encoded
CC   polypeptide (II) containing at least one region that encodes an enzymatic
CC   activity involved in biosynthesis of spinosyns. (I) are used (i) to
CC   identify, inactivate or modulate genes involved in the biosynthesis of
CC   (II); (ii) to generate a library of polyketide synthases; (iii) for
CC   adding forosamine or trimethylrhamnose to a spinosyn or polyketide
CC   aglycone; and (iv) for recombinant production of the corresponding
CC   enzymes, which are used for production of (II), their precursors or
CC   derivatives, including production of transgenic plants that express (II)
CC   and thus have increased resistance to insects. (I) are also useful as
CC   markers for sequencing of the Saccharopolyspora spinosa genome. (II) are
CC   macrolides with insecticidal, but not antibacterial, activity, and can
CC   also be used to raise specific antibodies, useful for identifying
CC   expression clones in a gene bank. Cells transformed with (I) may produce
CC   (II) at significantly increased levels or produce new derivatives of
CC   (II). This sequence represents a genomic DNA fragment of the S. spinosa
CC   genome which contains the coding regions for proteins involved in
CC   forosamine, trimethylrhamnose and polyketide synthase biosynthesis.
XX
SQ   Sequence 50000 BP; 6867 A; 14165 C; 19274 G; 9694 T; 0 other;

  Query Match             10.2%;  Score 3142;  DB 22;  Length 50000;
  Best Local Similarity   49.2%;  Pred. No. 0;
  Matches 15063;  Conservative    0;  Mismatches 12830;  Indels 2753;  Gaps  147;

Qy       1417 CACGGAGGCACGGCAGCGGCGGACGACCCGATCGCCATCATCGGCATGGCATGCCGTTTC 1476

Db      10123 CACGAGGCGGAGTCGGGAGAGCGGGAACCCATCGCGATCGTGGCGATGGGCTGCCGGTAC 10182

Qy       1477 CCGGGCGGAGTCCGGTCCCCGAAGGACCTGTGGGAGCTGGCCGCCTCGGGCGGAGACGCC 1536

Db      10183 CCGGGTGGGGTGCAGGACCCGGAAGGGCTGTGGAAACTGGTCGCCTCCGGTGGCGACGCC 10242

Qy       1537 ATCGGGCCGTTCCCCACCGACCGCGGATGGCCCACGGAACAGCGTCACGCCCAGGACCCC 1596

Db      10243 ATCGGTGAATTCCCCGCTGATCGTGGTTGGCACCTCGACGAGCTCTACGATCCCGACCCG 10302

Qy       1597 ACGCAGCCCGGCACGTTCTATCCGCAGGGAGGCGGGTTCCTTCACGACGCGGCGCACTTC 1656

Db      10303 GATCAGCCCGGAACCTGCTACACCCGGCACGGCGGCTTCCTCCACGACGCCGGCGAGTTC 10362

Qy       1657 GACGCCGGCTTCTTCGGAATCAGTCCACGTGAGGCACTGGCGATGGATCCGCAGCAGCGG 1716

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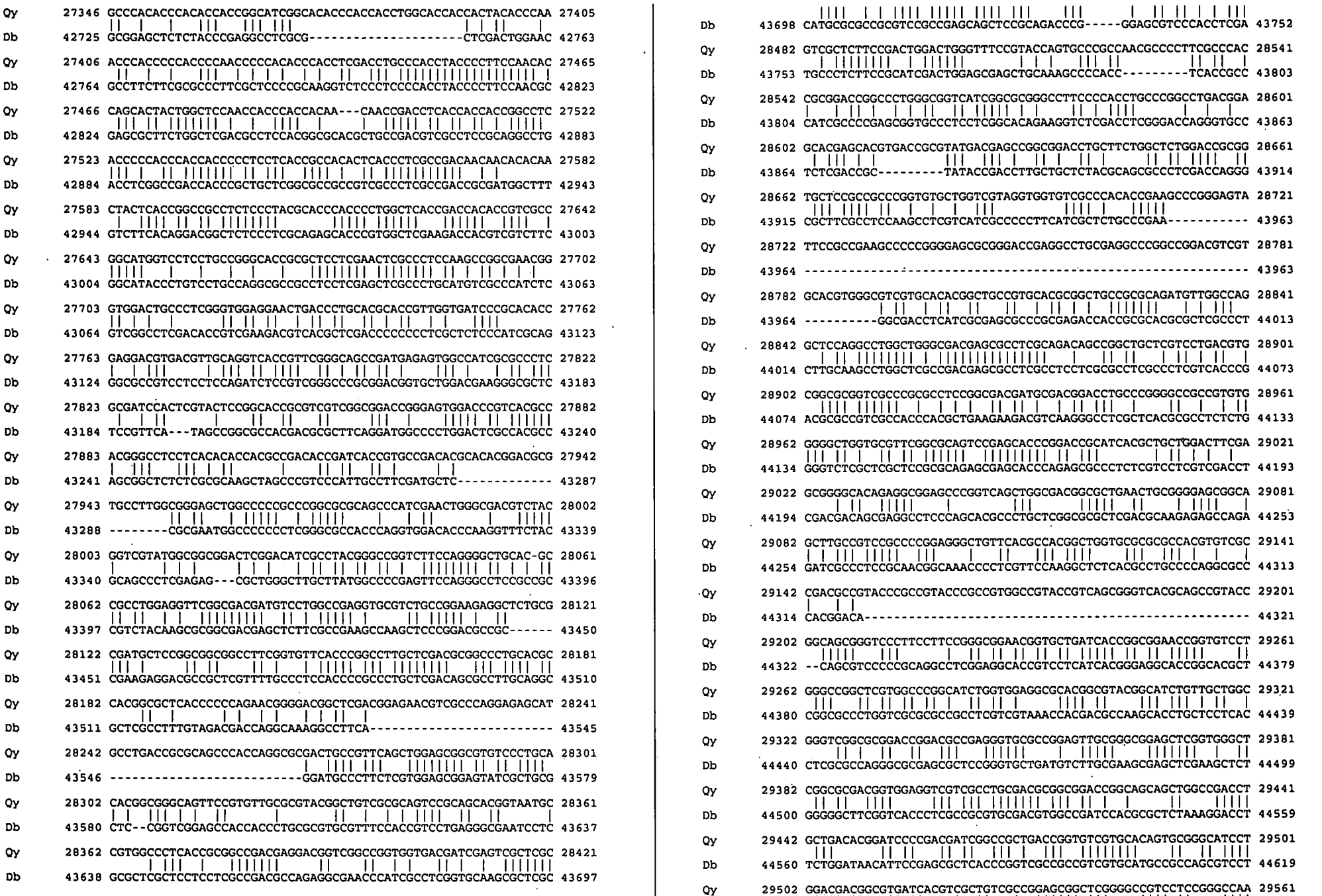
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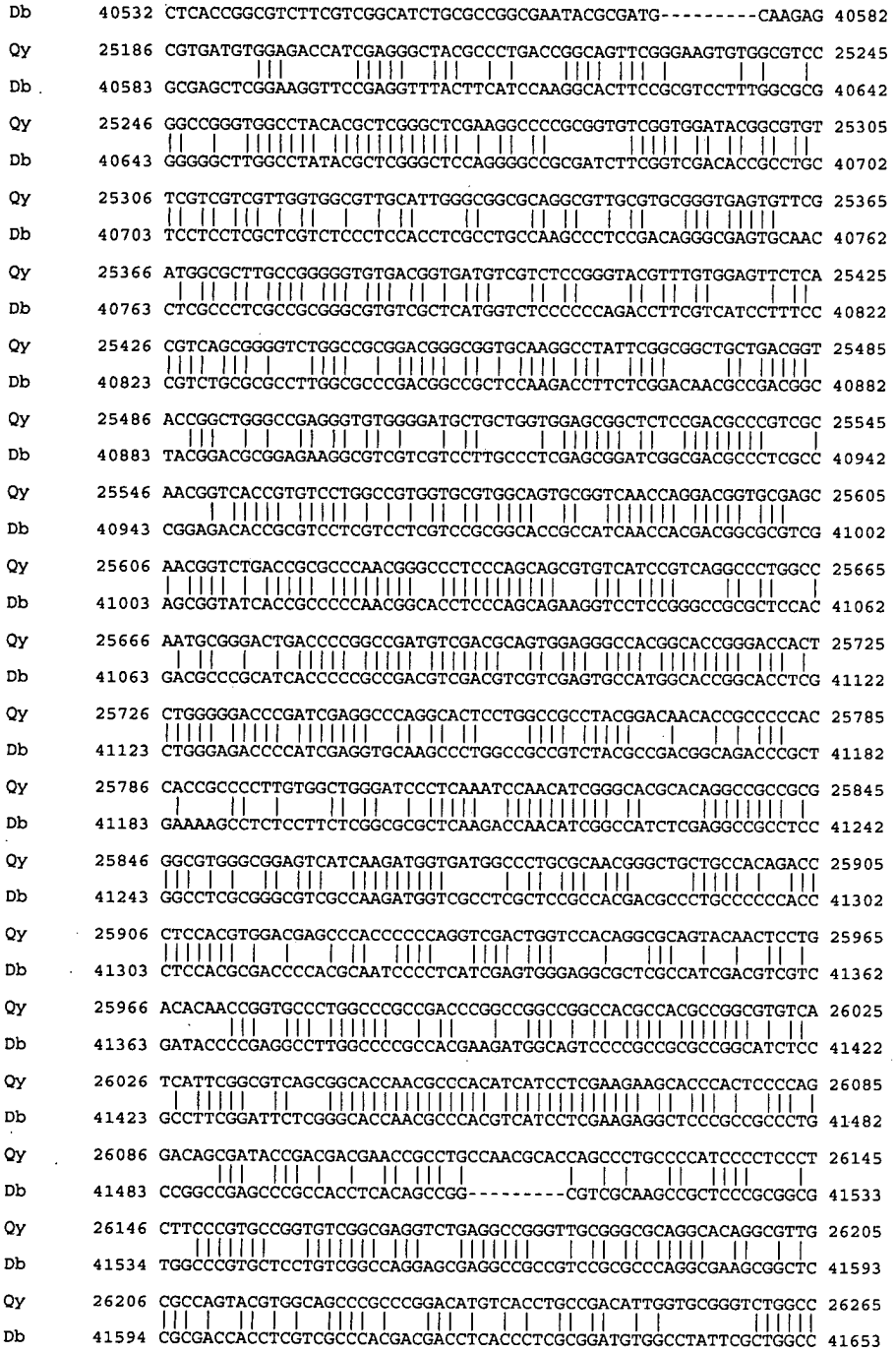
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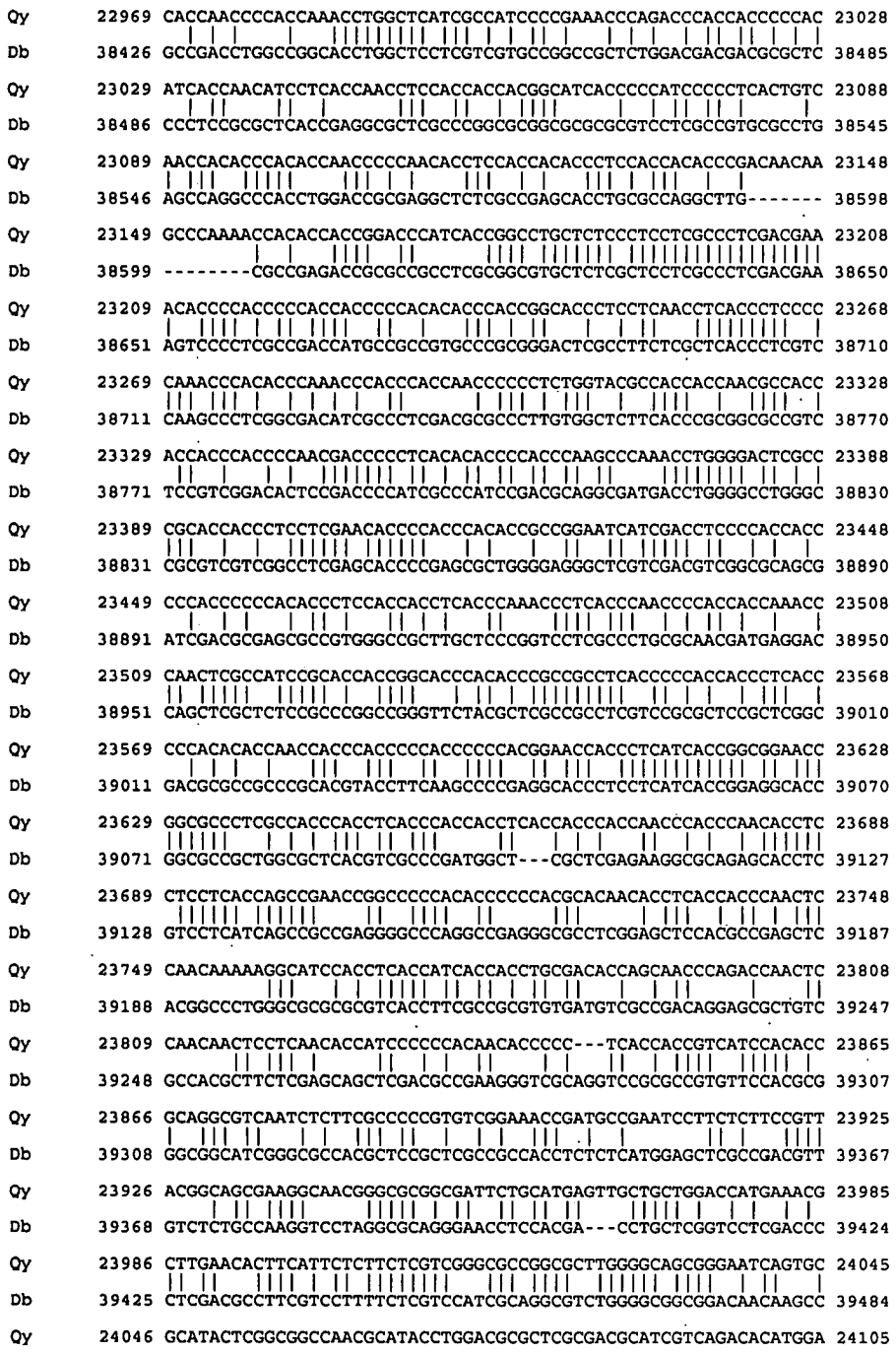
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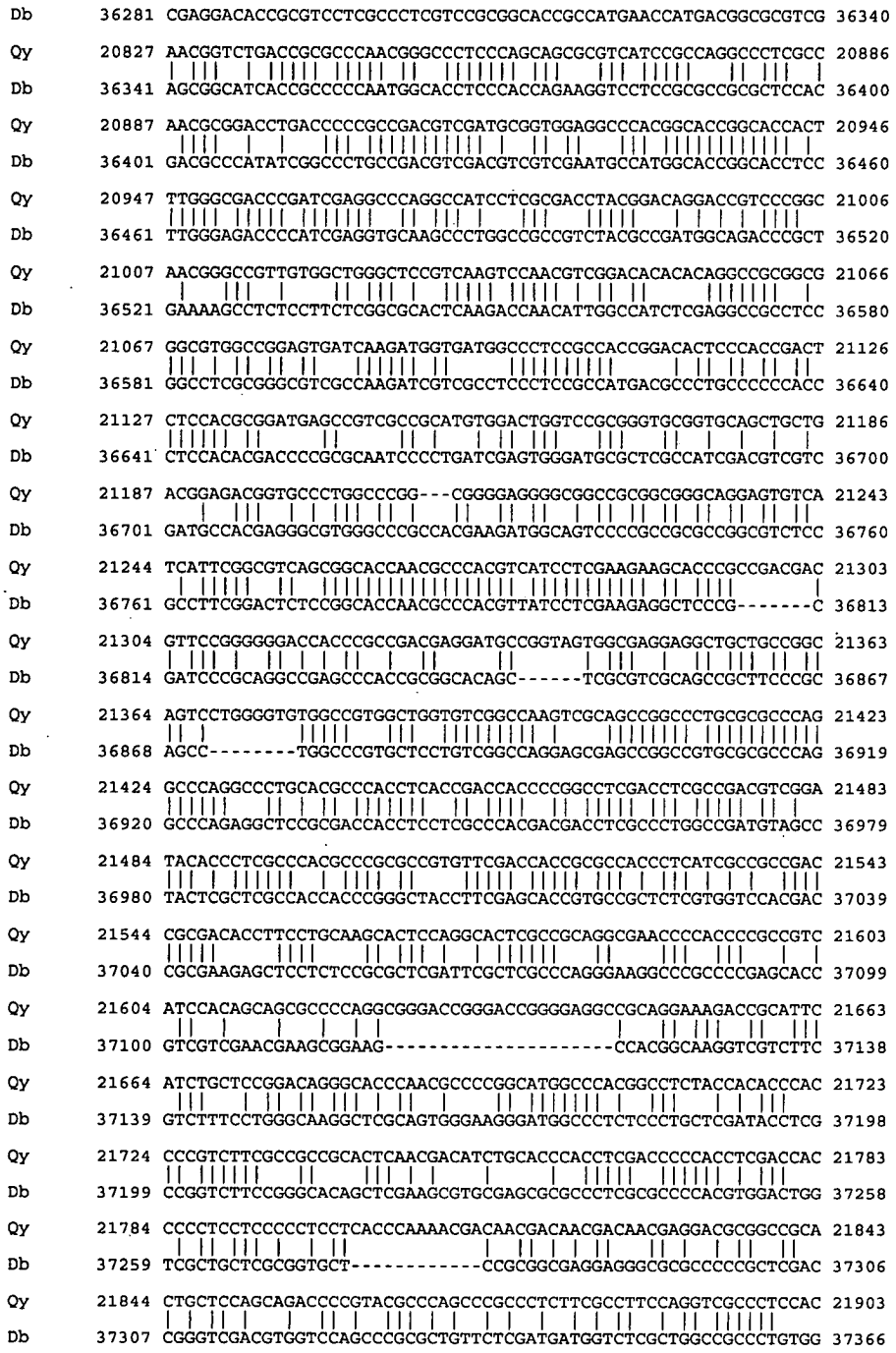
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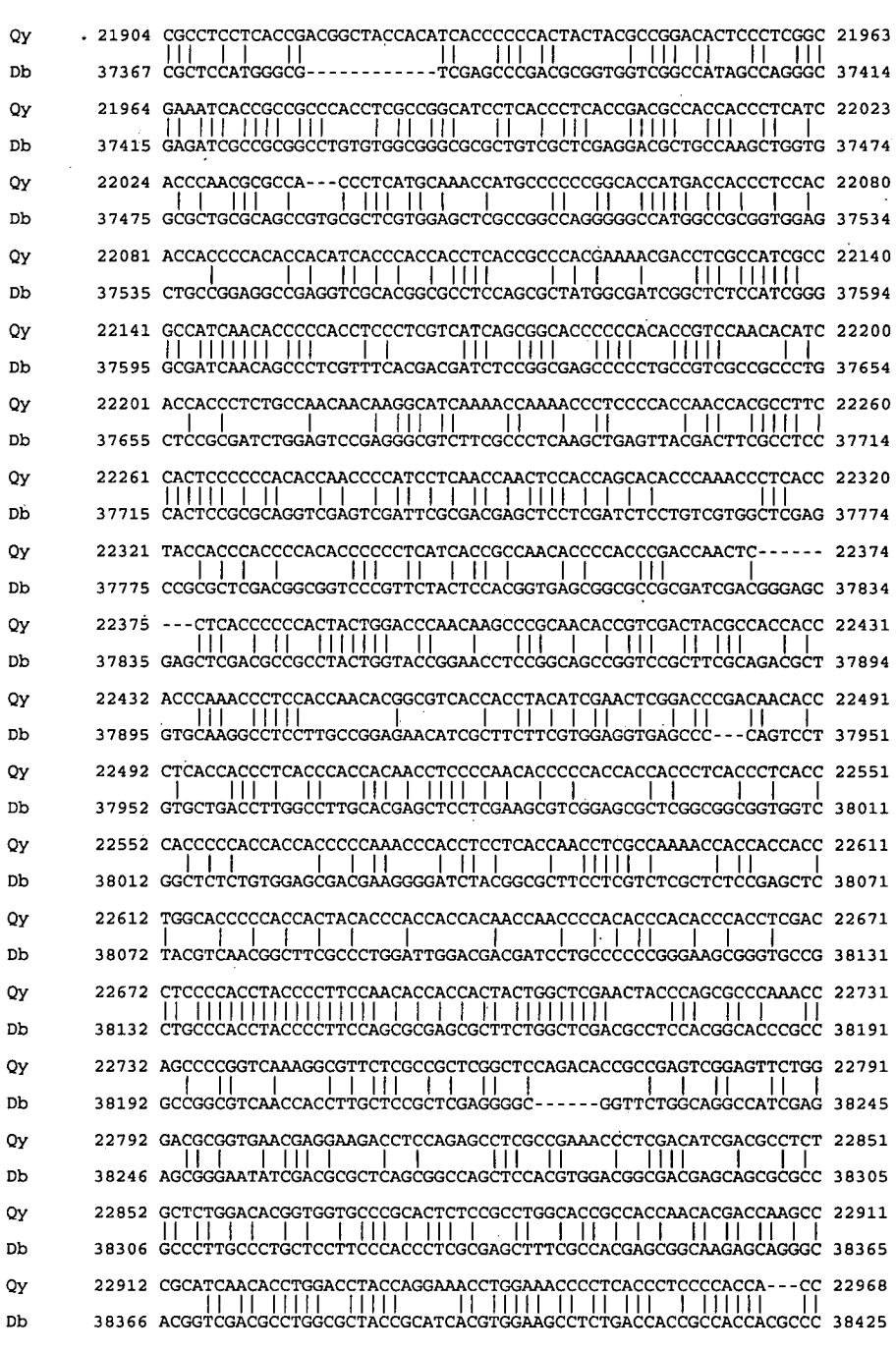
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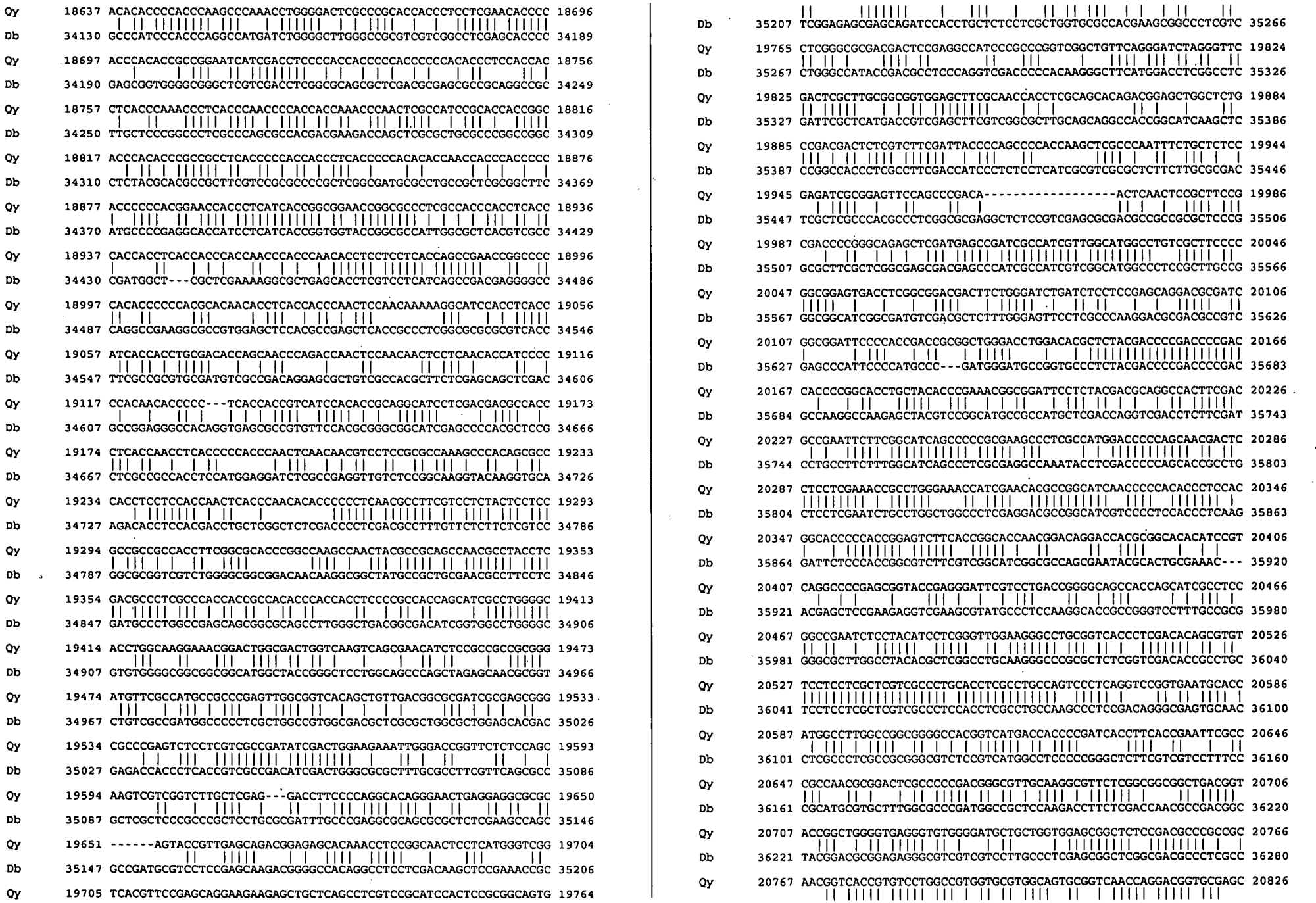


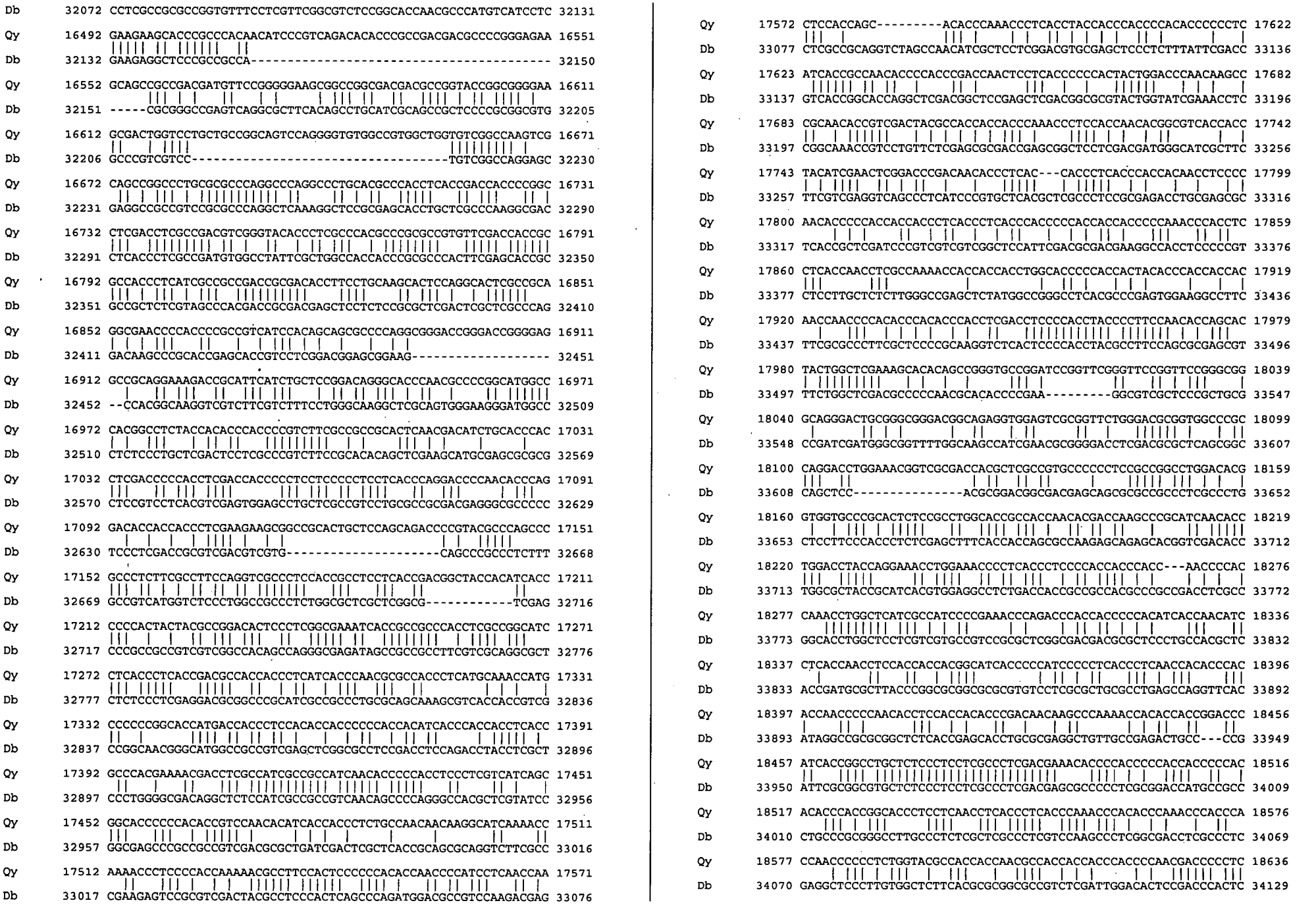

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Qy 25186 CGTGATGTGGAGACCATCGAGGGCTACGCCCTGACCGGCAGTTCGGGAAGTGTGGCGTCC 25245
Db 40583 GCGAGCTCGGAAGGTTCCGAGGTTTACTTCATCCAAGGCACTTCCGCGTCCTTTGGCGCG 40642
Qy 25246 GGCCGGGTGGCCTACACGCTCGGGCTCGAAGGCCCCGCGGTGTCGGTGGATACGGCGTGT 25305
Db 40643 GGGGGCTTGGCCTATACGCTCGGGCTCCAGGGGCCGCGATCTTCGGTCGACACCGCCTGC 40702
Qy 25306 TCGTCGTCGTTGGTGGCGTTGCATTGGGCGGCGCAGGCGTTGCGTGCGGGTGAGTGTTCG 25365
Db 40703 TCCTCCTCGCTCGTCTCCCTCCACCTCGCCTGCCAAGCCCTCCGACAGGGCGAGTGCAAC 40762
Qy 25366 ATGGCGCTTGCCGGGGGTGTGACGGTGATGTCGTCTCCGGGTACGTTTGTGGAGTTCTCA 25425
Db 40763 CTCGCCCTCGCCGCGGGCGTGTCGCTCATGGTCTCCCCCCAGACCTTCGTCATCCTTTCC 40822
Qy 25426 CGTCAGCGGGGTCTGGCCGCGGACGGGCGGTGCAAGGCCTATTCGGCGGCTGCTGACGGT 25485
Db 40823 CGTCTGCGCGCCTTGGCGCCCGACGGCCGCTCCAAGACCTTCTCGGACAACGCCGACGGC 40882
Qy 25486 ACCGGCTGGGCCGAGGGTGTGGGGATGCTGCTGGTGGAGCGGCTCTCCGACGCCCGTCGC 25545
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Qy 25546 AACGGTCACCGTGTCCTGGCCGTGGTGCGTGGCAGTGCGGTCAACCAGGACGGTGCGAGC 25605
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Qy 25846 GGCGTGGGCGGAGTCATCAAGATGGTGATGGCCCTGCGCAACGGGCTGCTGCCACAGACC 25905
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Db 41363 GATACCCCGAGGCCTTGGCCCCGCCACGAAGATGGCAGTCCCCGCCGCGCCGGCATCTCC 41422
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Db 41423 GCCTTCGGATTCTCGGGCACCAACGCCCACGTCATCCTCGAAGAGGCTCCCGCCGCCCTG 41482
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Db 41483 CCGGCCGAGCCCGCCACCTCACAGCCGG---------CGTCGCAAGCCGCTCCCGCGGCG 41533
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PN US5716849-A.
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PD 10-FEB-1998.
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PF 14-DEC-1996; 96US-0764233.
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PR 24-AUG-1993; 93WO-US07954.
PR 08-JUN-1994; 94US-0258261.
PR 09-OCT-1996; 96US-0729214.
XX
PA (NOVS) NOVARTIS FINANCE CORP.
XX
PI Beck JJ, Hill DS, Ligon JM, Neff S, Ryals JA, Schupp T;
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DR WPI; 1998-158369/14.
XX
PT DNA encoding Sorangium cellulosum polypeptide(s) - used for, e.g.
PT biosynthesis of soraphen useful as antimicrobial agent against
PT phytopathogenic fungi
XX
PS Claim 2; Columns 47-90; 64pp; English.
XX
CC The present sequence contains a cluster of genes that encode polyketide
CC synthases (PKSs) that are involved in the synthesis of soraphens in
CC Sorangium cellulosum. The proteins encoded by the present sequence are
CC SorR, SorA, SorB and SorM. SorA and SorB contain biosynthetic modules
CC which contain a beta-ketoacylsynthase, an acyltransferase, a
CC ketoreductase and an acyl carrier protein domain, as well as beta-ketone
CC processing domains. S. cellulosum soraphens are useful as a cytostatic
CC and antimicrobial agent active against phytopathogenic fungi.
CC Soraphen-producing transgenic plants or biological control agents can
CC also be produced, which may reduce crop losses and nutritional
CC deprivation for local populations in many parts of the world.
XX
SQ Sequence 49377 BP; 7247 A; 19522 C; 14477 G; 8131 T; 0 other;

Query Match 10.4%; Score 3194.8; DB 19; Length 49377;
Best Local Similarity 54.1%; Pred. No. 0;
Matches 8389; Conservative 0; Mismatches 6392; Indels 719; Gaps 64;

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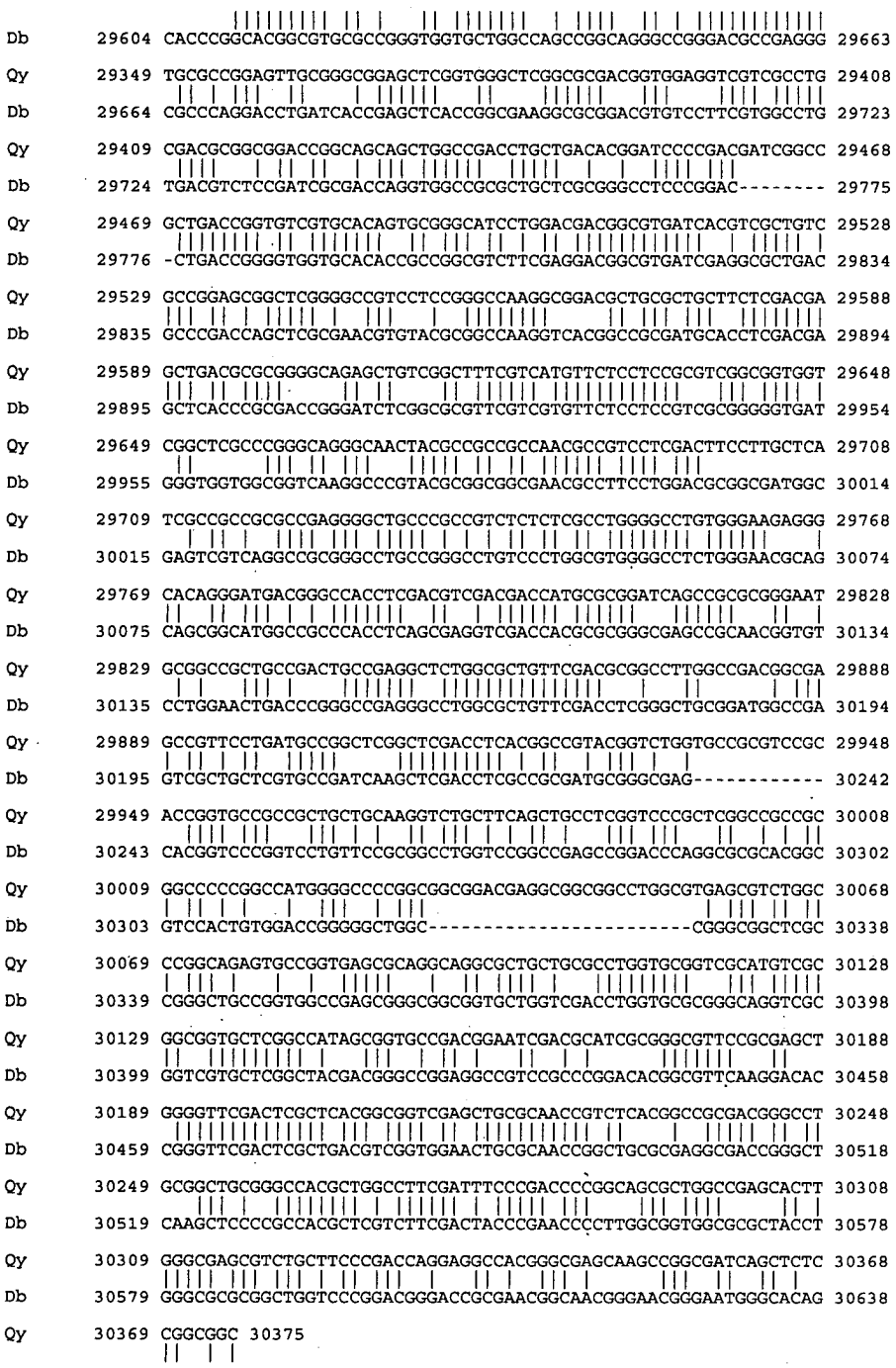
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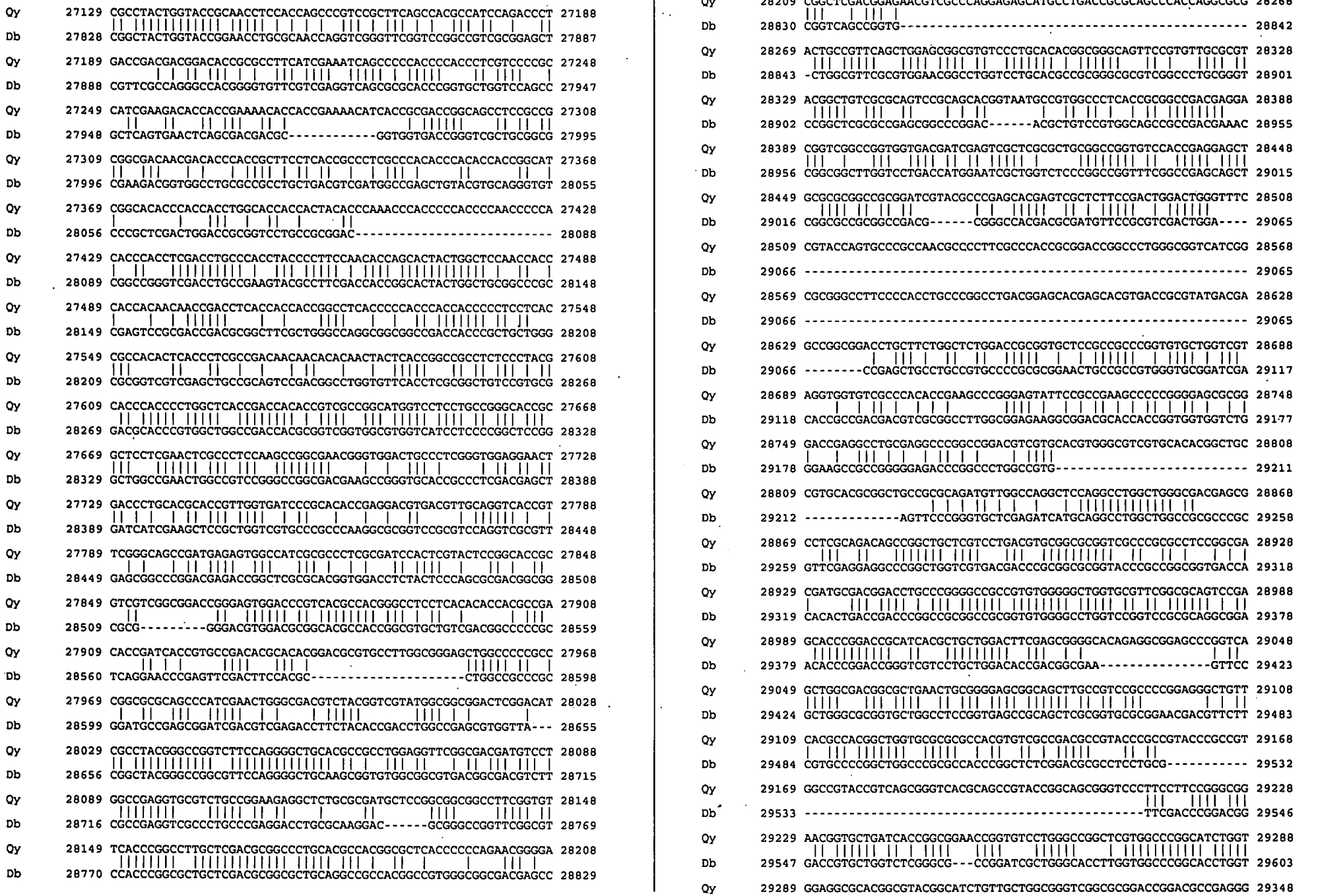
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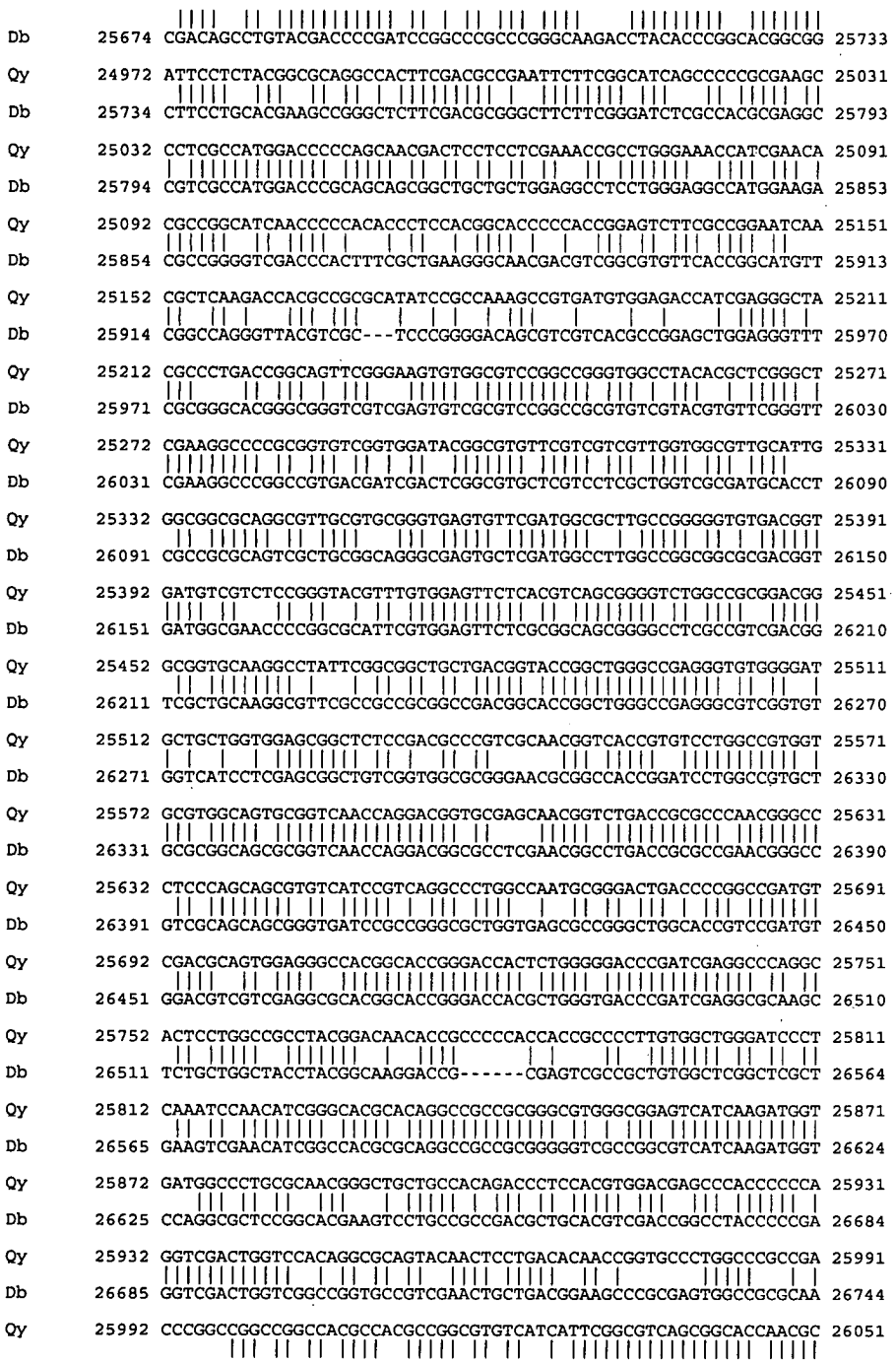
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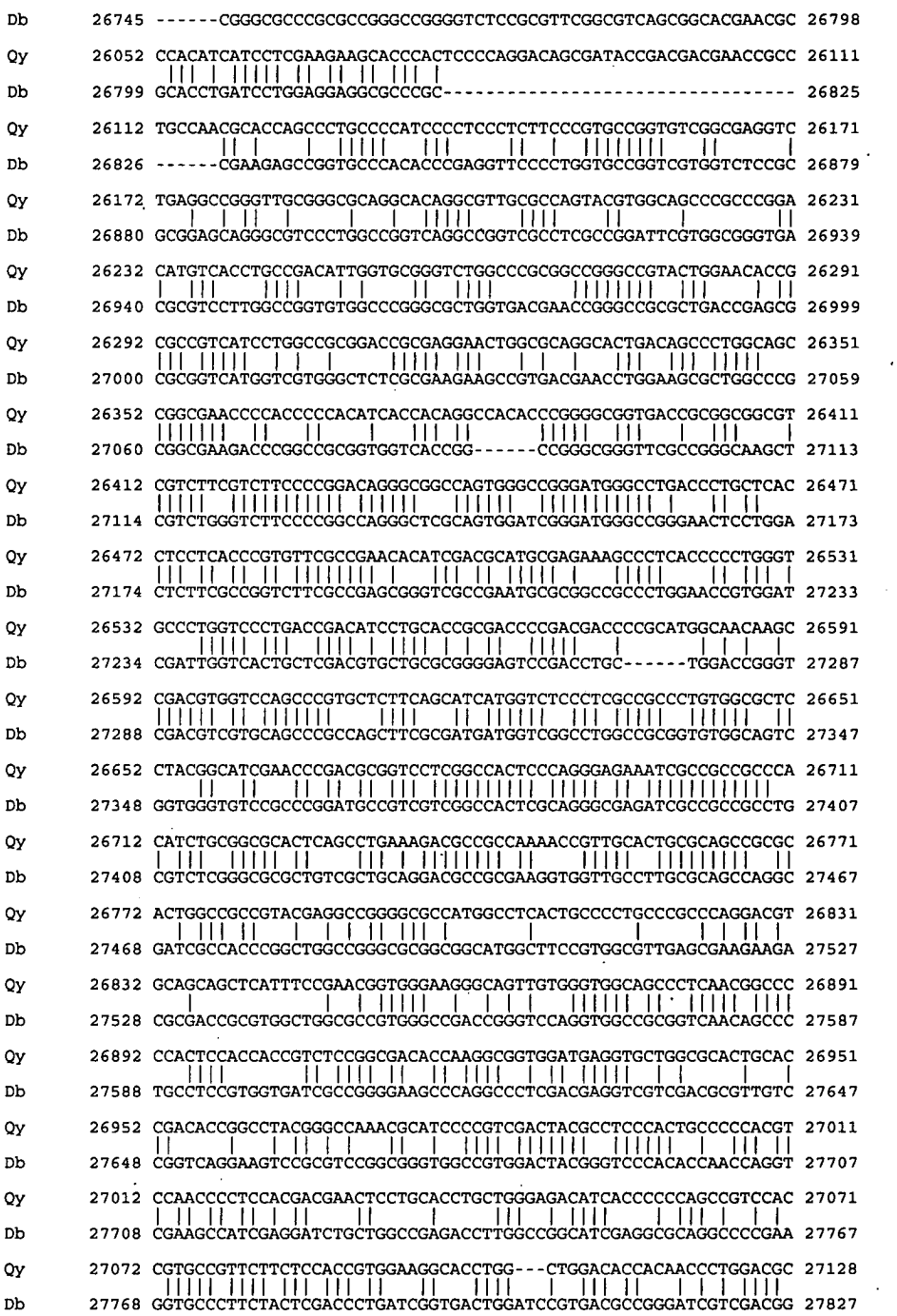
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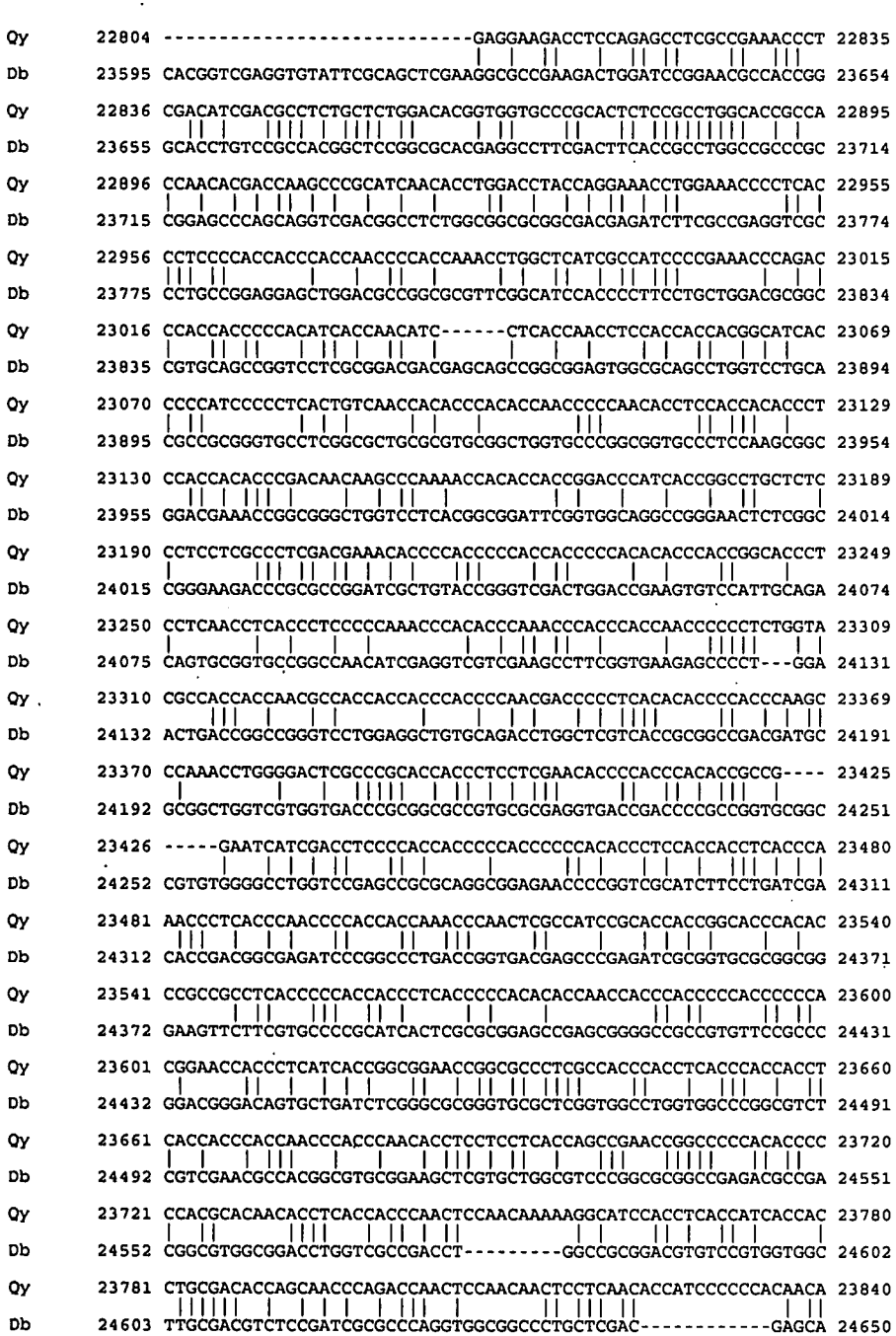
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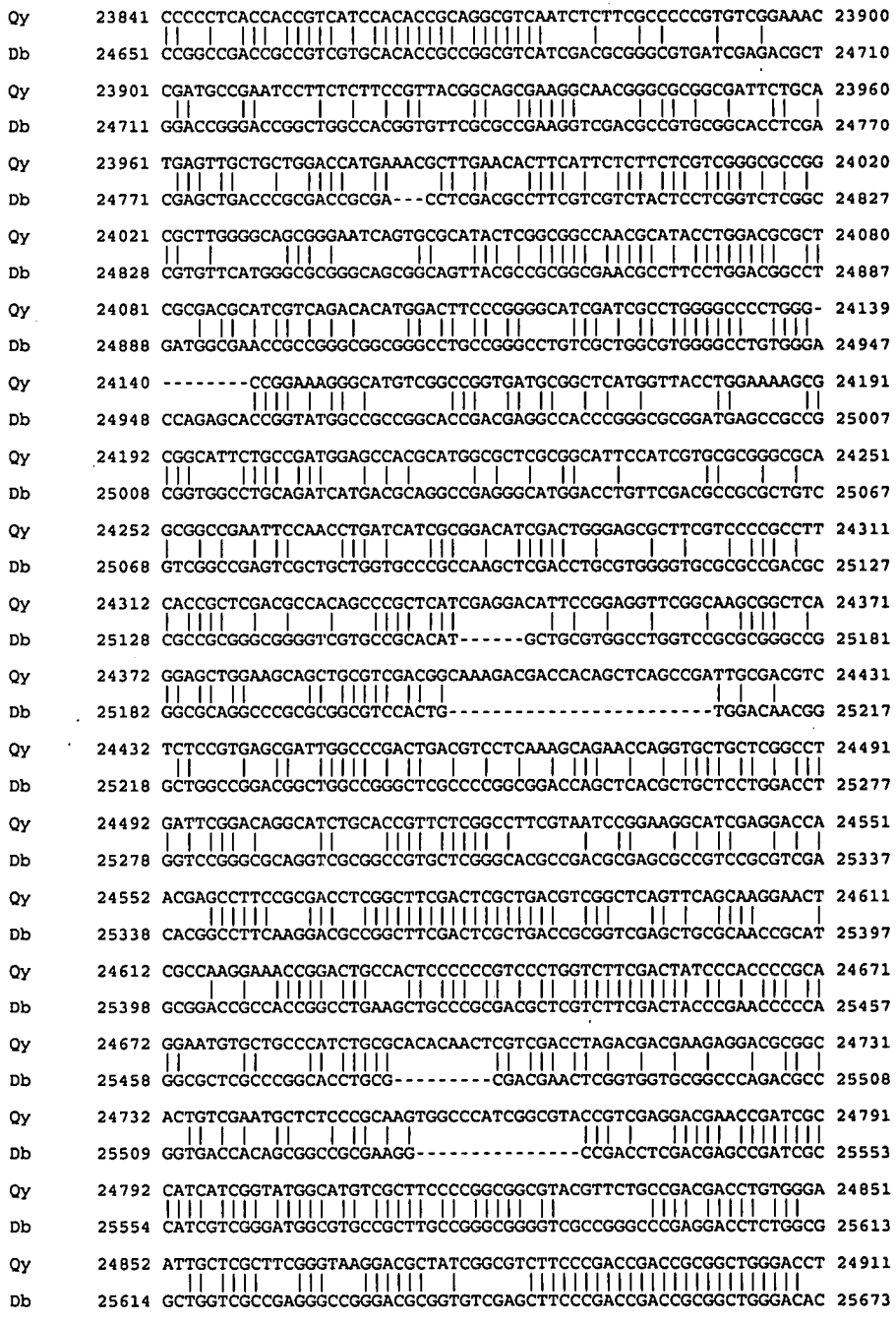

RESULT 11
AAV05287
ID   AAV05287 standard; DNA; 49377 BP.
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AC   AAV05287;
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DT   21-MAY-1998  (first entry)
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DE   The soraphen biosynthesis gene cluster from Sorangium cellulosum.
XX
KW   Polyketide synthase; PKS; biosynthesis; soraphen; SorR; SorA; SorB;
KW   SorM; biosynthetic module; beta-ketoacylsynthase; acyltransferase;
KW   ketoreductase; beta-ketone processing domain; cytostatic agent;
KW   antimicrobial agent; phytopathogenic fungi; transgenic plant;
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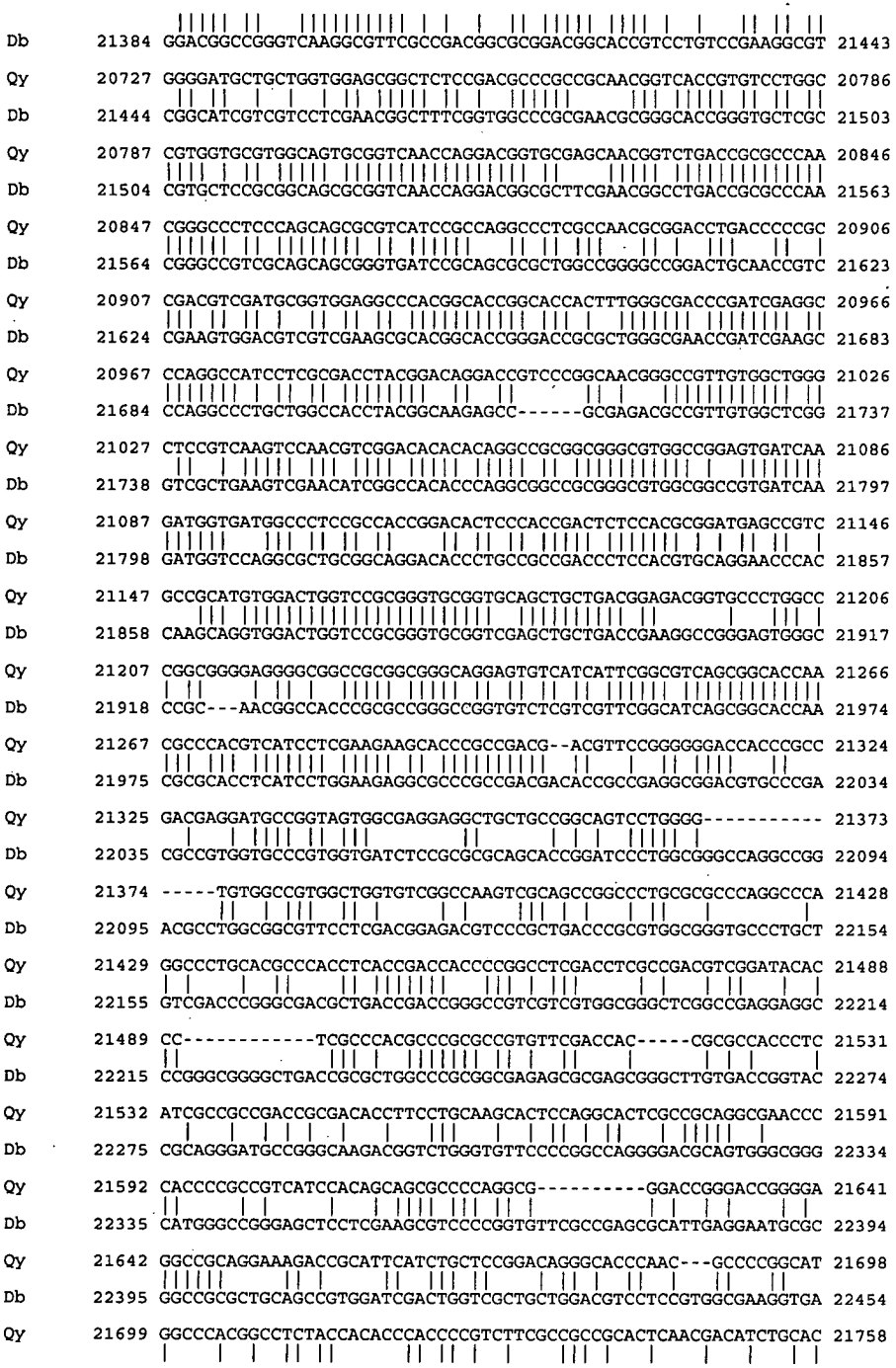


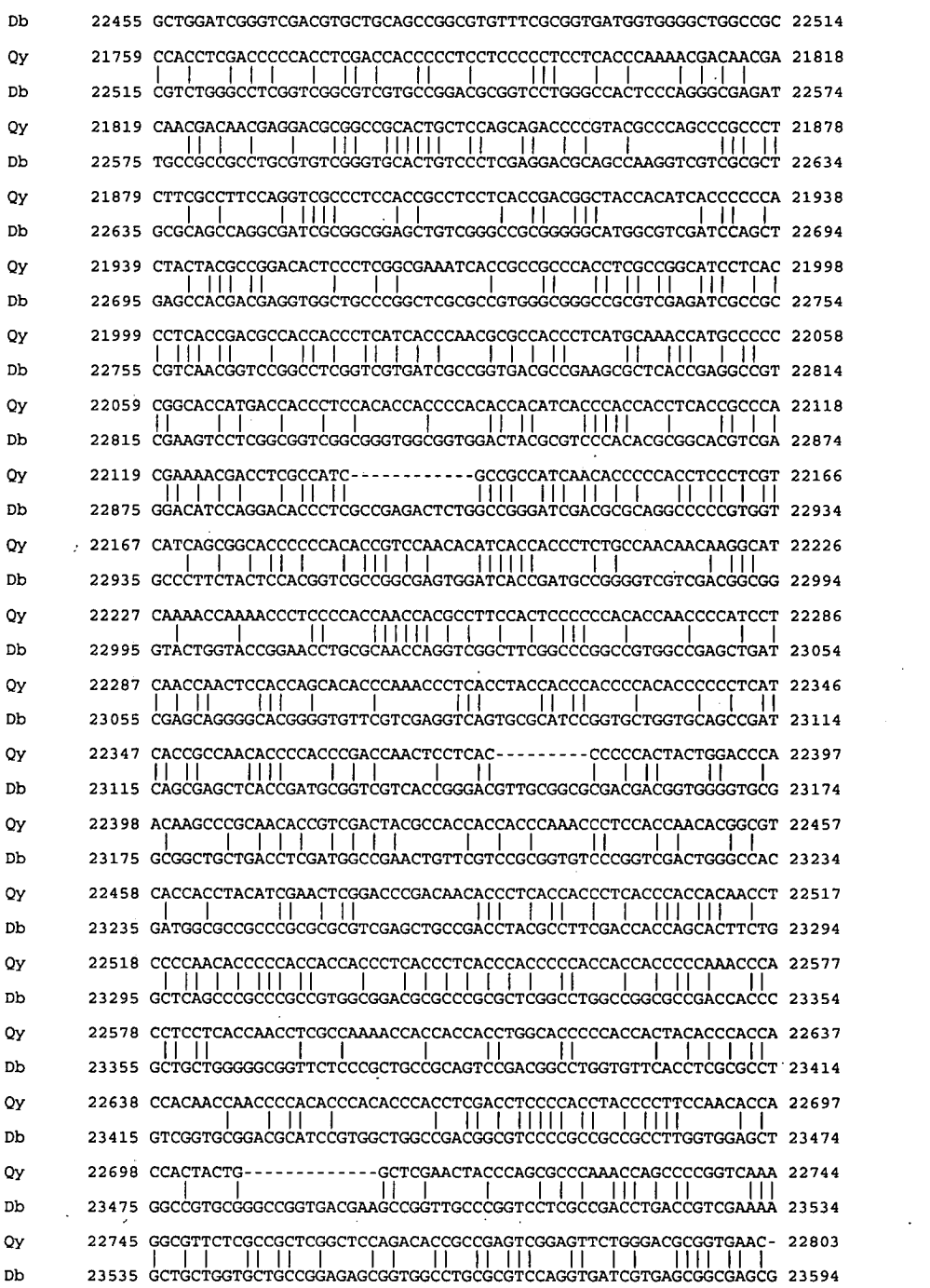

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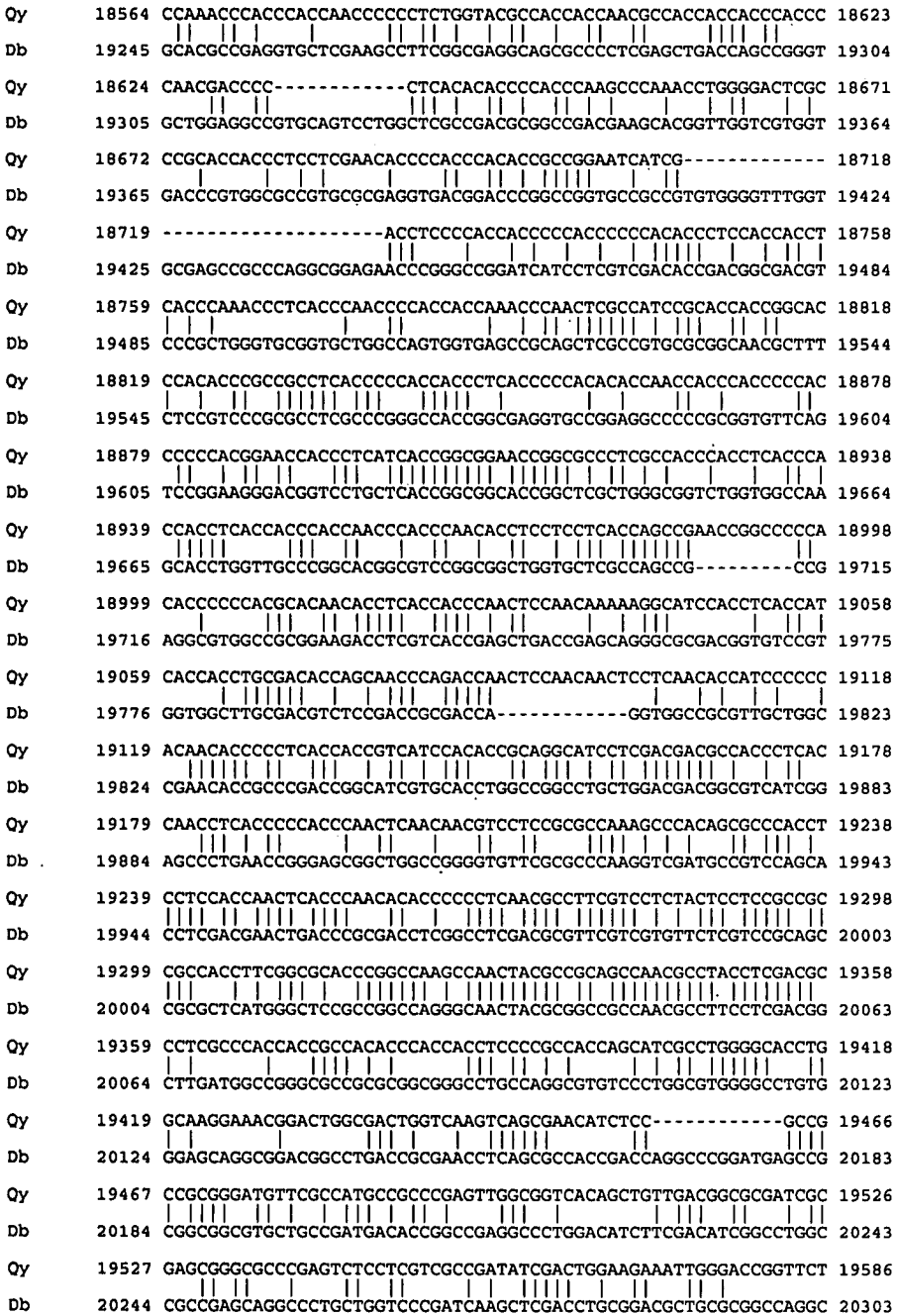

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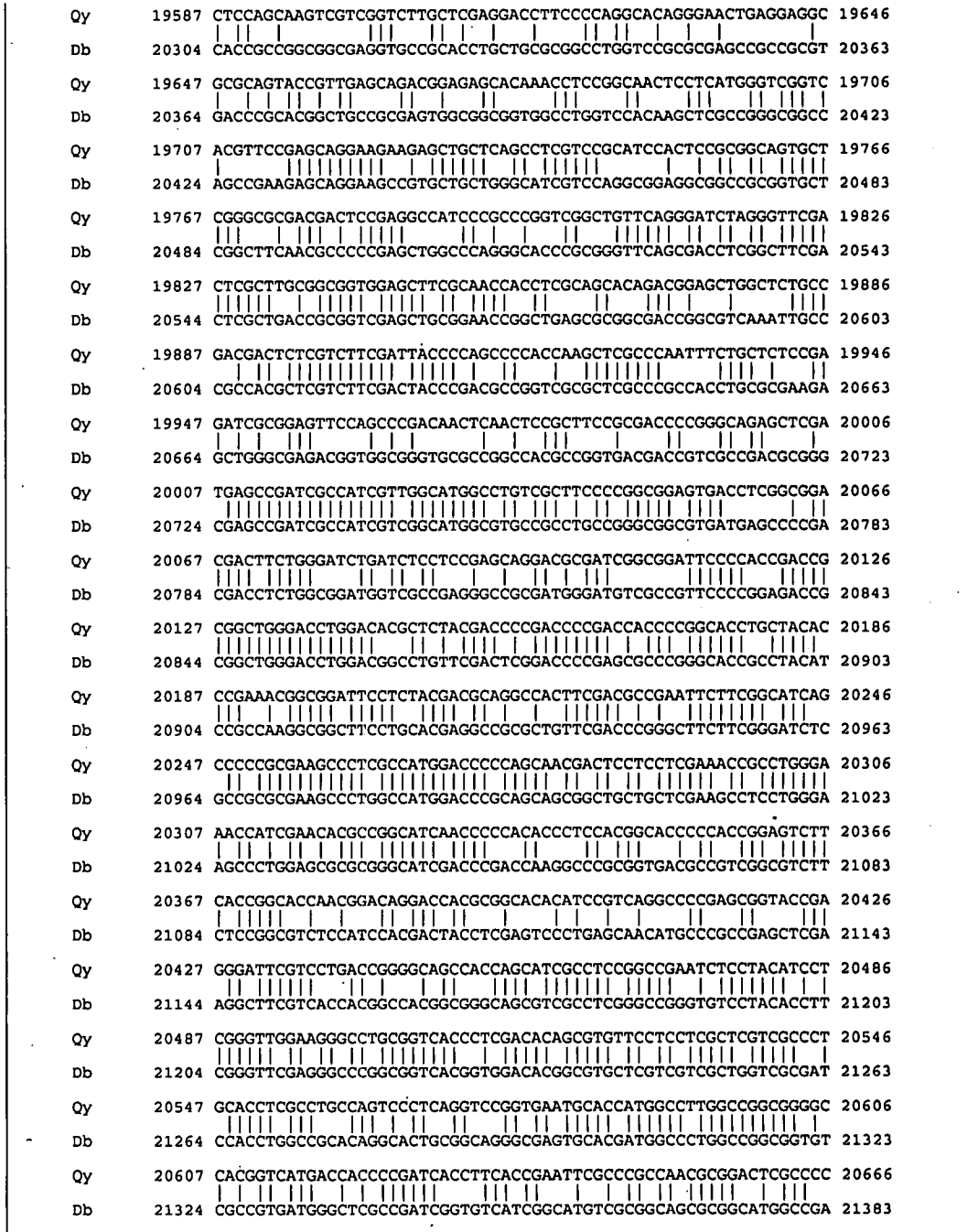


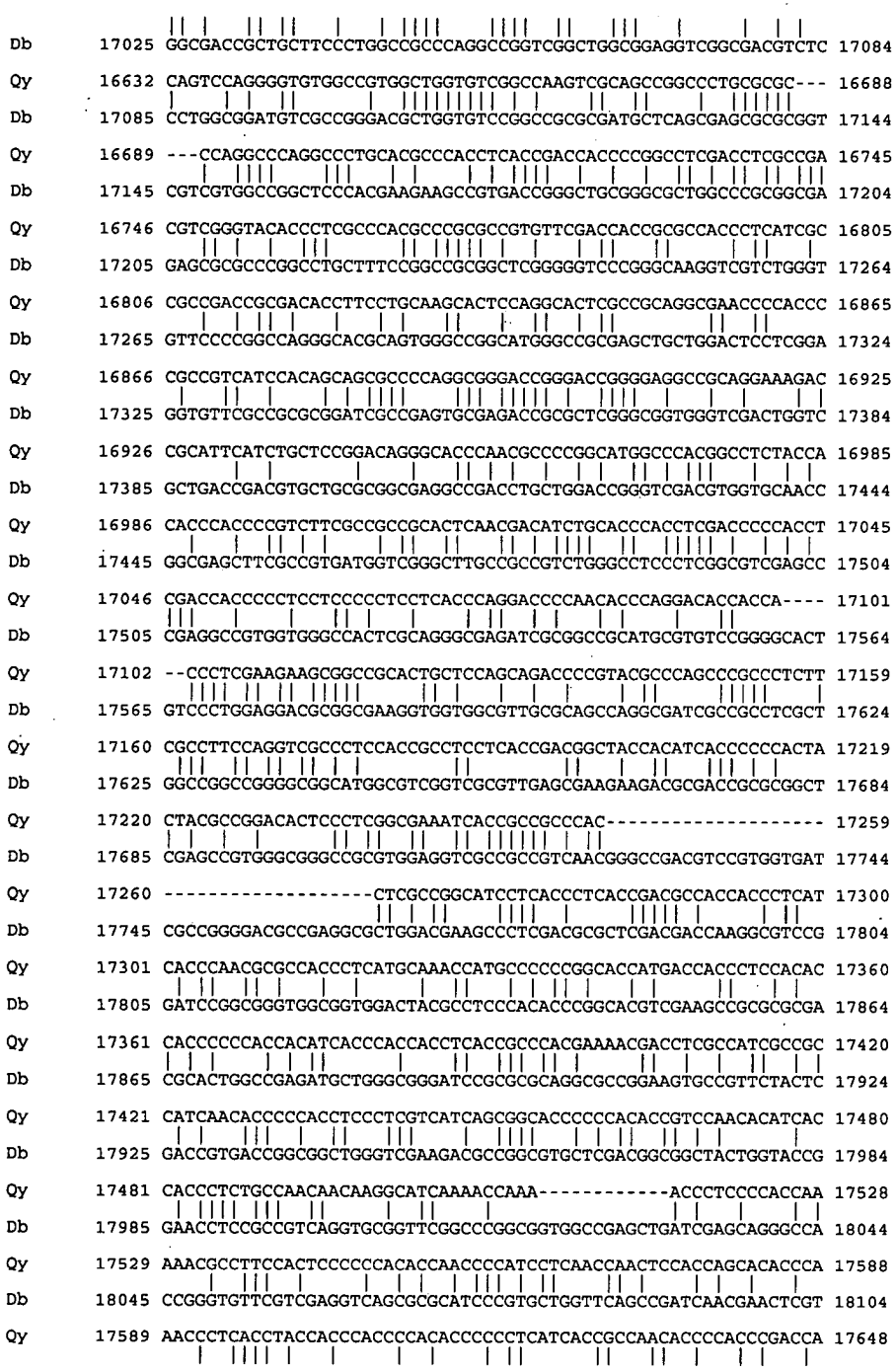


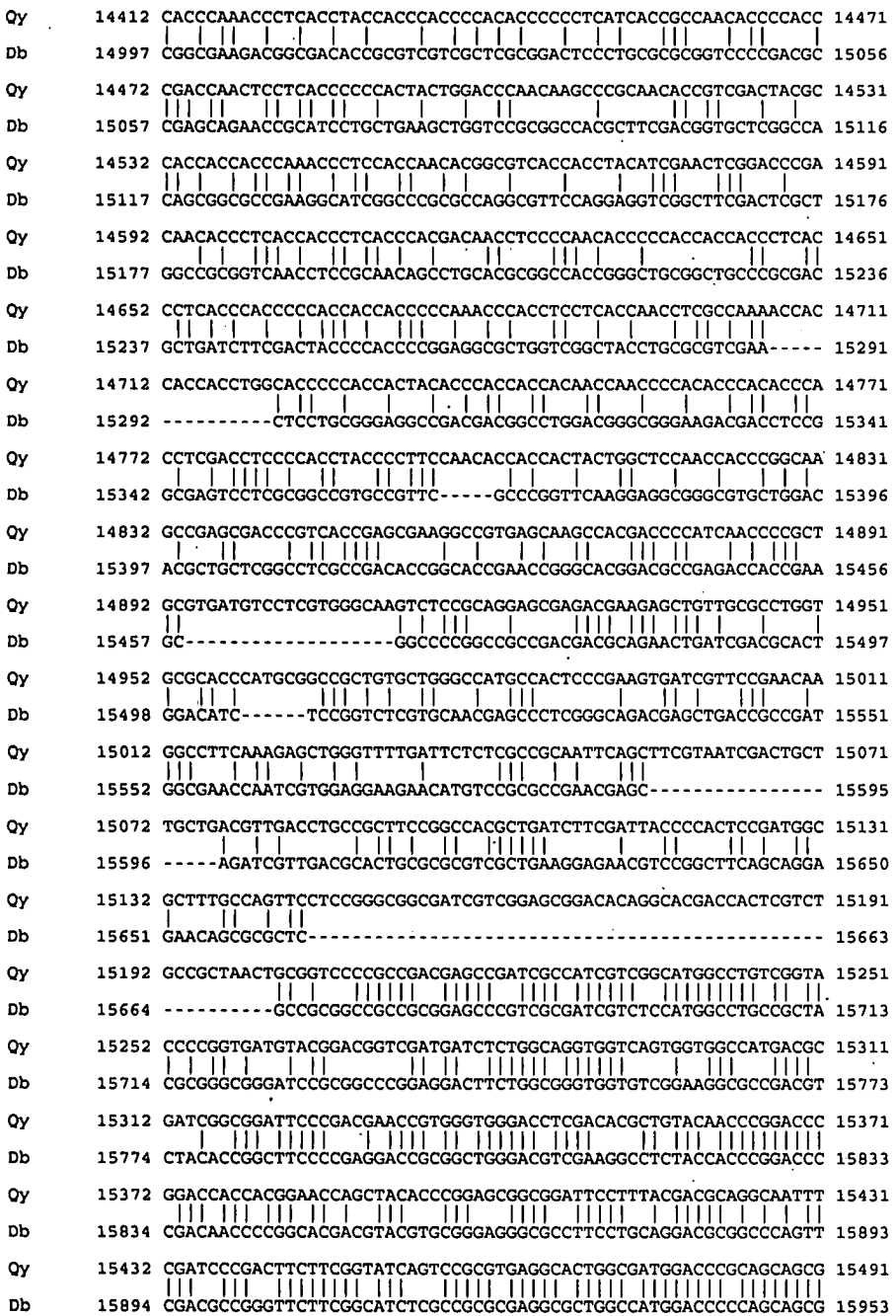


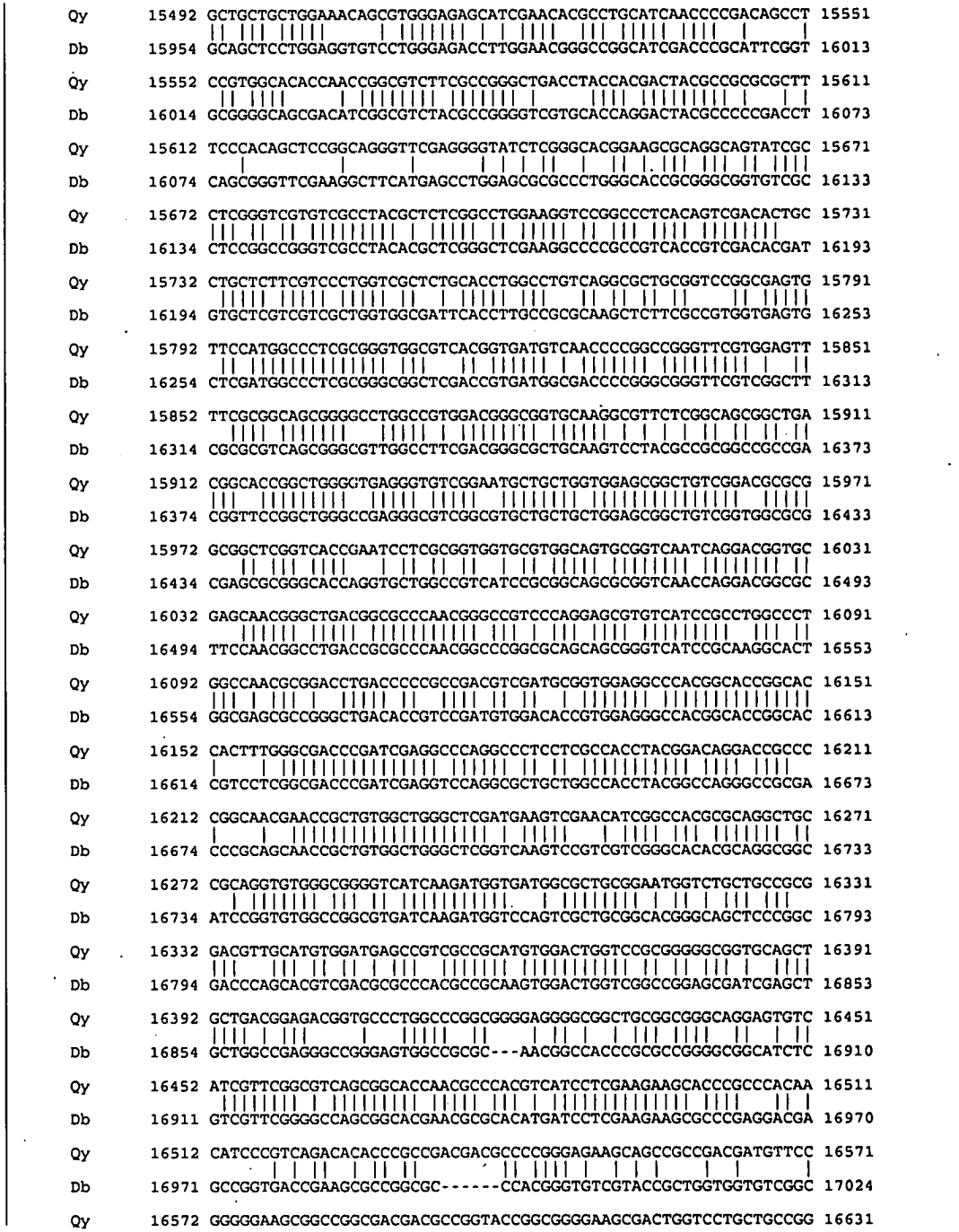


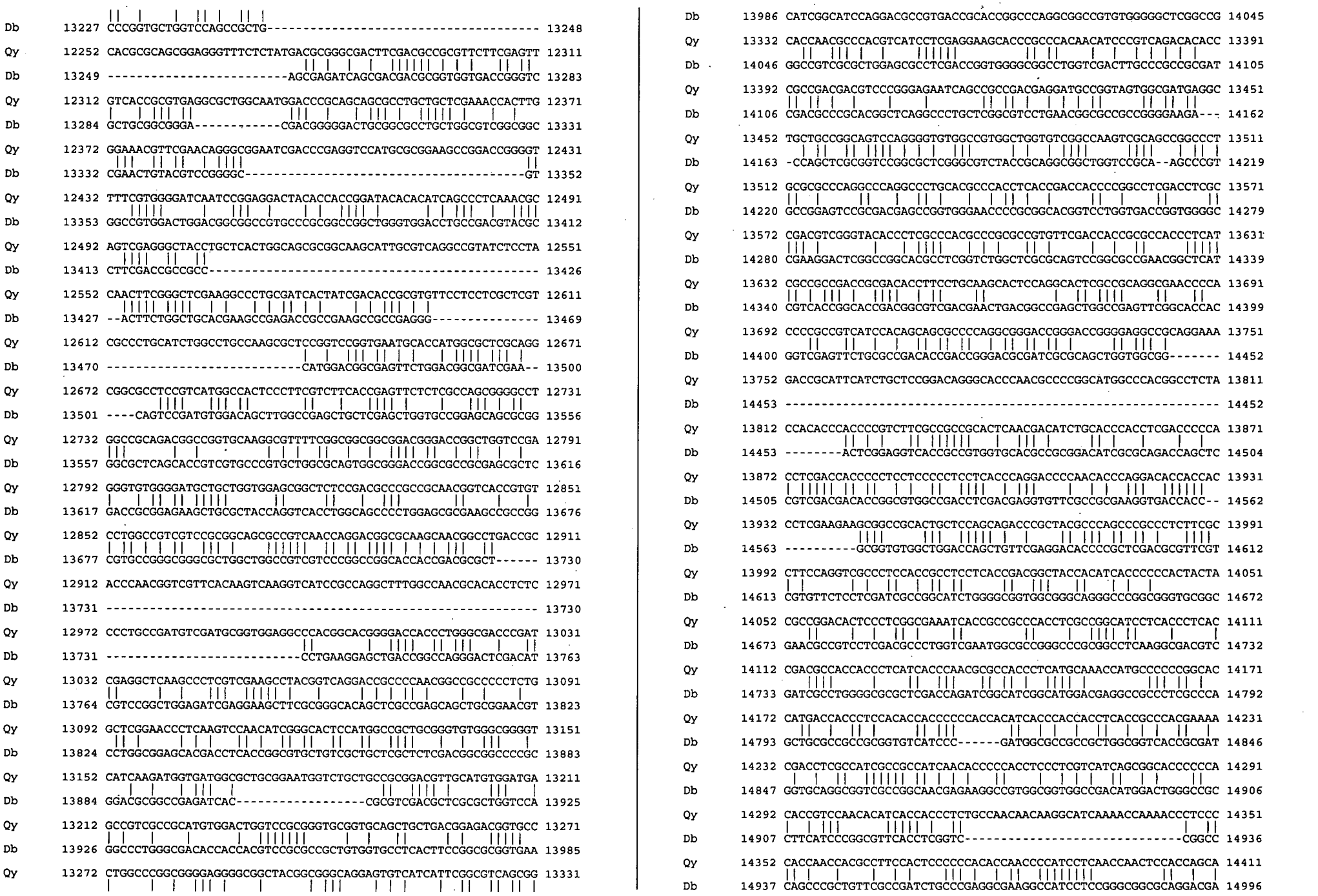


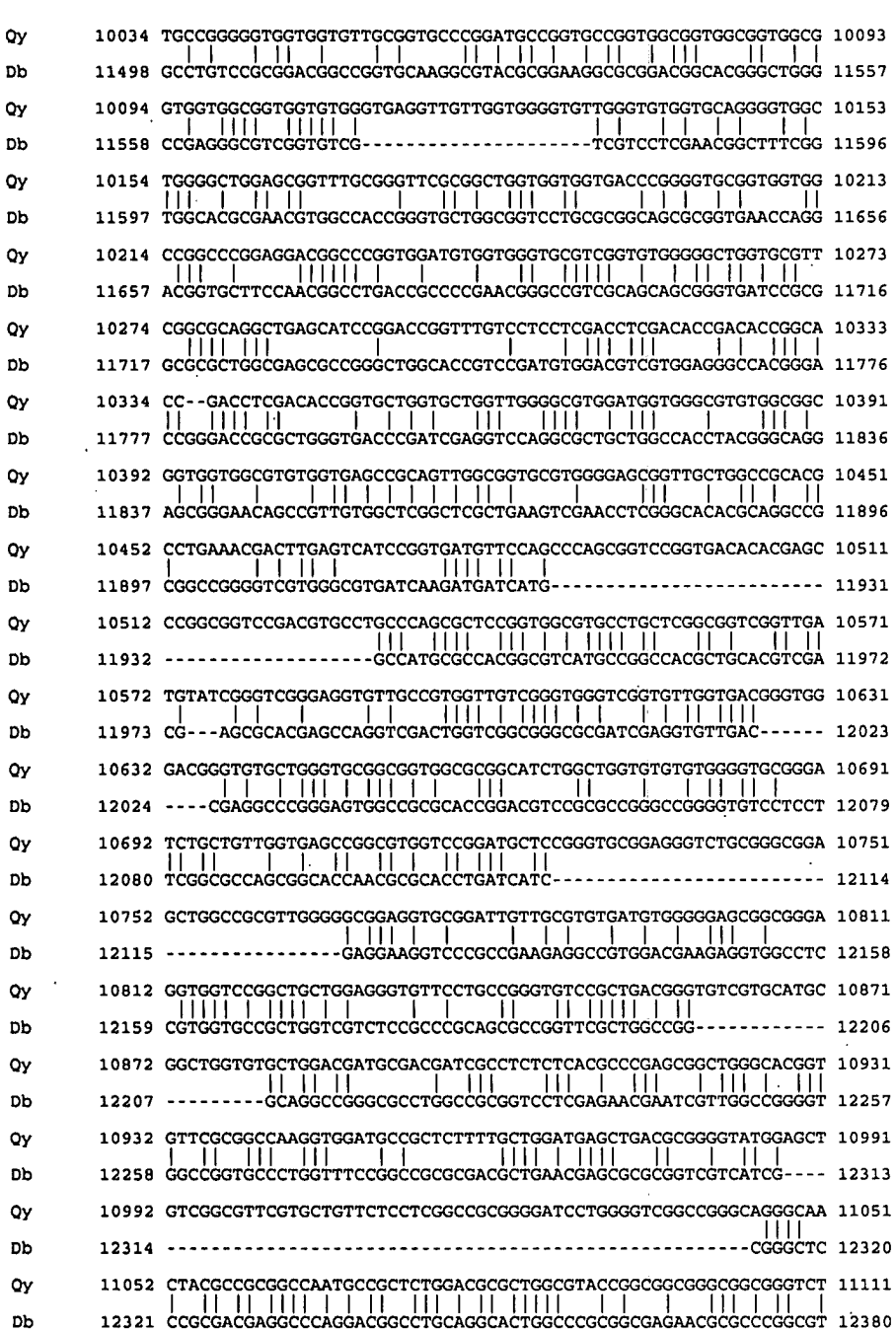


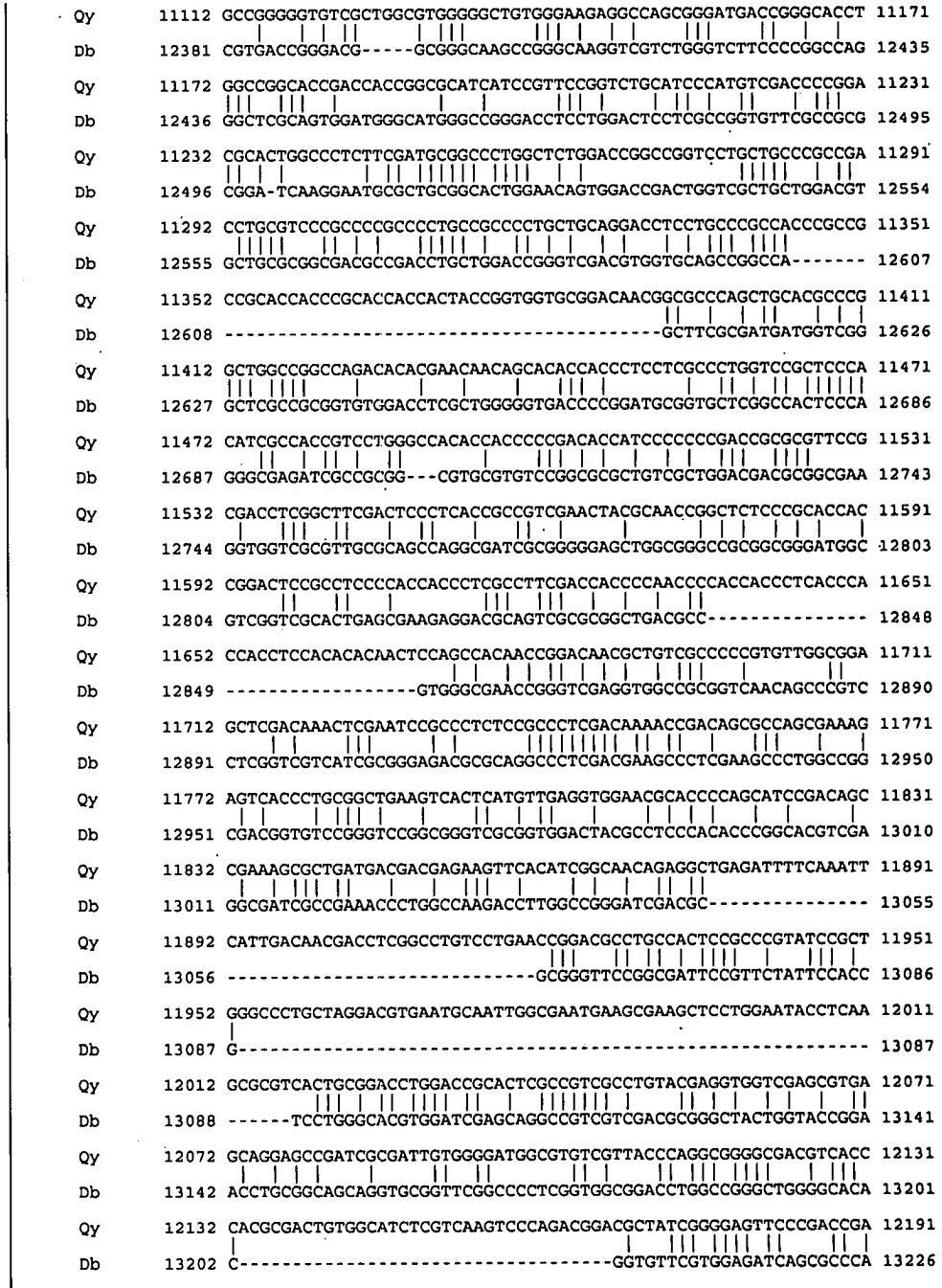

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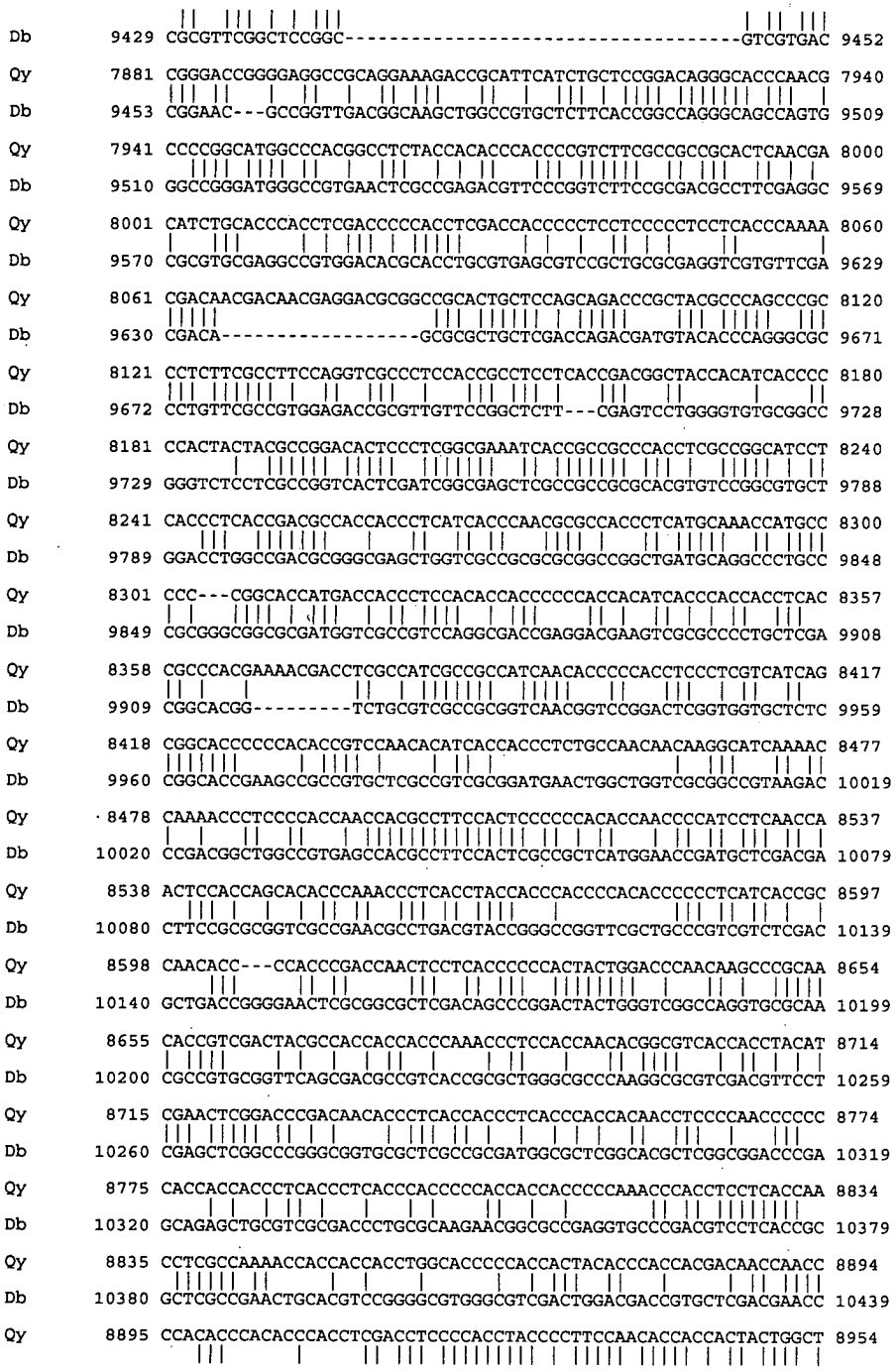


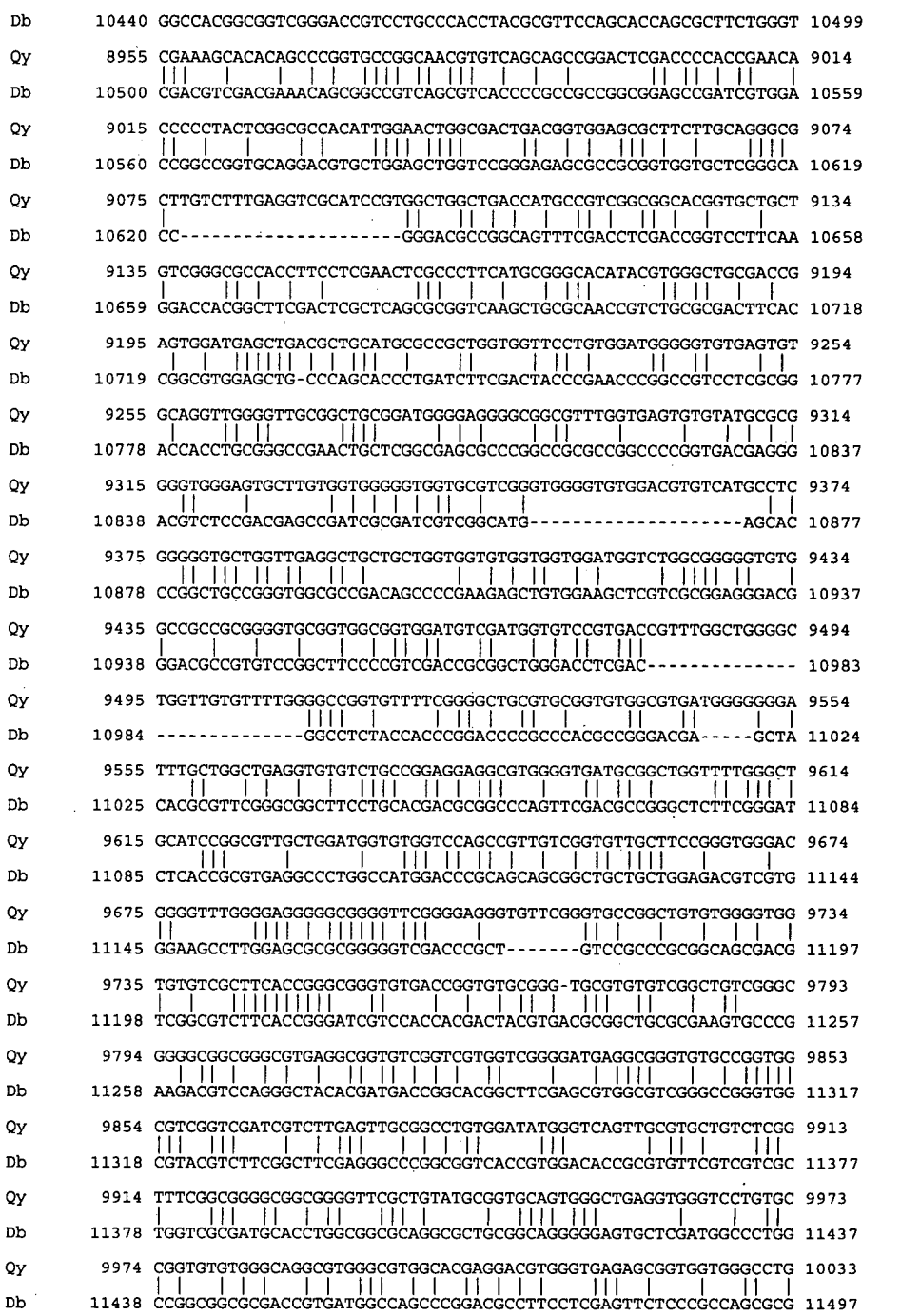


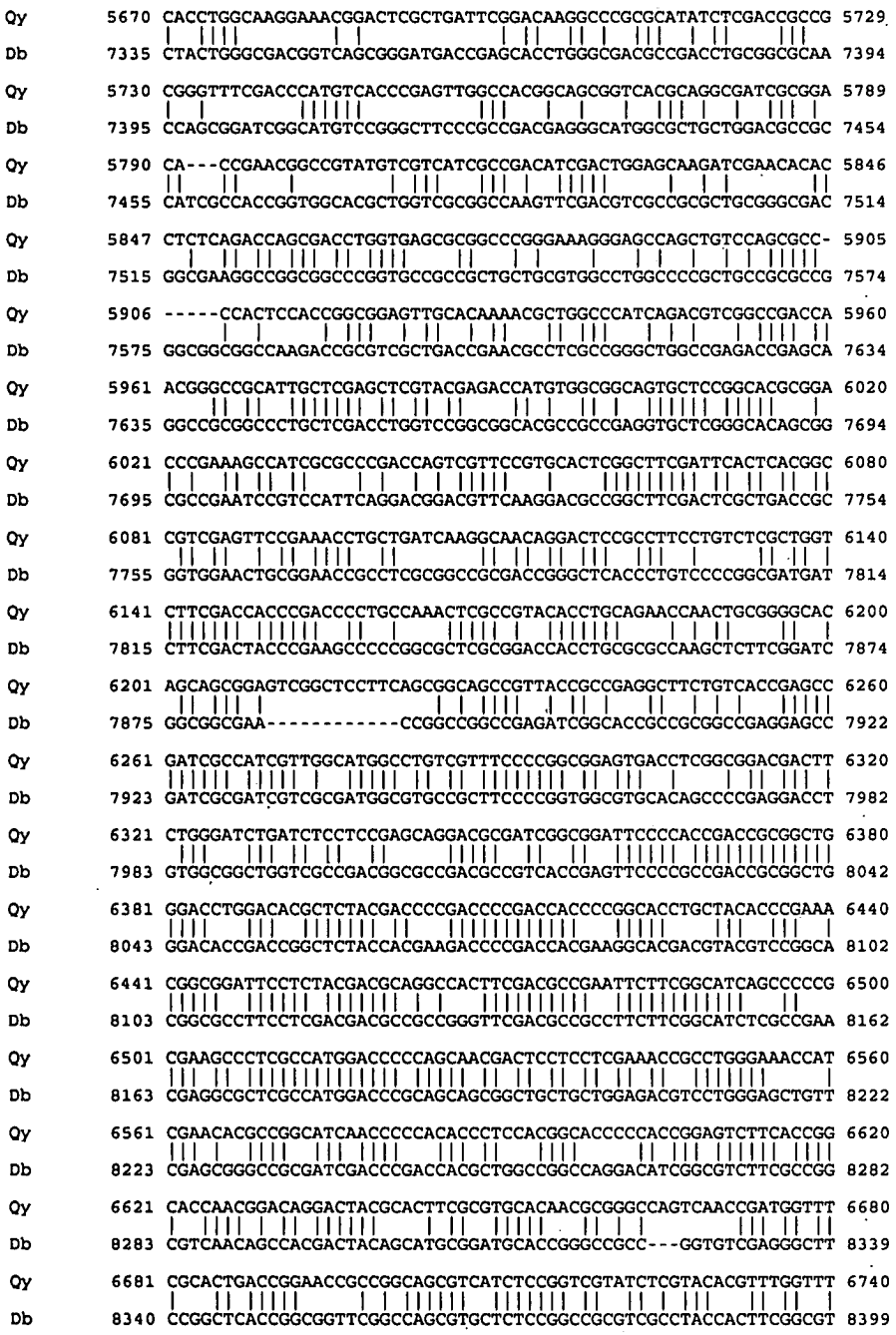


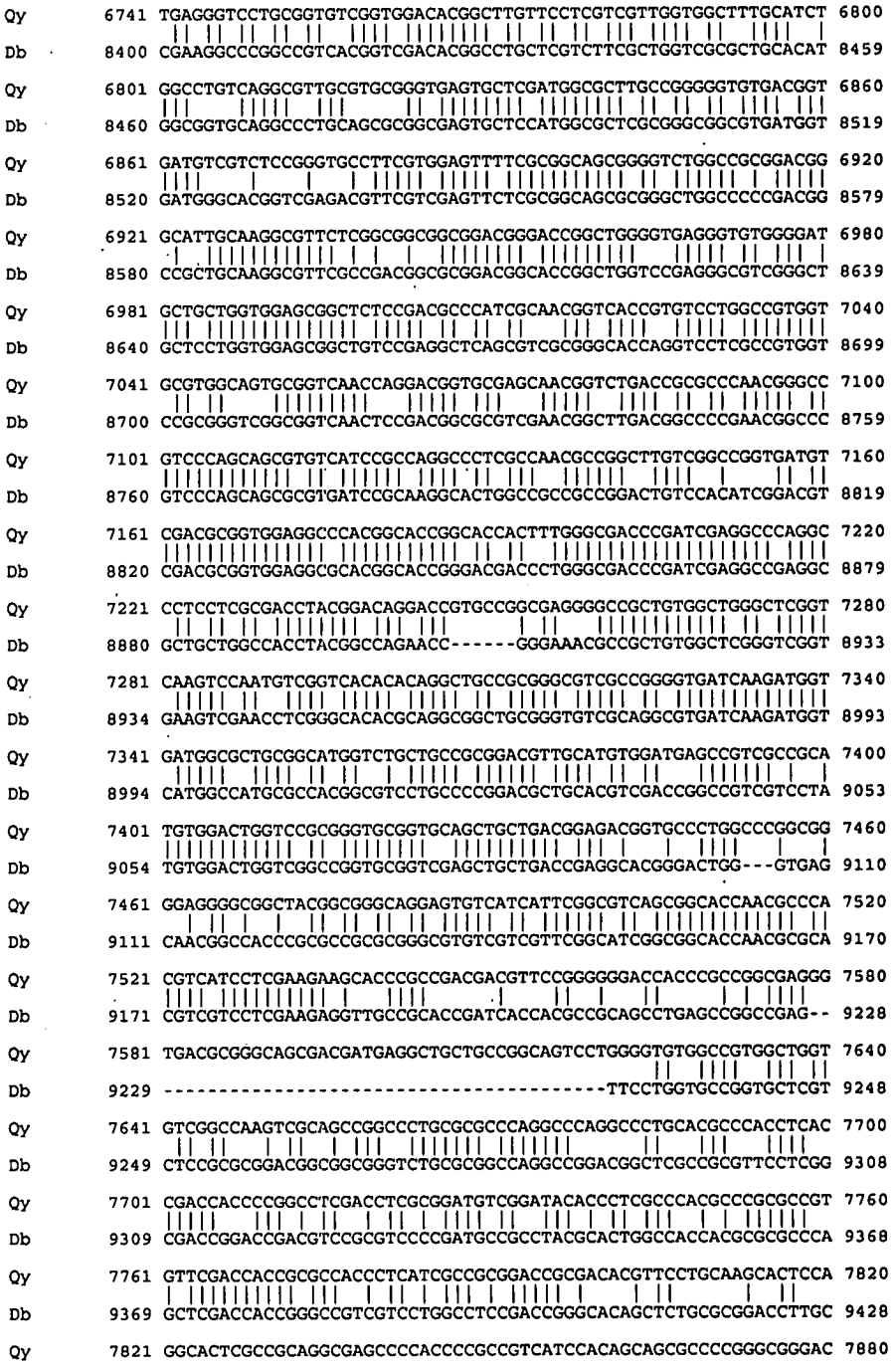


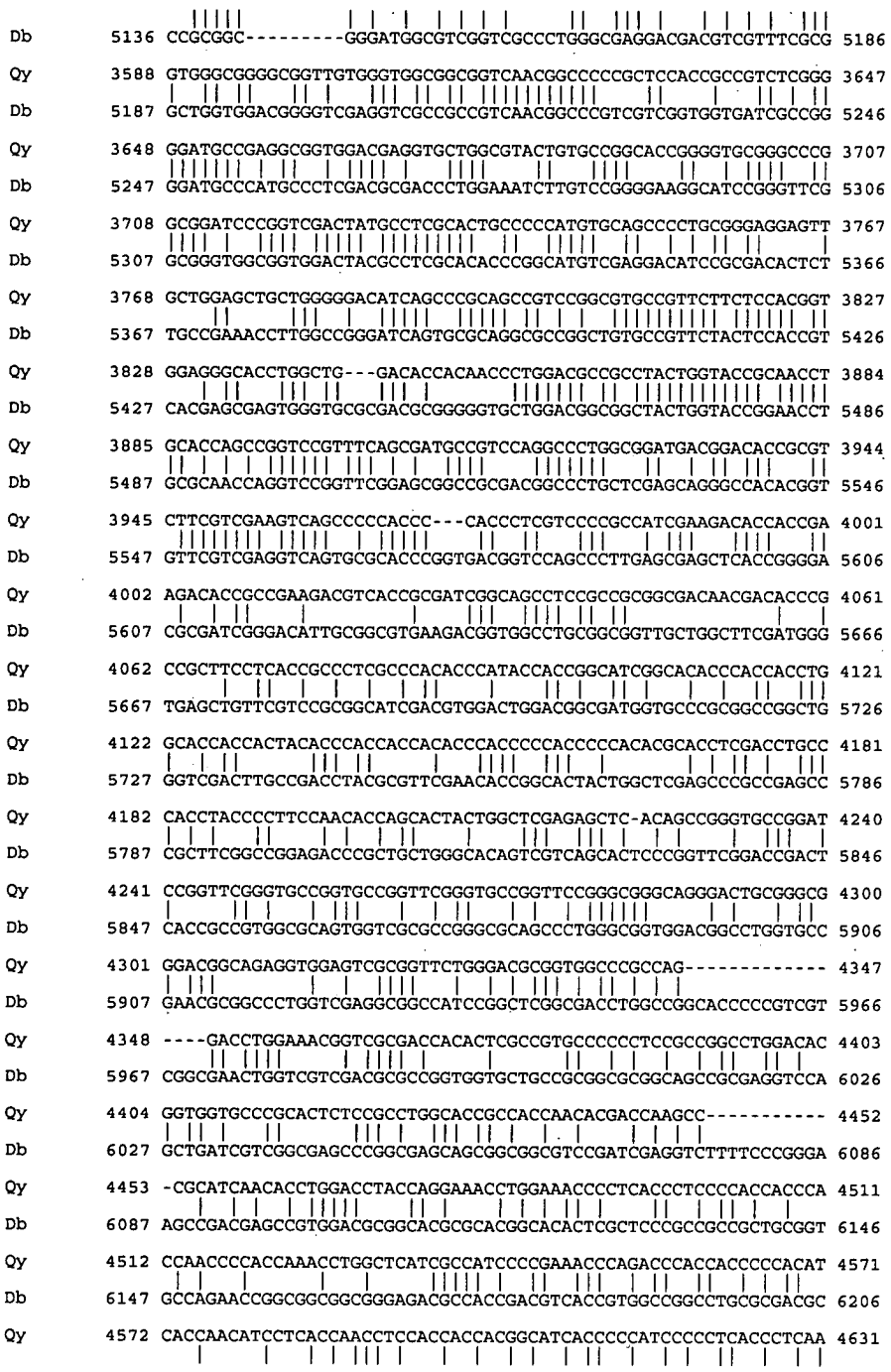


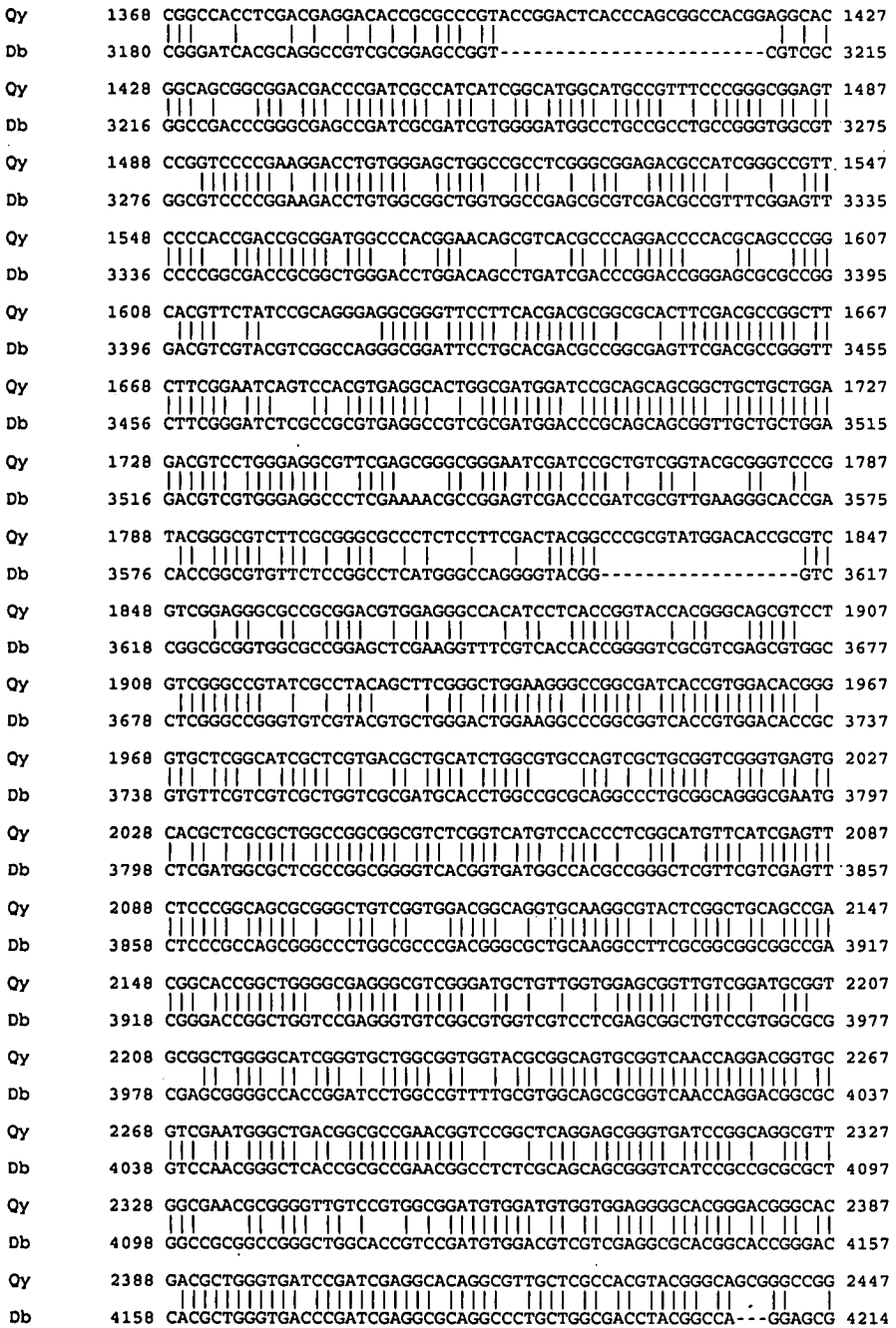


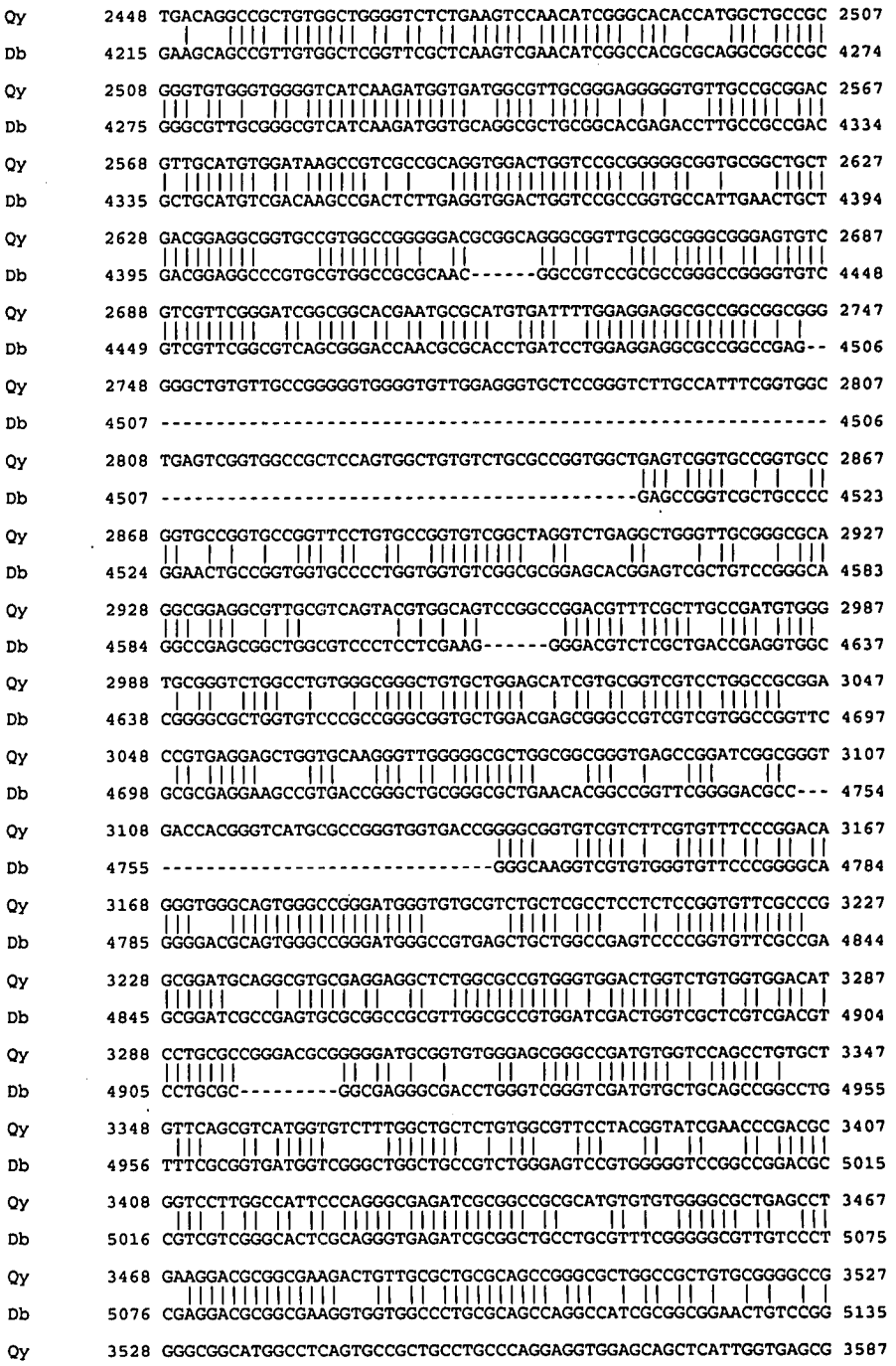







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AAV21187
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XX
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PI   Engel N,  Schupp T,  Toupet C;
XX
DR   WPI; 1998-169172/15.
DR   P-PSDB; AAW52845-W52850.
XX
PT   Amycolatopsis mediterranei rifamycin synthesis gene cluster - used
PT   to produce rifamycin and rifamycin analogues
XX
PS   Claim 4; Page 53-102; 205pp; English.
XX
CC   The present sequence represents a Amycolatopsis mediterranei rifamycin
CC   synthesis gene cluster DNA fragment from the present invention. The
CC   DNA fragment comprises a DNA region involved directly or indirectly
CC   in the gene cluster responsible for rifamycin synthesis, including
CC   the adjacent DNA regions to the right and left which, by reason of
CC   their function in connection with rifamycin biosynthesis, qualify
CC   as constituents of this rifamycin gene cluster, and functional
CC   fragments, derivatives or constituents of these. The Amycolatopsis
CC   mediterranei rifamycin synthesis gene cluster DNA fragment can be used
CC   for producing rifamycin, rifamycin analogues or precursors. It can also
CC   be used for inactivating or modifying genes involved in ansamycin or
CC   rifamycin biosynthesis. The DNA can be used for constructing mutant
CC   actinomycetes strains from which the natural rifamycin or ansamycin
CC   biosynthesis gene cluster has been partly or completely deleted. The
CC   DNA fragment can be used for assembling a library of polyketide
CC   synthases, which can be used for assembling a library of polyketides.
CC   A hybridisation probe of the invention can be used for identifying DNA
CC   fragments involved in the biosynthesis of ansamycins.
XX
SQ   Sequence 53789 BP; 6707 A; 19183 C; 20504 G; 7395 T; 0 other;

  Query Match            11.1%;  Score 3399.8;  DB 19;  Length 53789;
  Best Local Similarity  49.6%;  Pred. No. 0;
  Matches 15100;  Conservative    0;  Mismatches 12717;  Indels 2610;  Gaps  146;

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Qy       534 CAACCCGGCGCGGCTCGCCGTCGCAGCCGTCAACGGACCCCGGAGCACAGTCGTTTCCGG 593
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Qy       594 TGCCCGCGAGGCCGTCGCGGACCTGGTGGCCGACCTCACCGCCGCGCAGGTGCGCACGCG 653
Db      2424 GAACGTCATGCTCGGCTACCACAACAGCCCGGAGGCGACCGCCGCGGCGATGCGGGACGG 2483

Qy       654 CATGATCCCGGTGGACGTTCCCGCCCACTCCCCCCTGATGTACGCCATCGAGGAACGGGT 713
Db      2484 CTGGTTCCGGACCGGGGACCTGGCCCGCCGCGACGACGCCGGTTACTTCACCATCTGCGG 2543

Qy       714 CGTCAGCGGCCTGCTGCCCATCACCCCACGCCCCTCCCGCATCCCCTTCCACTCCTCGGT 773
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Qy       831 GTCGAGCACGGTCCGGTTCGAGCCCGCCGCCCGGCTGCTTCTGCAGCAGGGGCCCAAGAC 890
Db      2664 GCTCGGCGAGGTGCCGGTCGCCTACGTCATCCCCGGACCGACCGGTTTCGATCCTGCGGC 2723

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Db      2724 GTTGATCGAGAAGTGCCGCGAACAGCTGTCCGCCTACAAGGTGCCGGACCGGATCCTCGA 2783

Qy       951 CCTGGGCGACACCACCGGCACCGCCGACACCGTGATCATGGGCACGCTGCGCCGCGGCCA 1010
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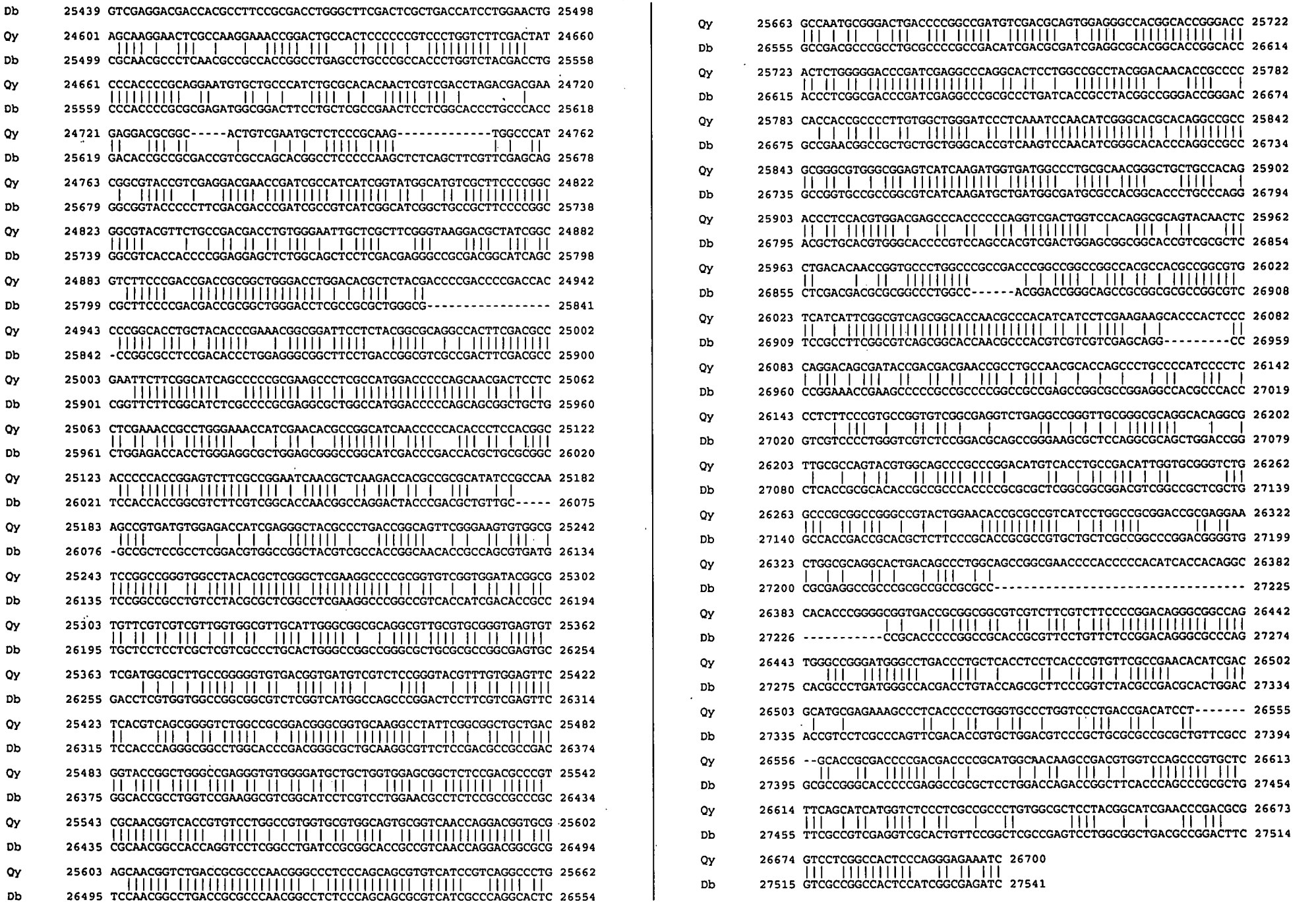
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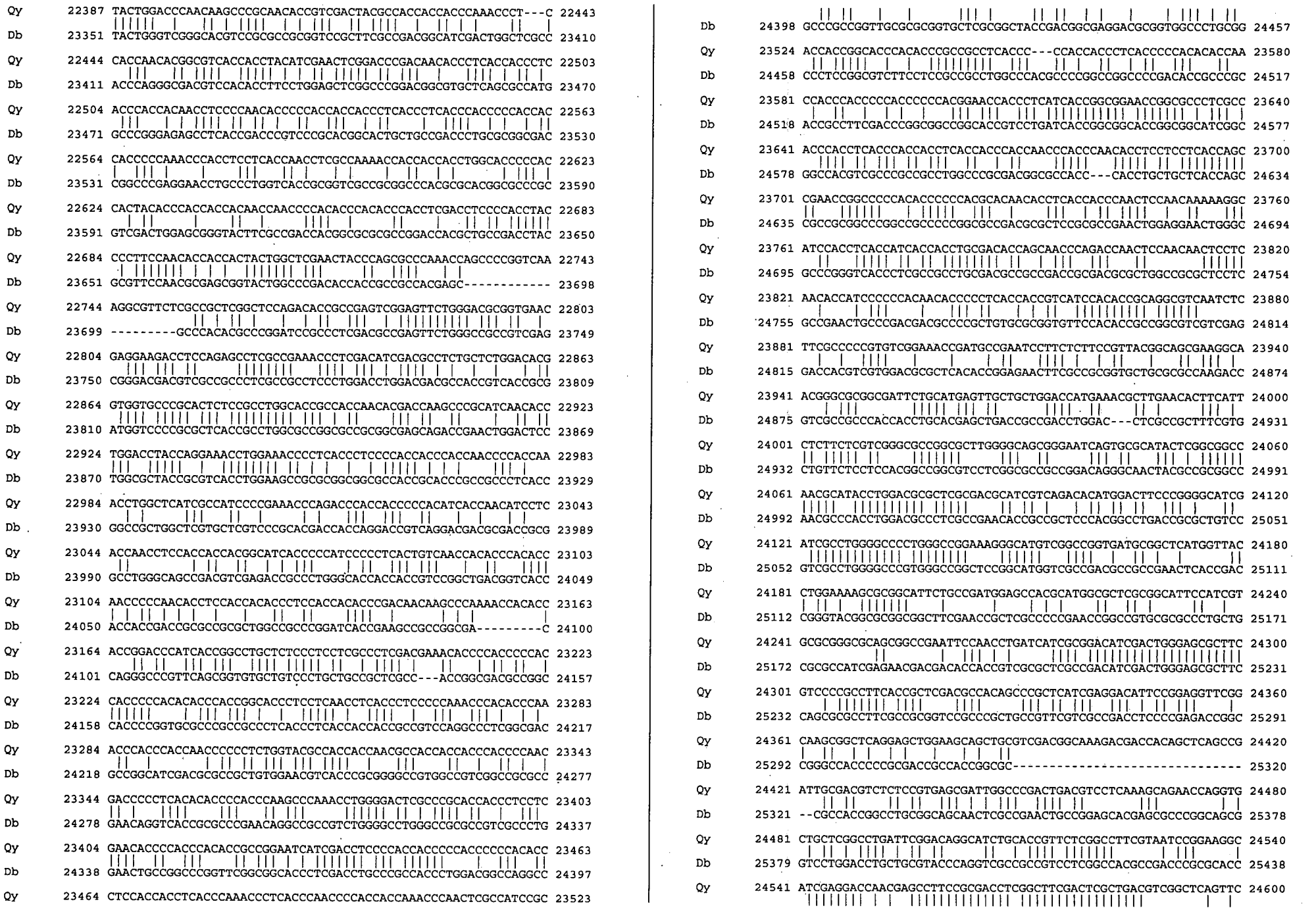
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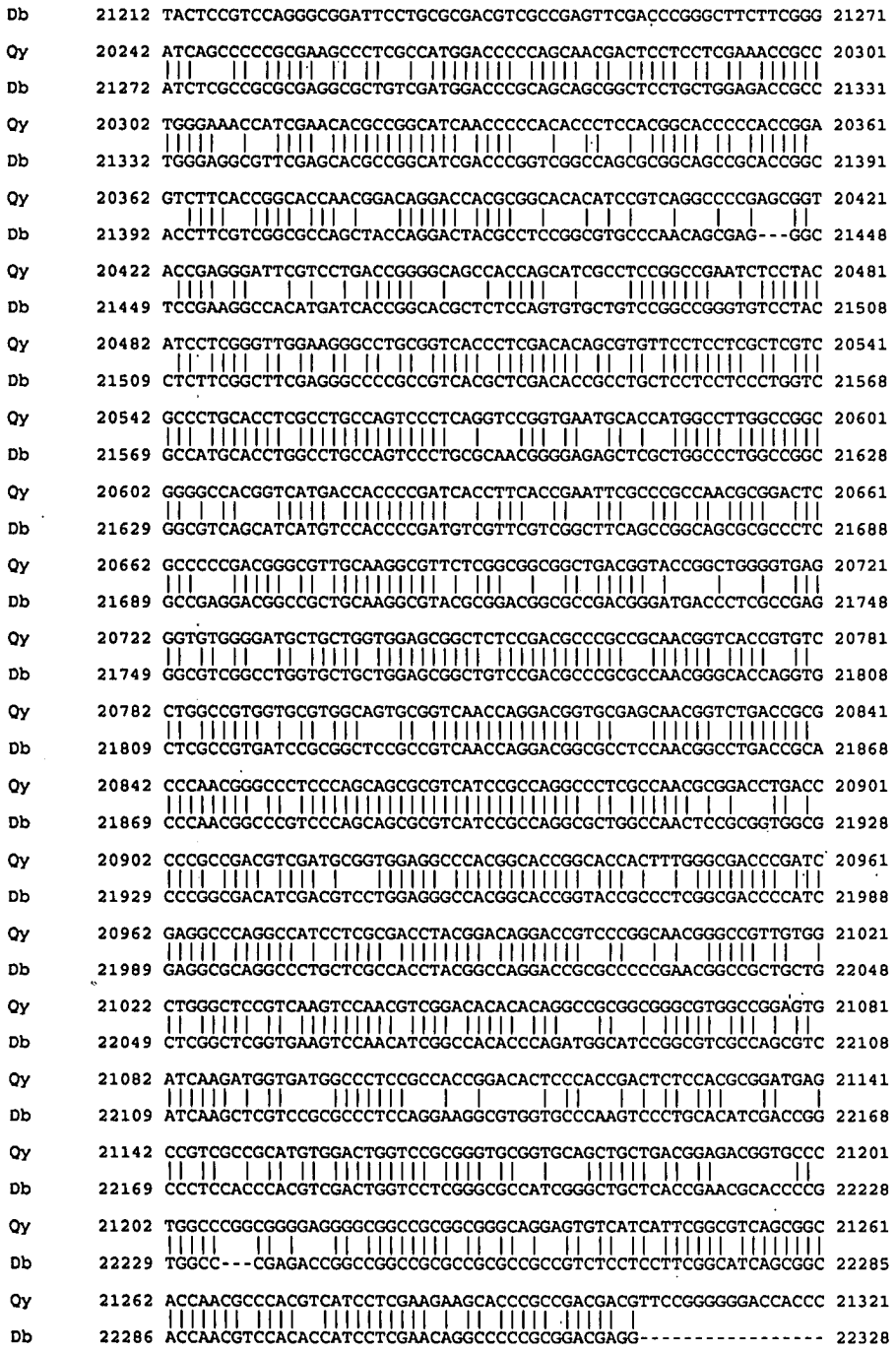
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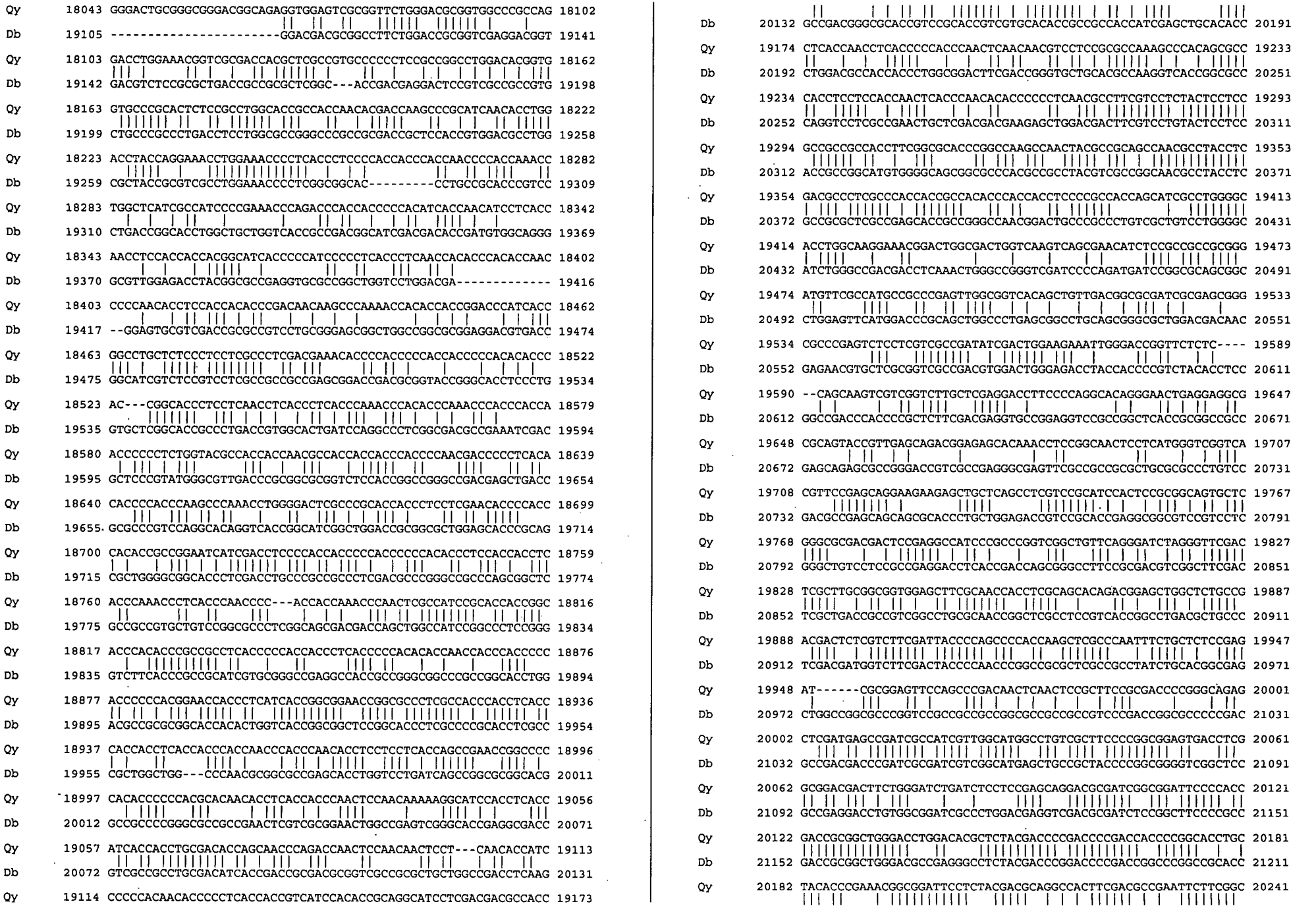
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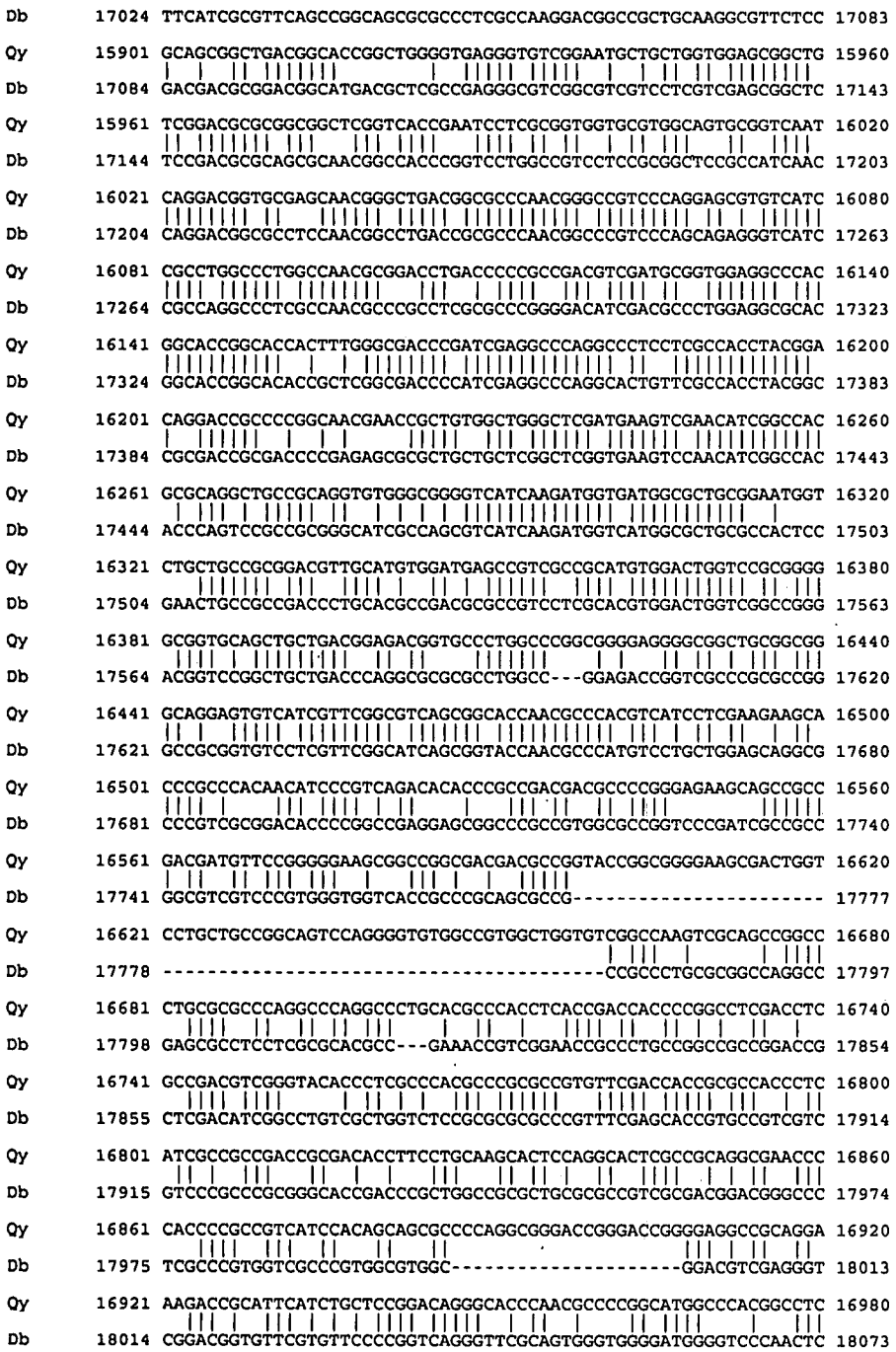
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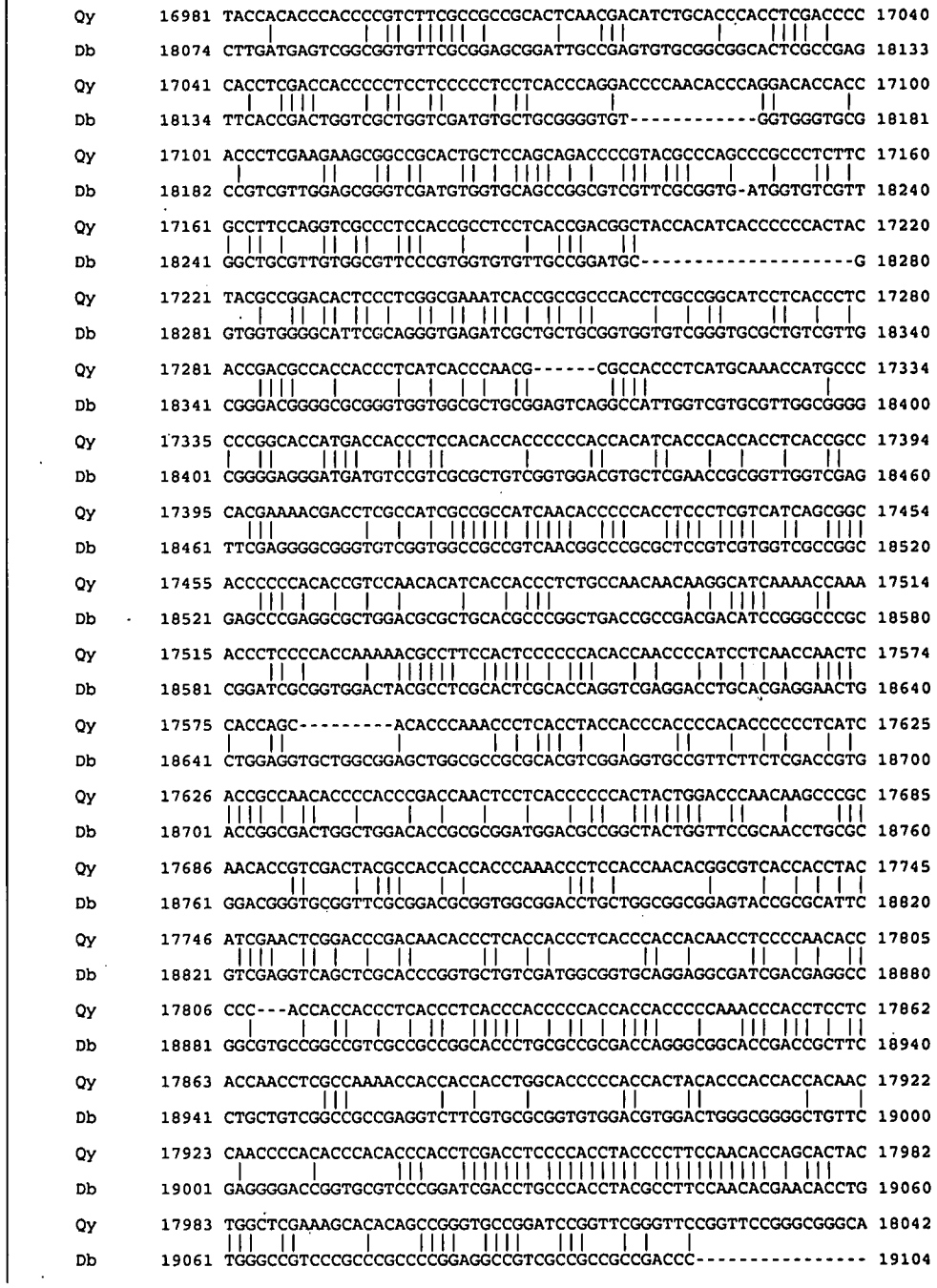


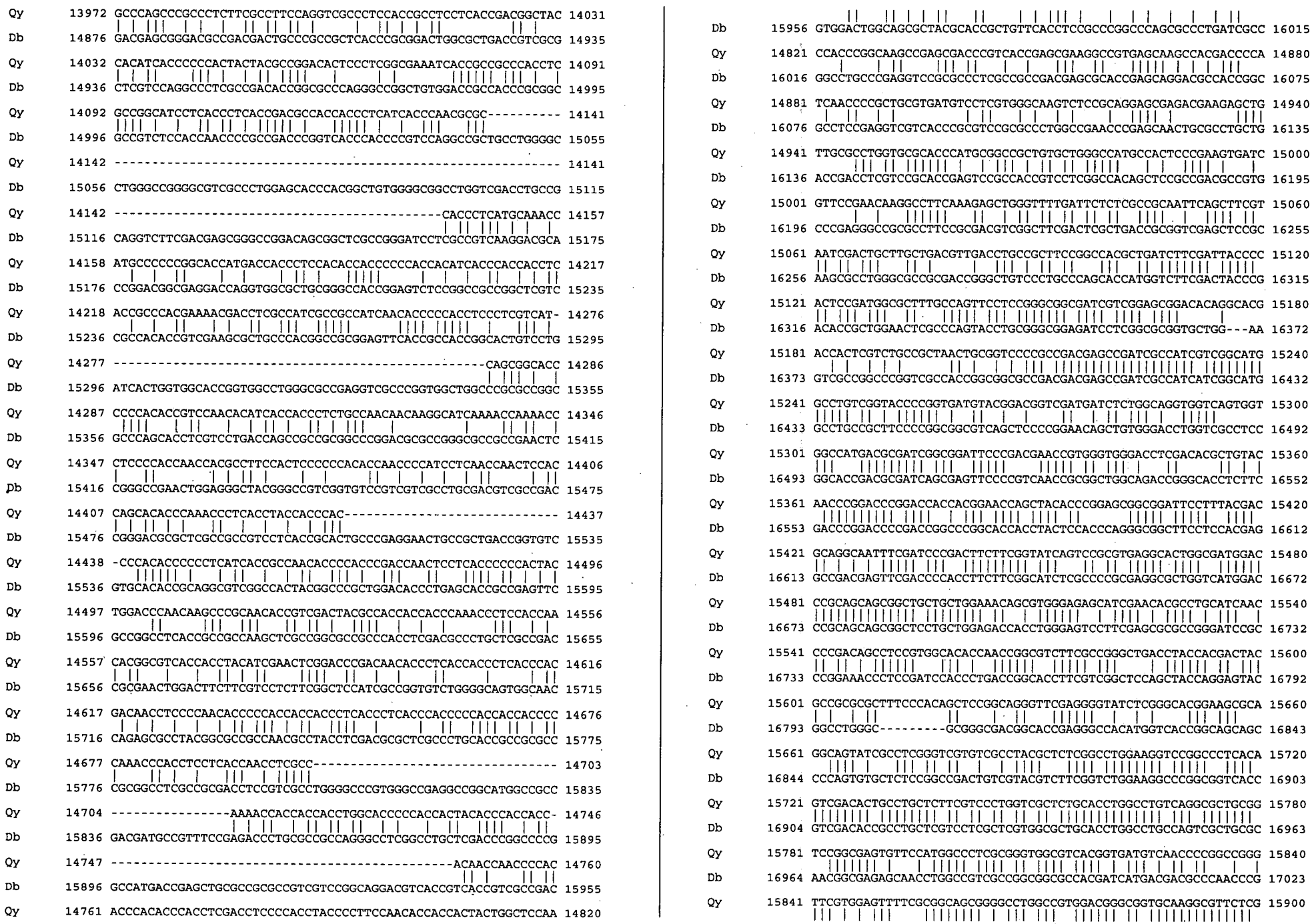


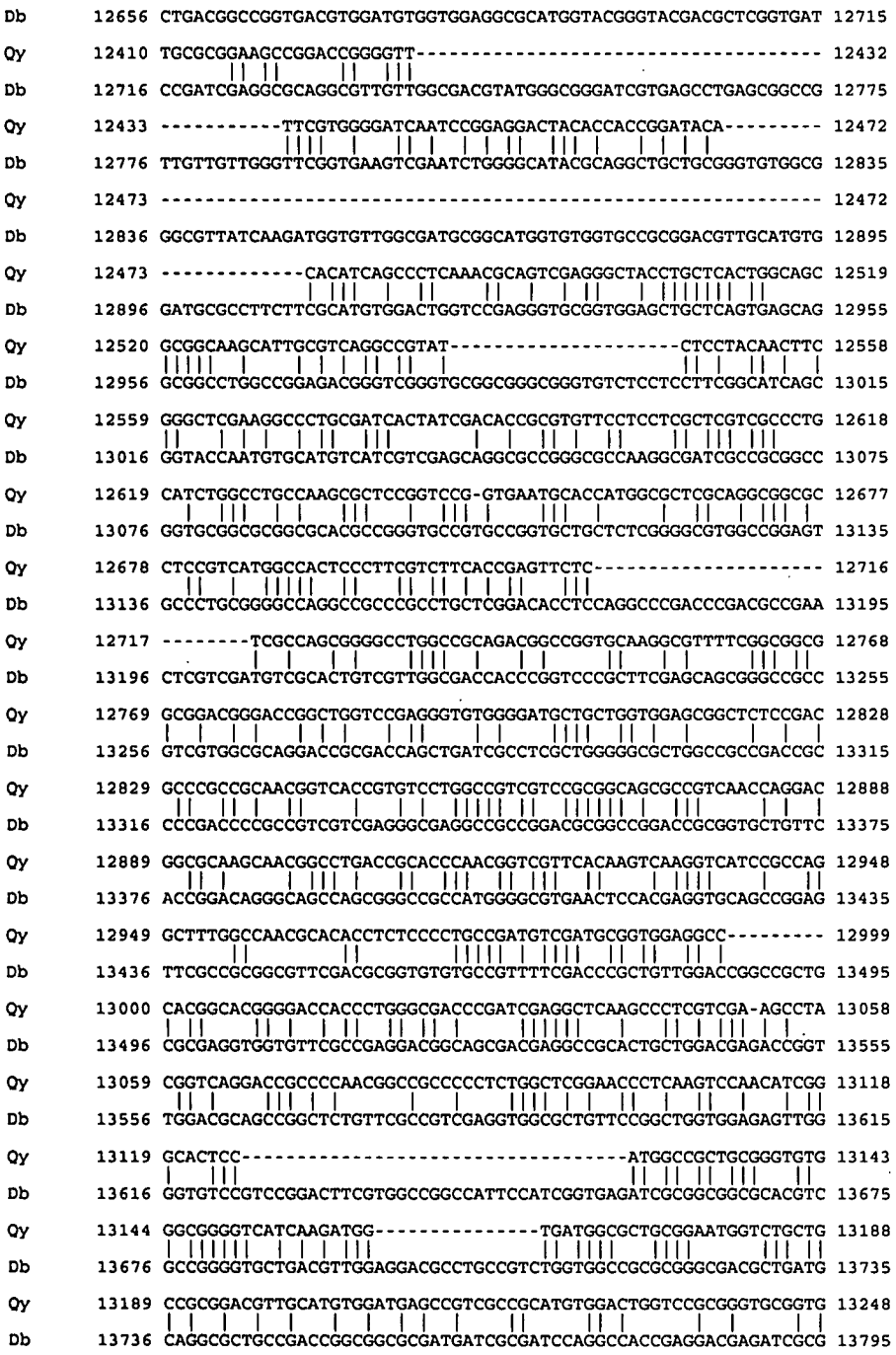

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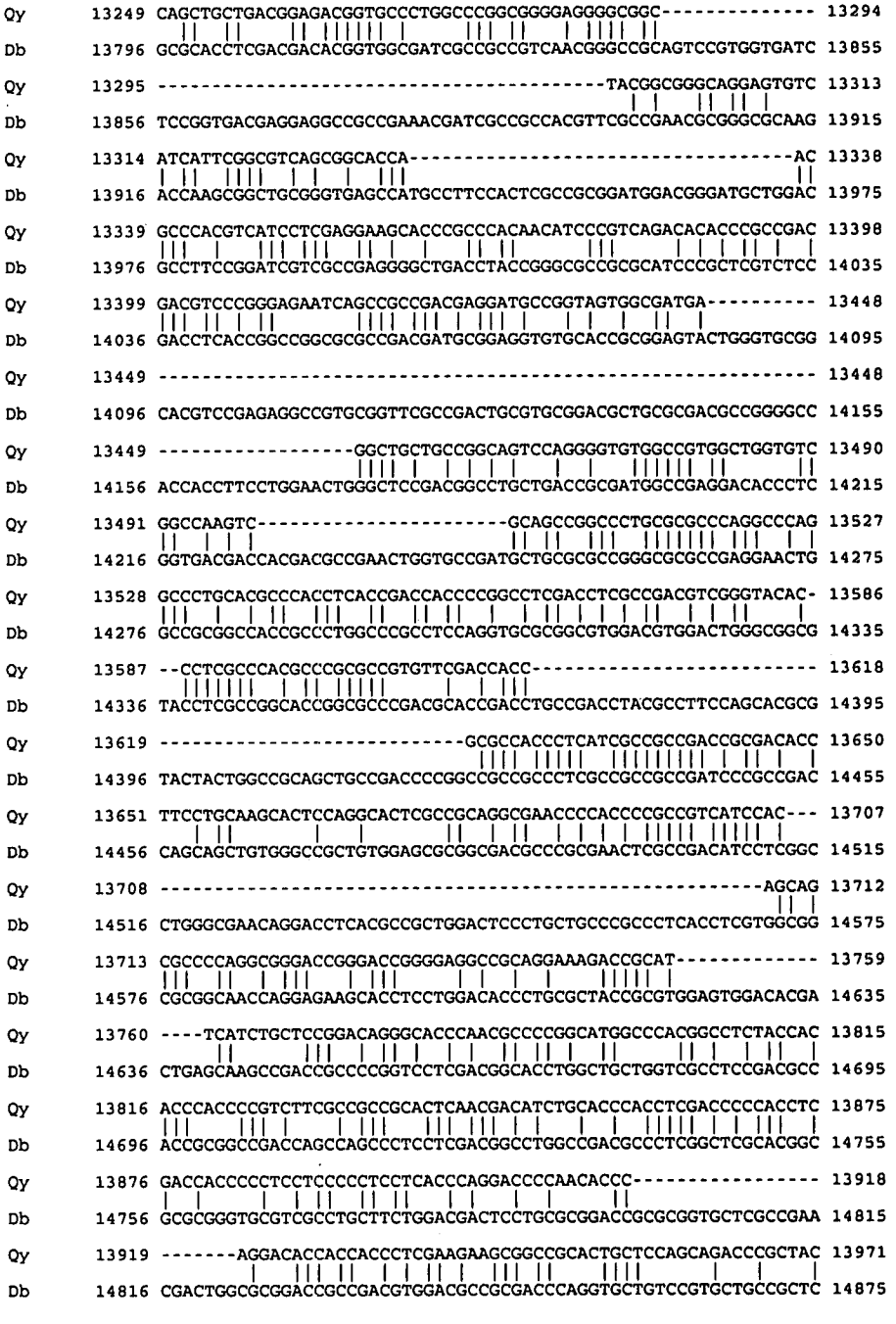


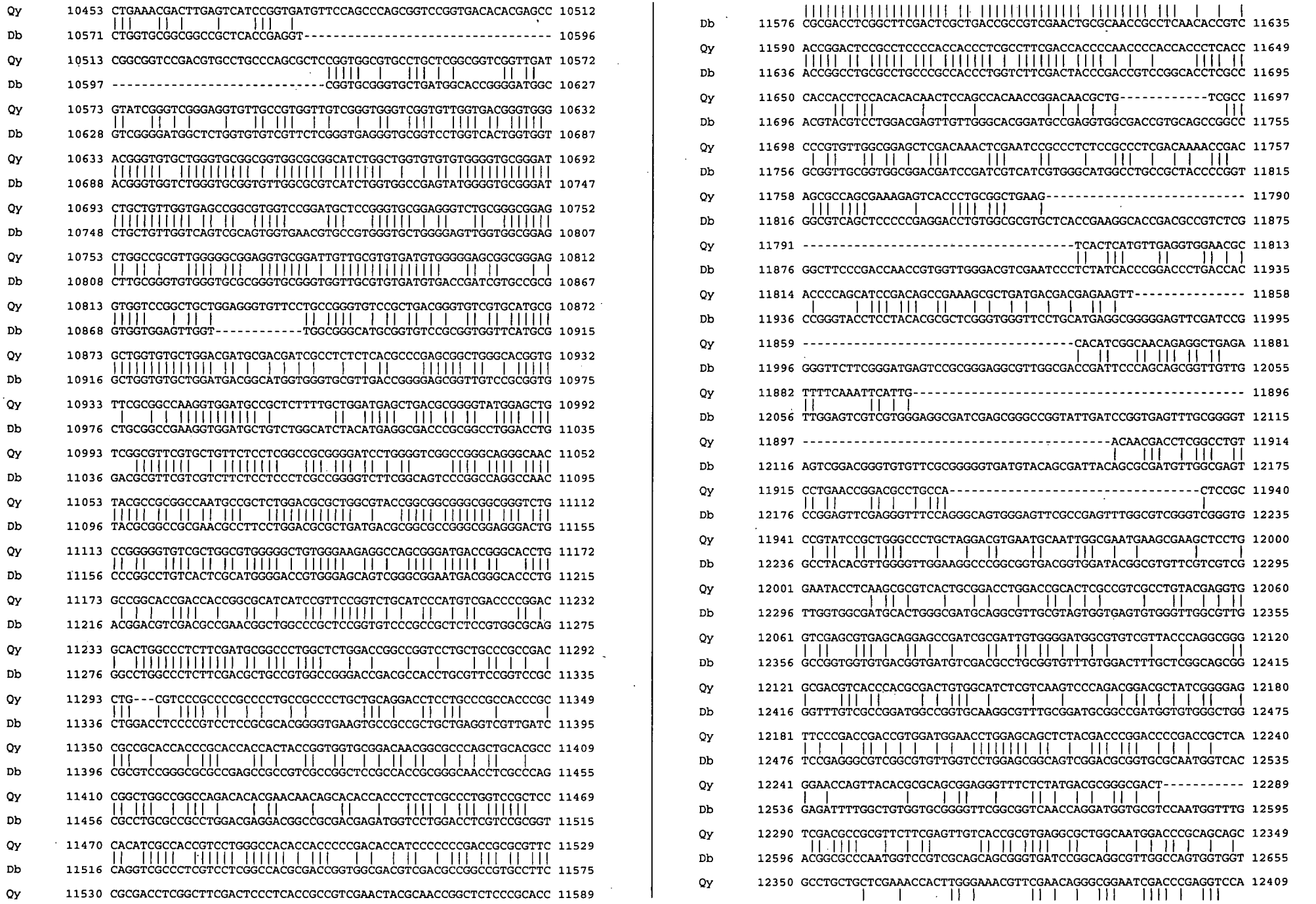


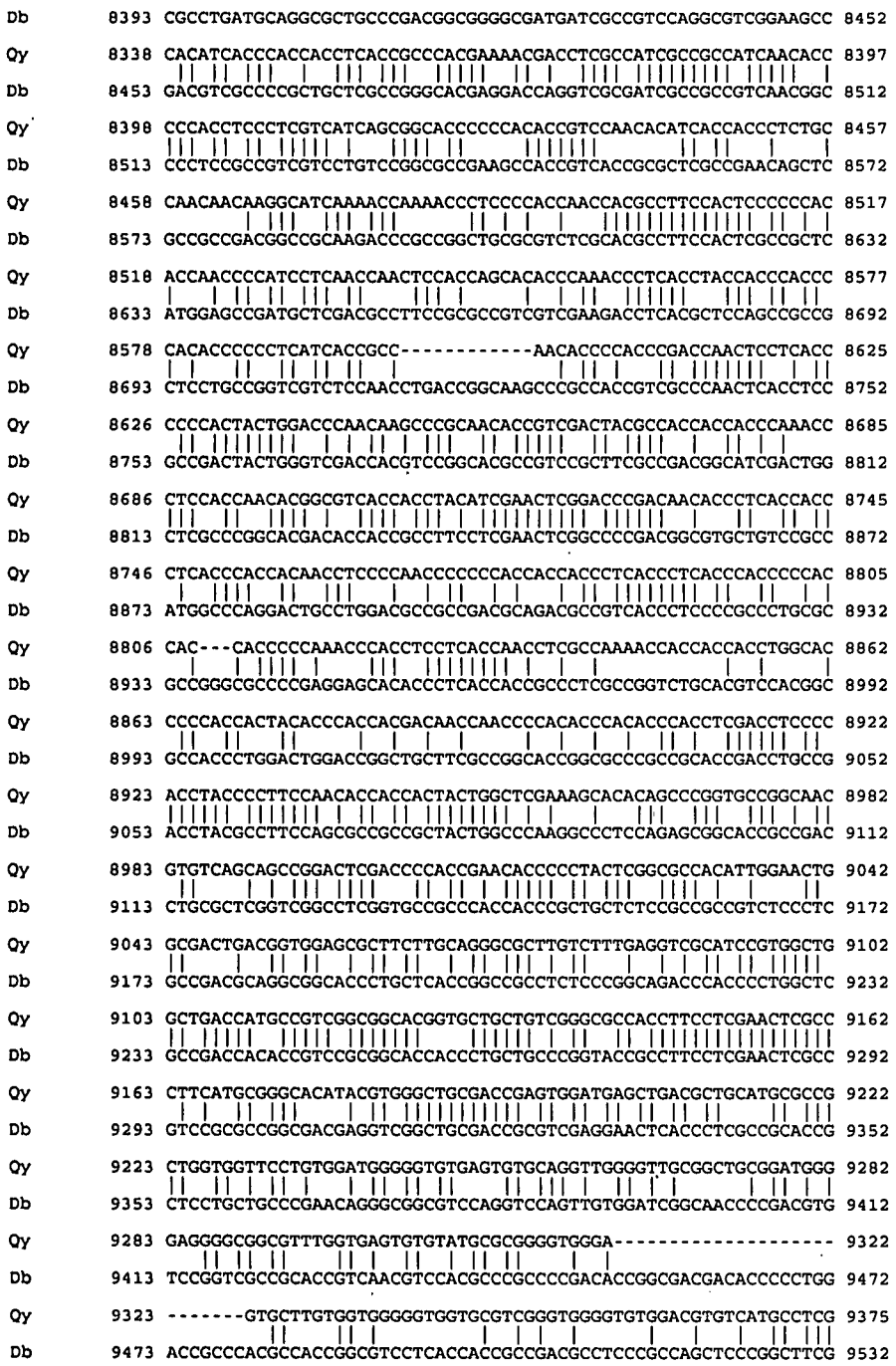


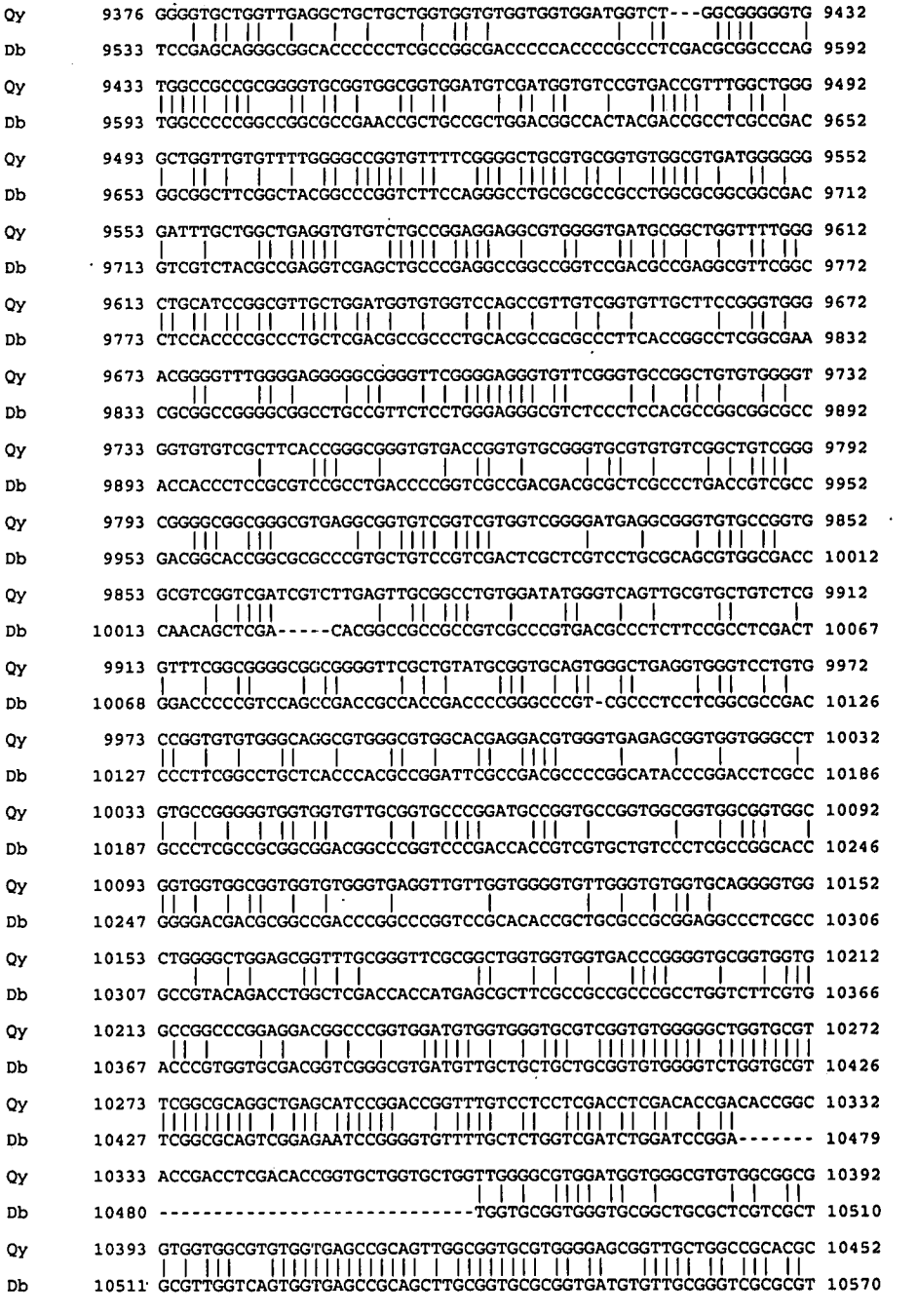












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XX
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  Query Match            11.2%;  Score 3443.4;  DB 22;  Length 27541;
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  Matches 11367;  Conservative    0;  Mismatches 8466;  Indels 1914;  Gaps   93;

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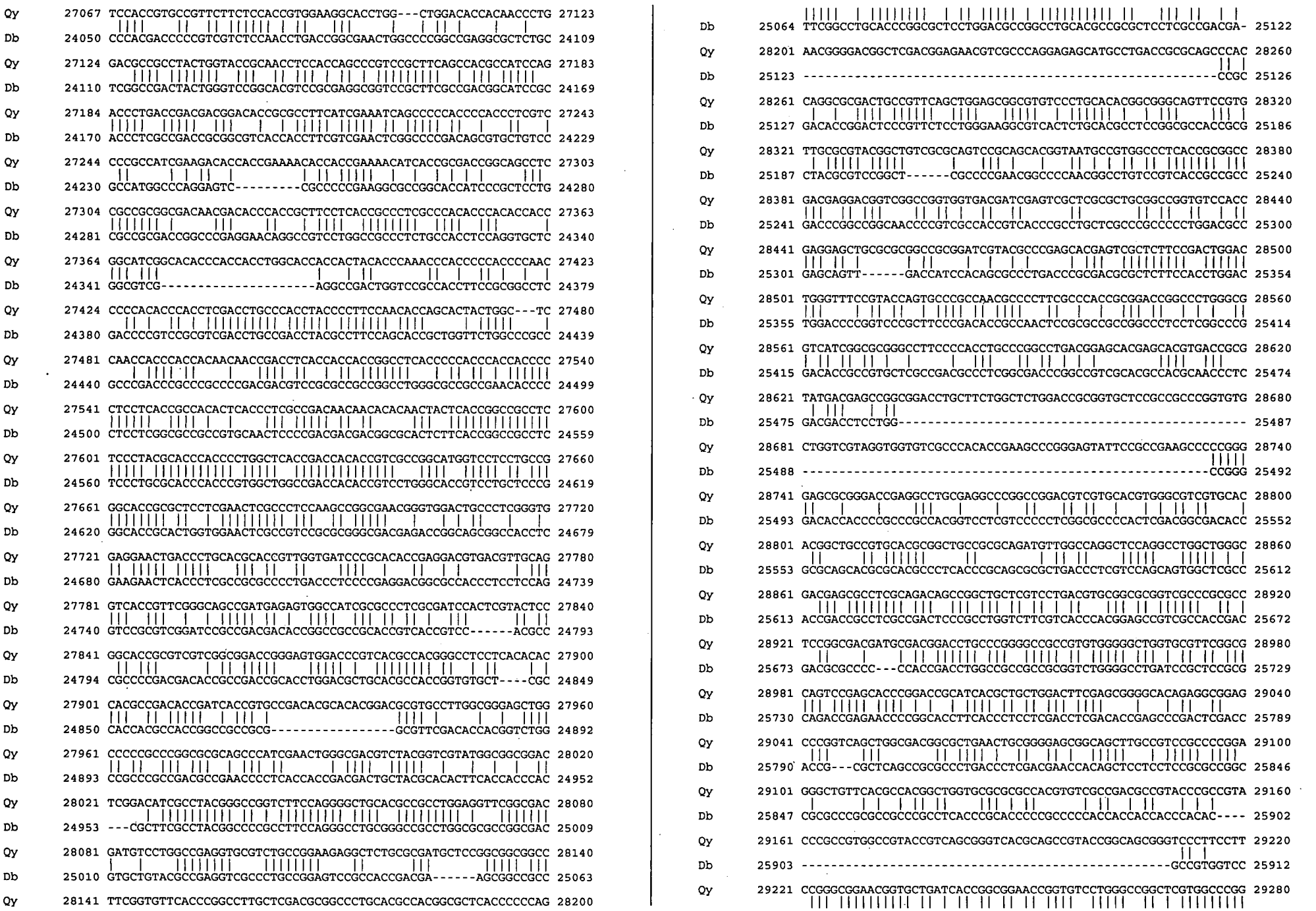
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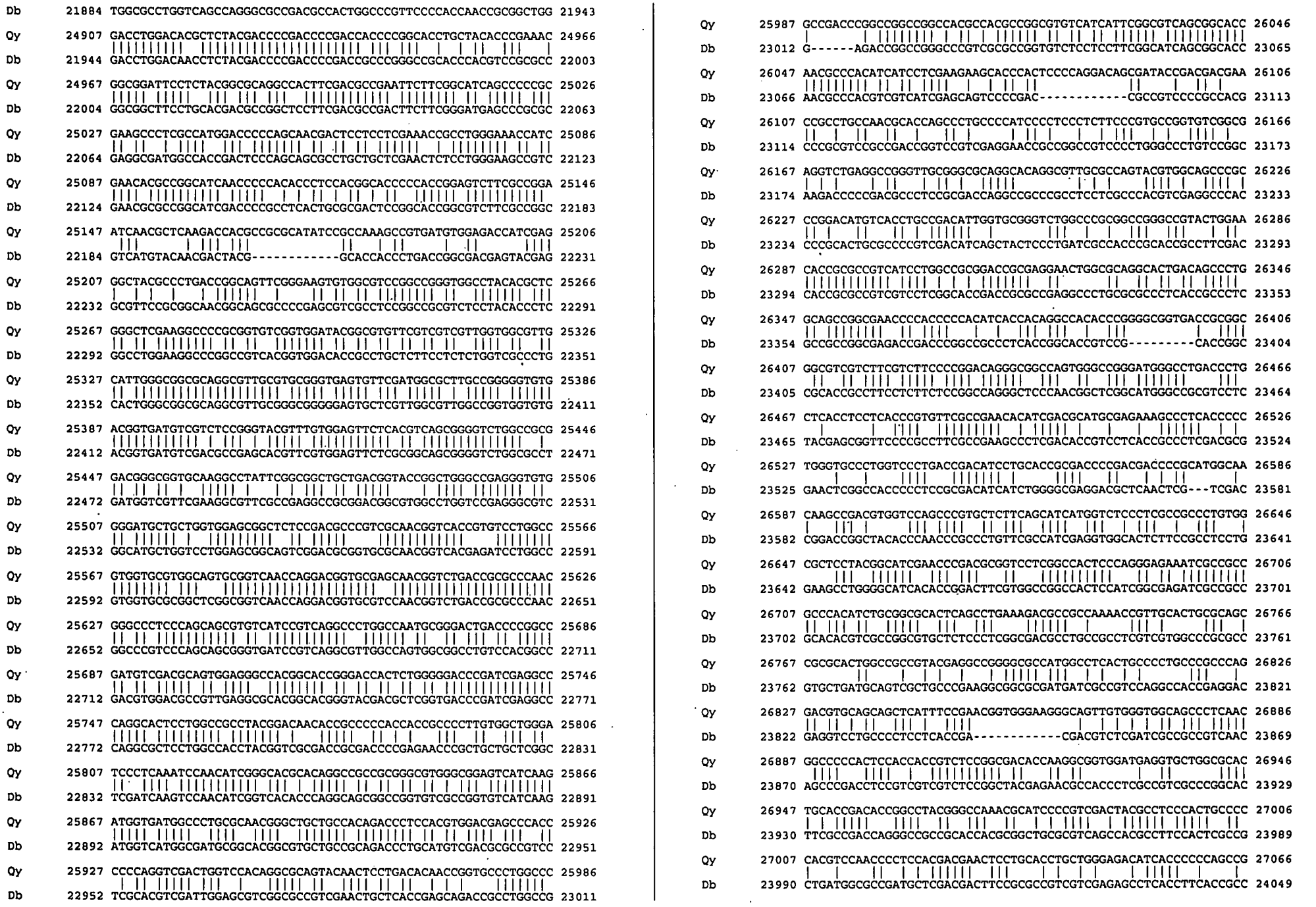
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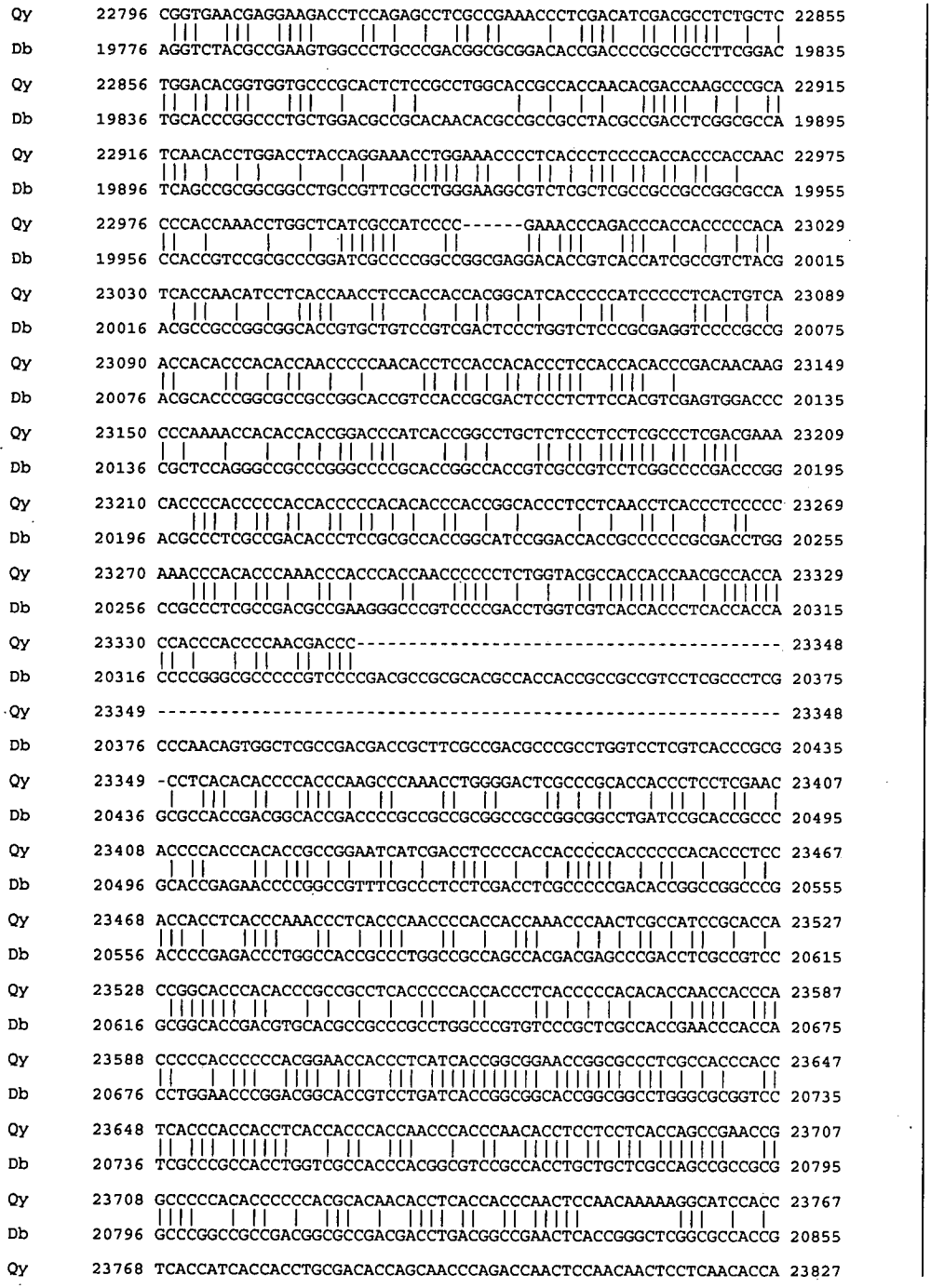
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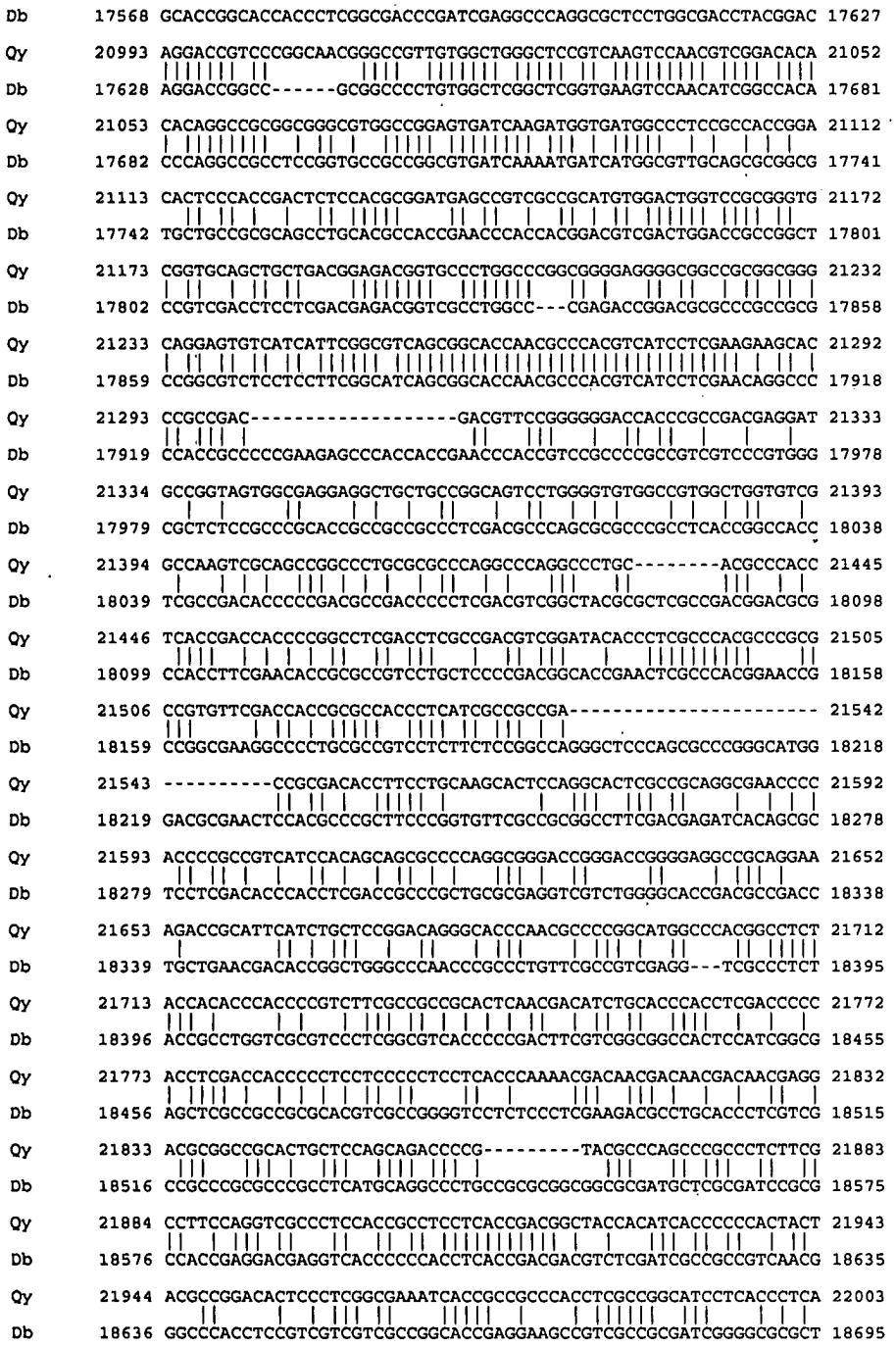
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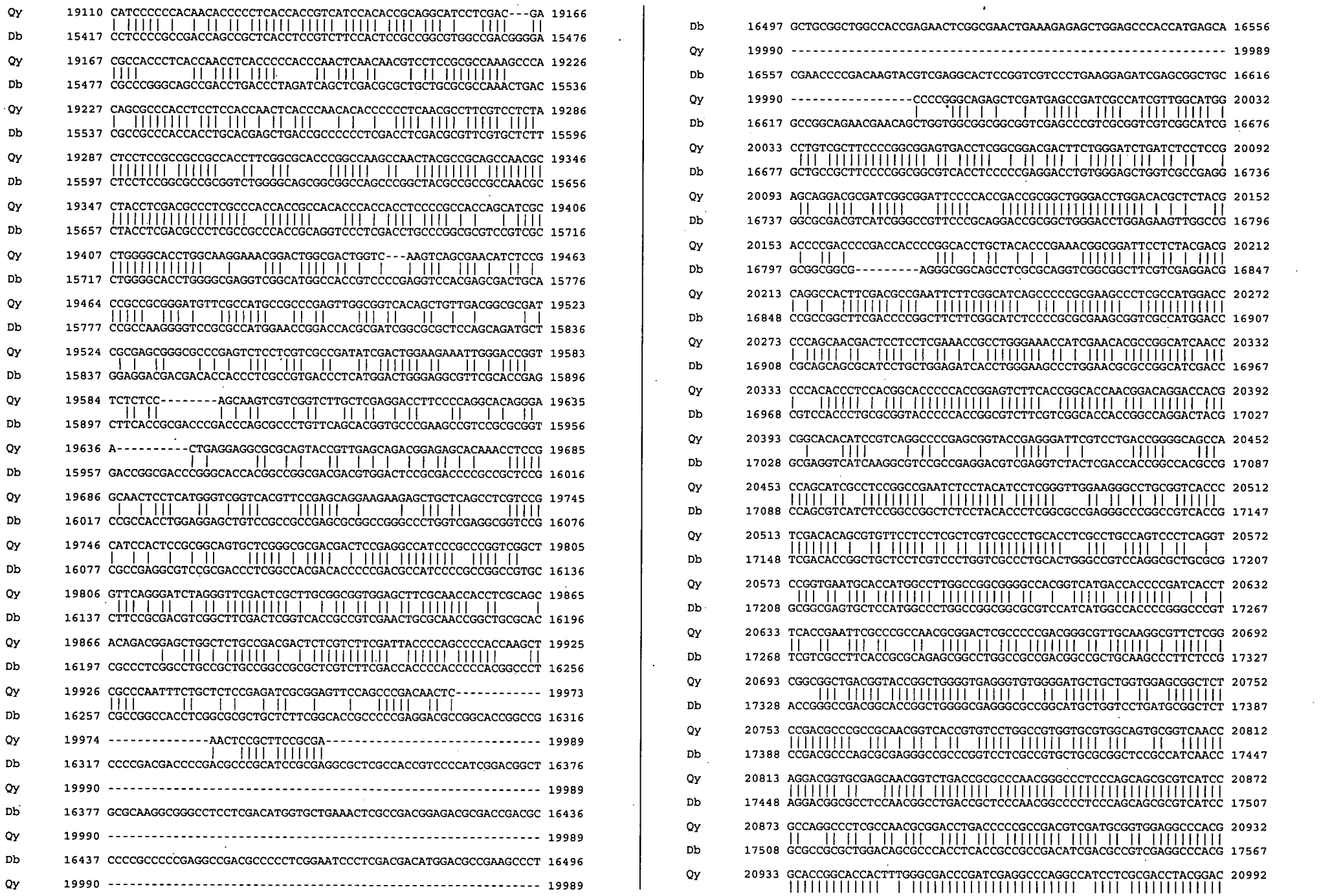
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XX
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PA   (ALPH-) ALPHARMA AS.
PA   (SINV-) SINVENT AS.
PA   (DZIE/) DZIEGLEWSKA H.
PA   (ZOTC/) ZOTCHEV S B.
PA   (SEKU/) SEKUROVA O N.
PA   (FJAE/) FJAERVIK E.
PA   (BRAU/) BRAUTASET T.
PA   (STRO/) STROM A R.
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DR   WPI; 2001-557614/62.
DR   P-PSDB; AAE10138, AAE10139, AAE10140, AAE10141, AAE10142.
XX
PT   New nystatin polyketide synthase polynucleotides and polypeptides,
PT   useful as antibiotics and antifungals -
XX
PS   Claim 2; Page 151-166; 266pp; English.
XX
CC   The present invention relates to the cloning and sequencing of the gene
CC   cluster encoding a modular type I polyketide synthase (PKS) enzyme
CC   involved in the biosynthesis of the macrolide antibiotic nystatin.
CC   The nystatin PKS is useful as antifungal antibiotics. The present
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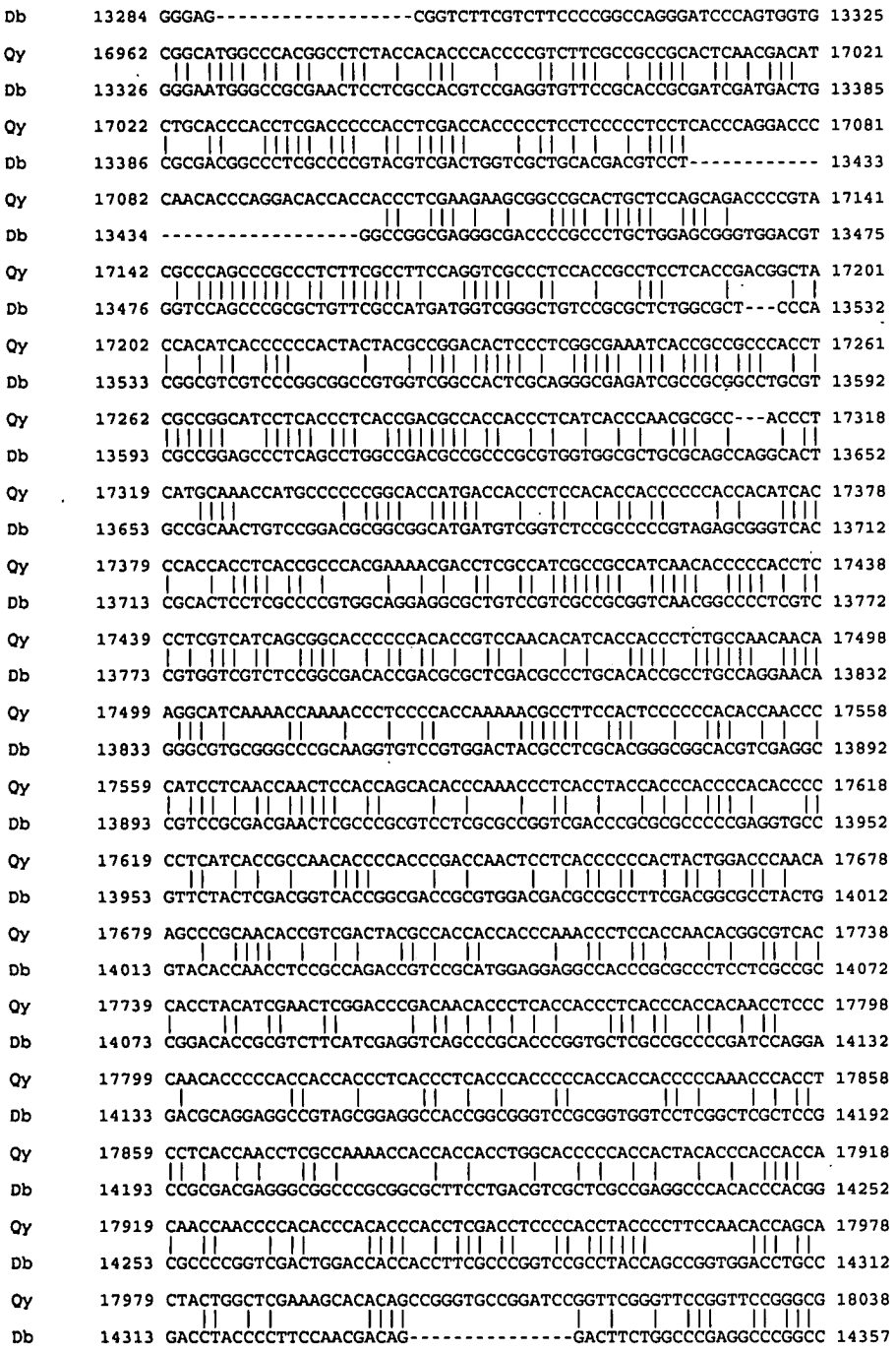


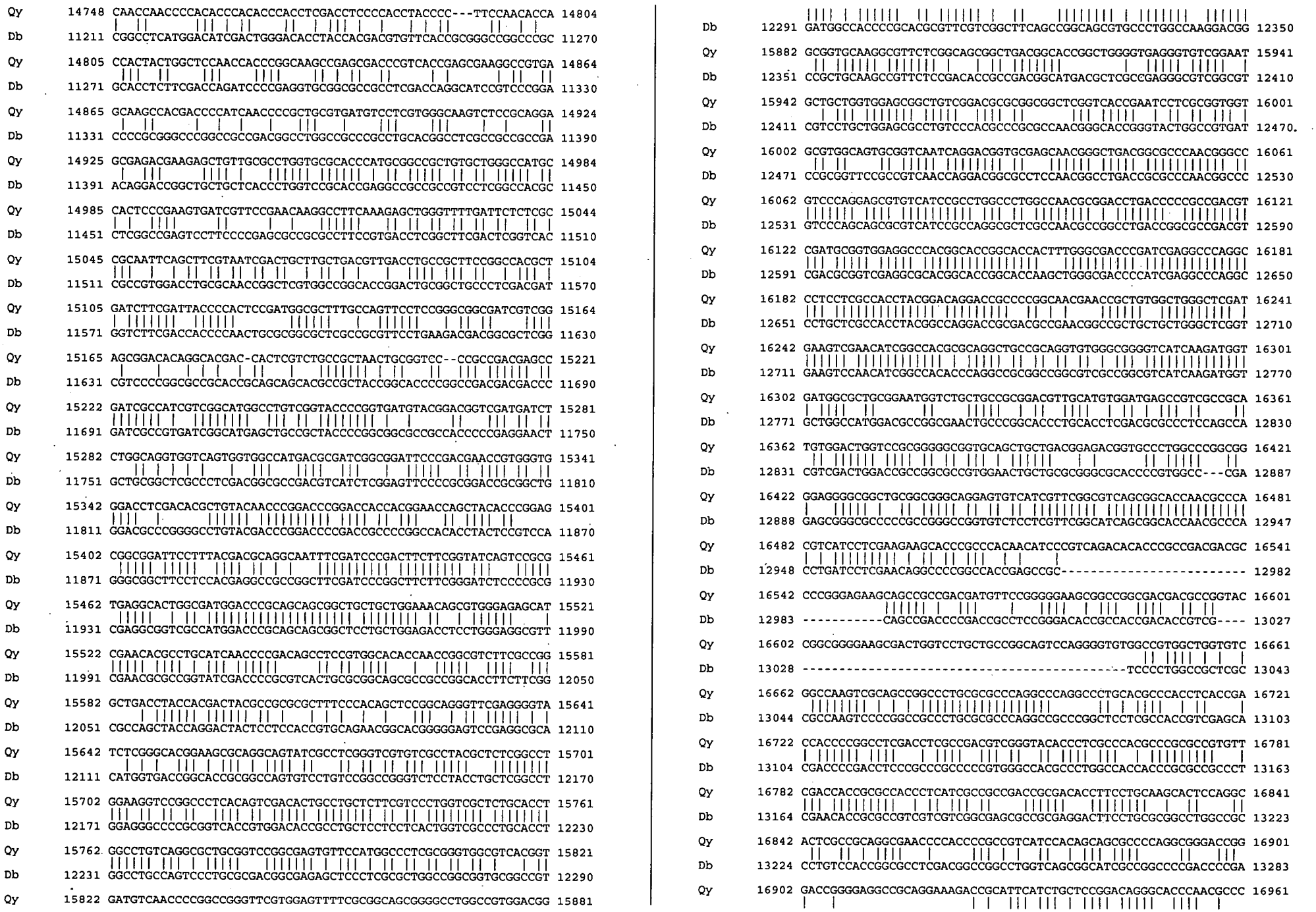


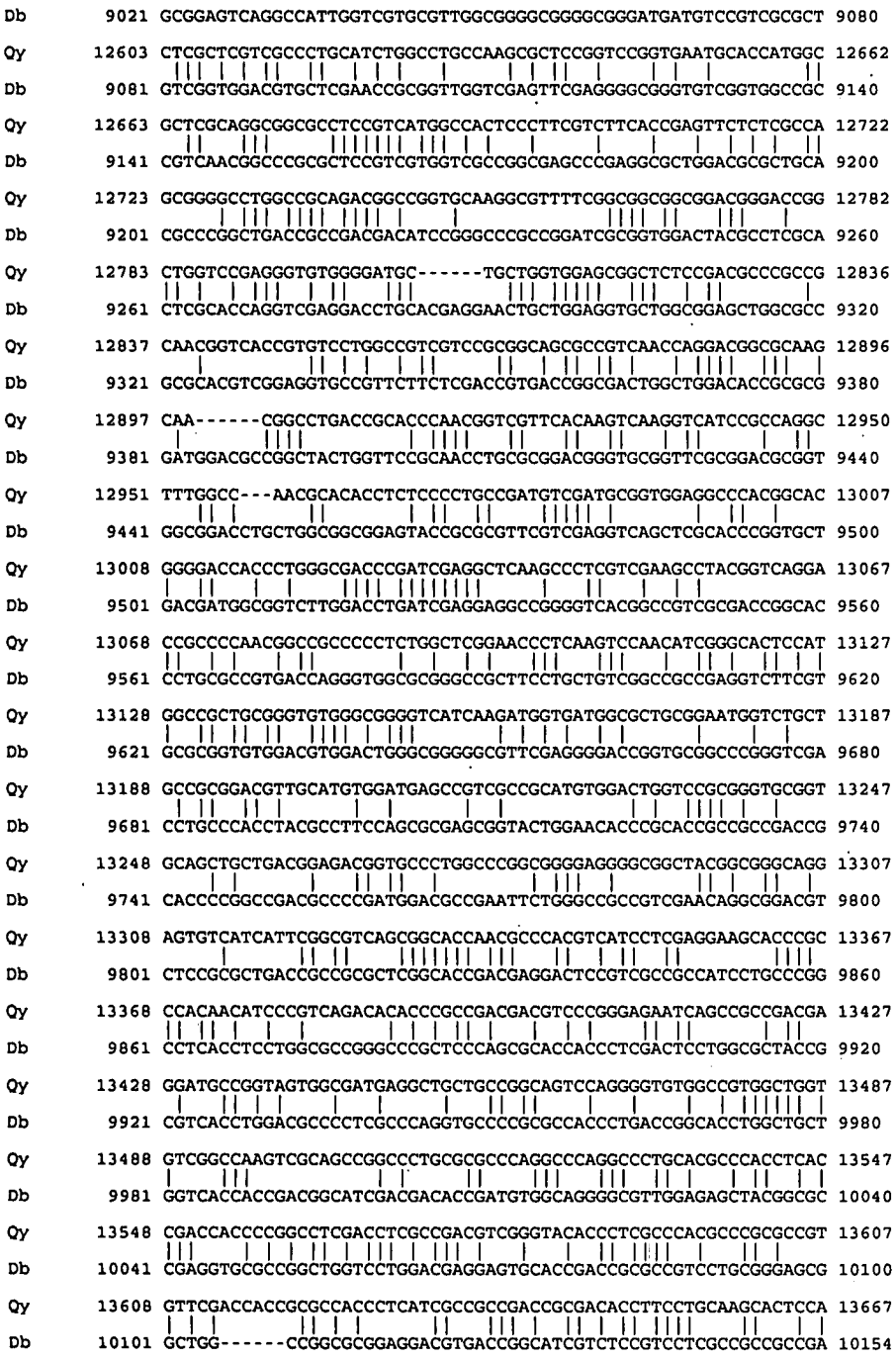

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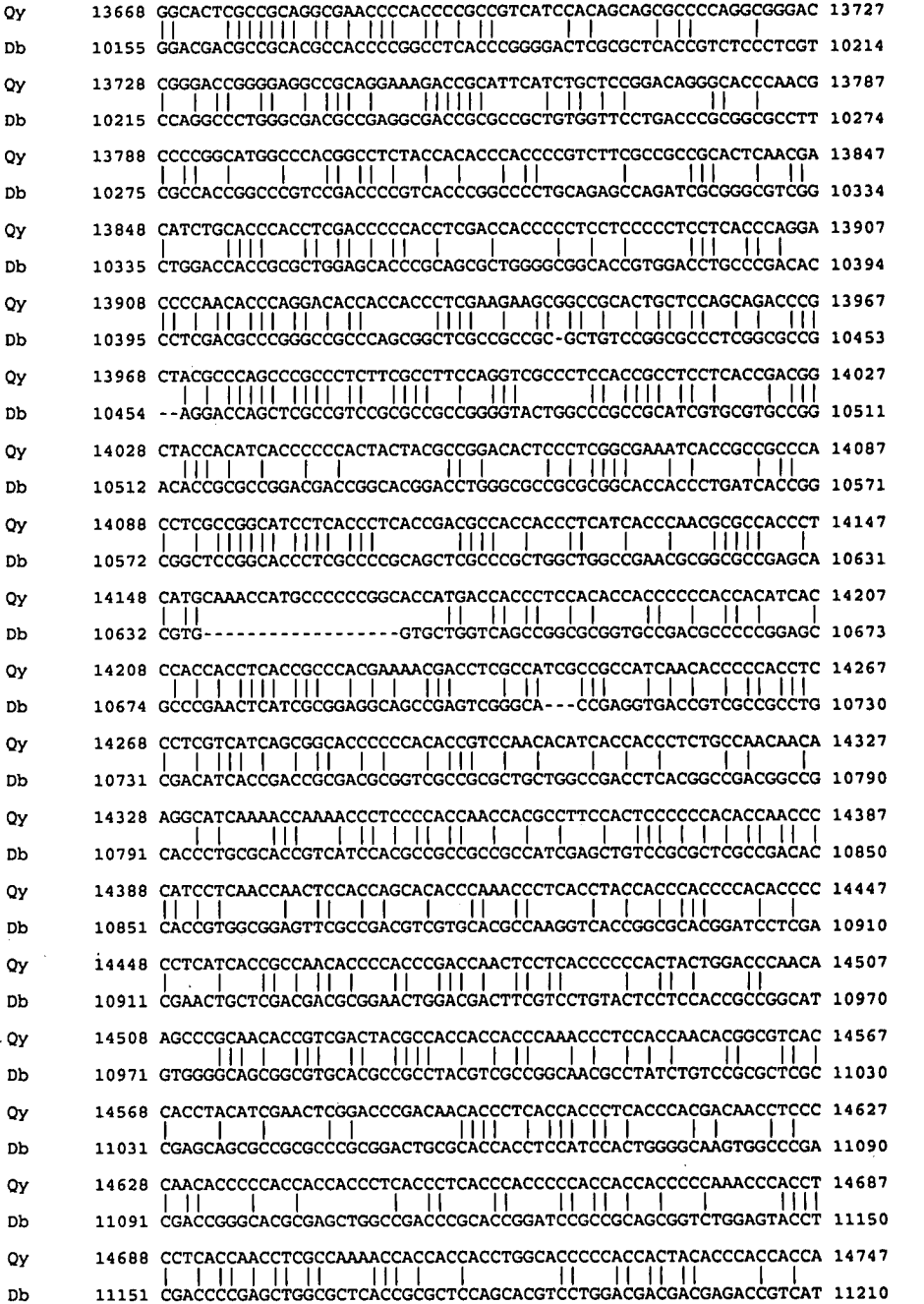

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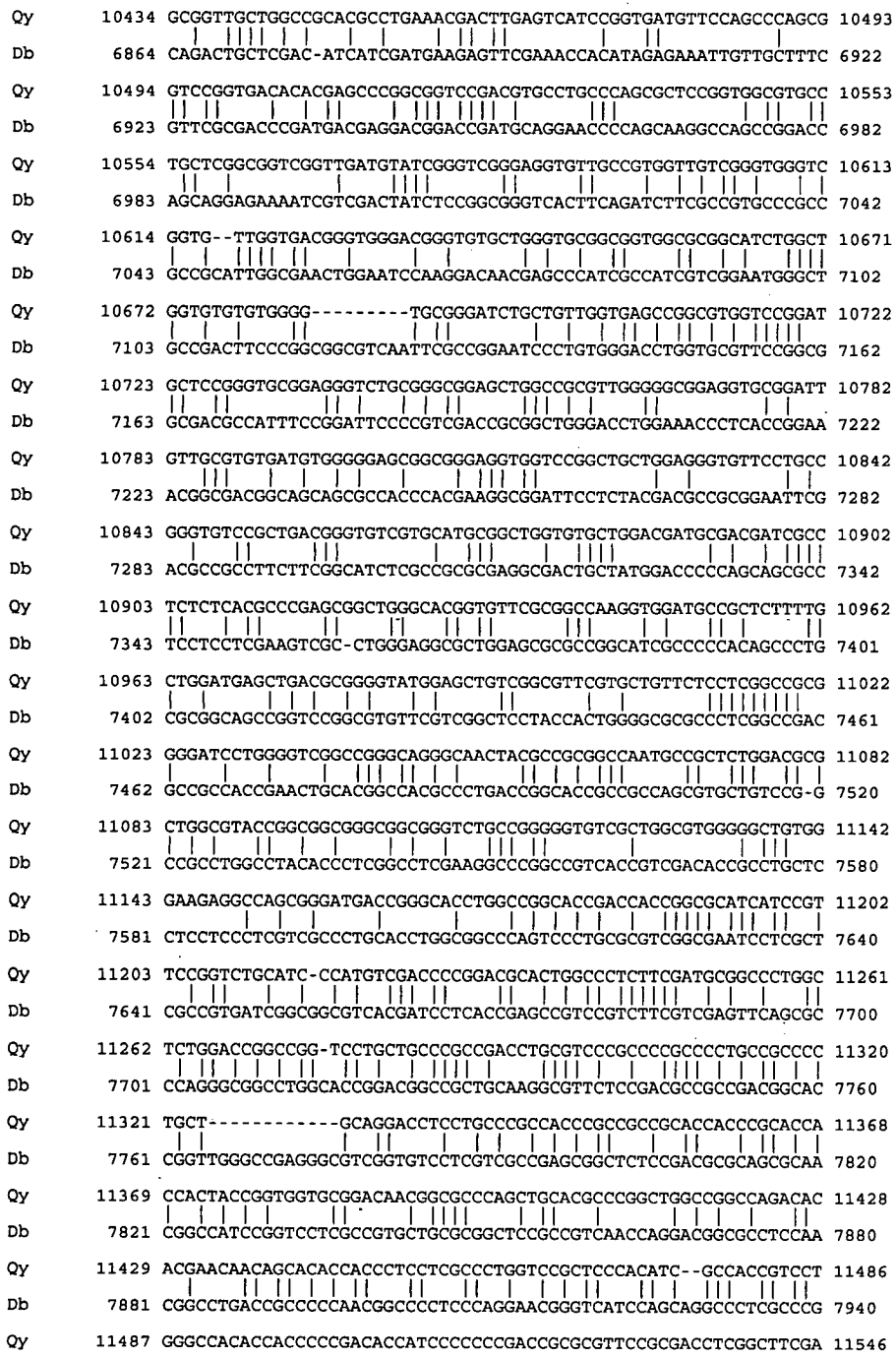


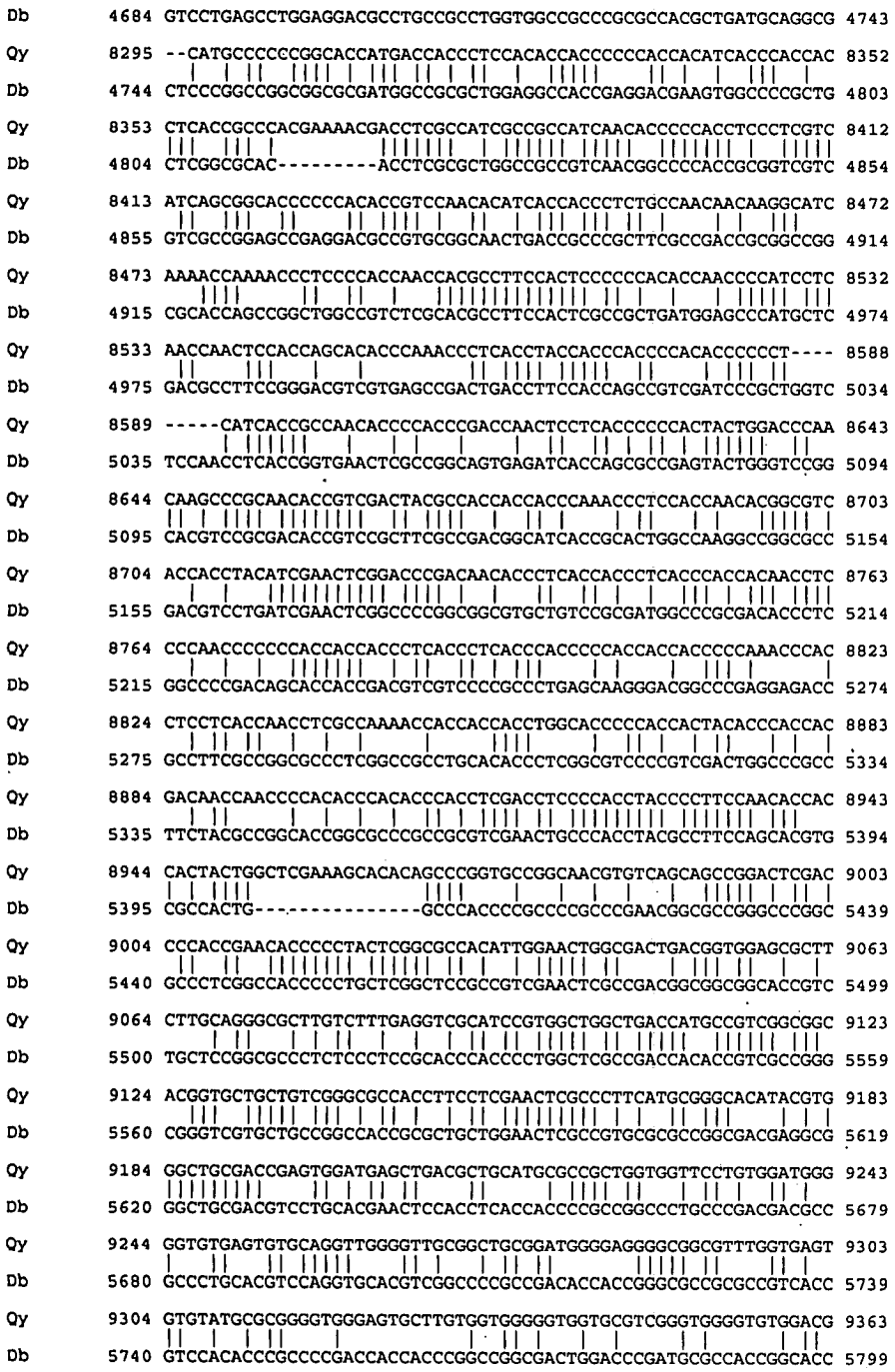

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Db 14418 CCAGGACCTCGCCGCGCTCGCCGACGCGCTCGGCGTCCCCGCCGACGACGAGCACACCGC 14477
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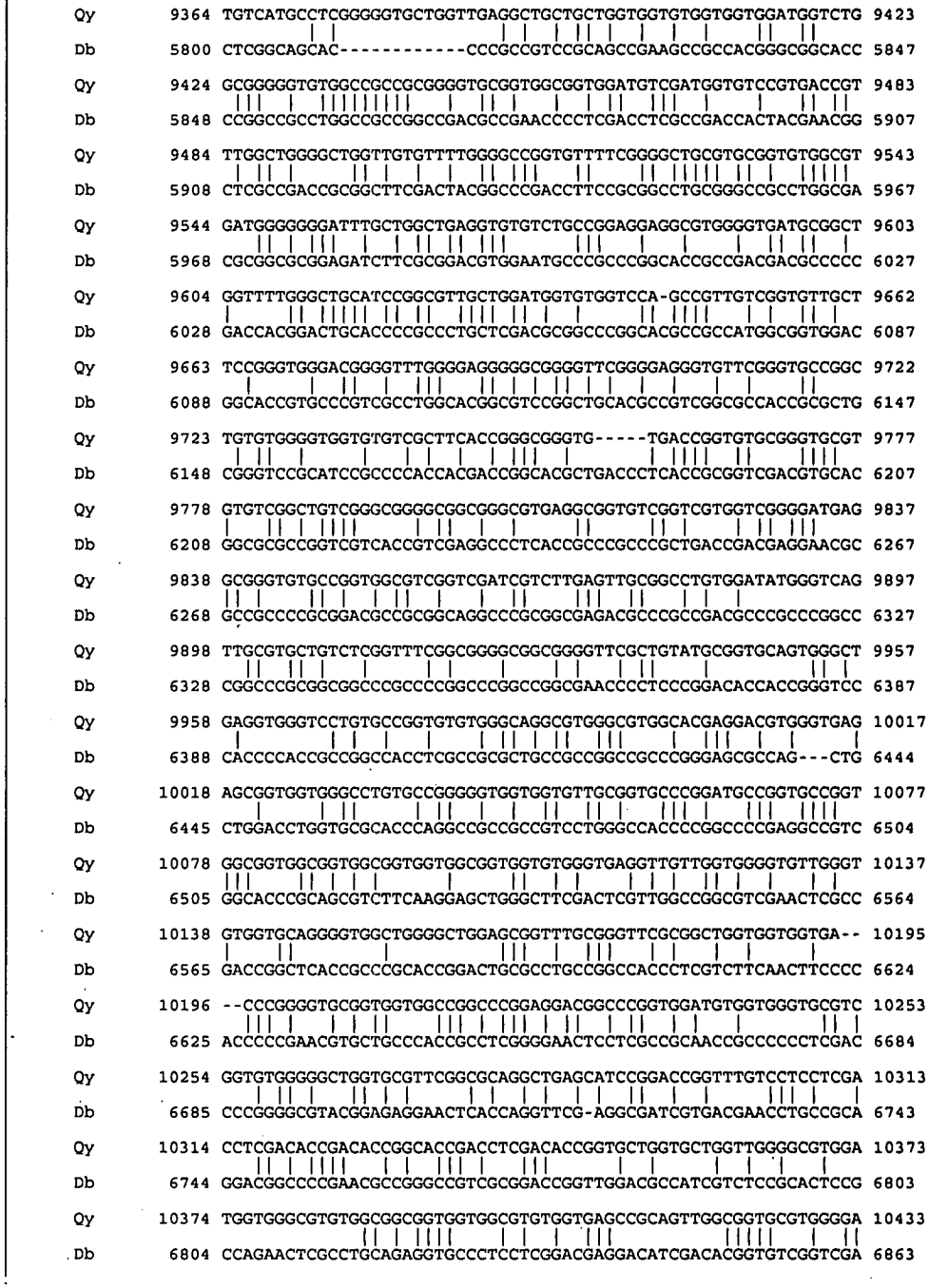







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Qy 12543 TATCTCCTACAACTTCGGGCTCGAAGGCCCTGCGATCACTATCGACACCGCGTGTTCCTC 12602





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CC   The present invention relates to the cloning and sequencing of the gene
CC   cluster encoding a modular type I polyketide synthase (PKS) enzyme
CC   involved in the biosynthesis of the macrolide antibiotic nystatin.
CC   The nystatin PKS is useful as antifungal antibiotics. The present
CC   sequence is a Streptomyces noursei nys1 DNA of nystatin PKS gene cluster.
XX
SQ   Sequence 65140 BP; 8270 A; 25171 C; 22273 G; 9426 T; 0 other;

  Query Match            12.3%;  Score 3788.2;  DB 22;  Length 65140;
  Best Local Similarity  51.4%;  Pred. No. 0;
  Matches 12852;  Conservative    0;  Mismatches 10418;  Indels 1733;  Gaps  108;

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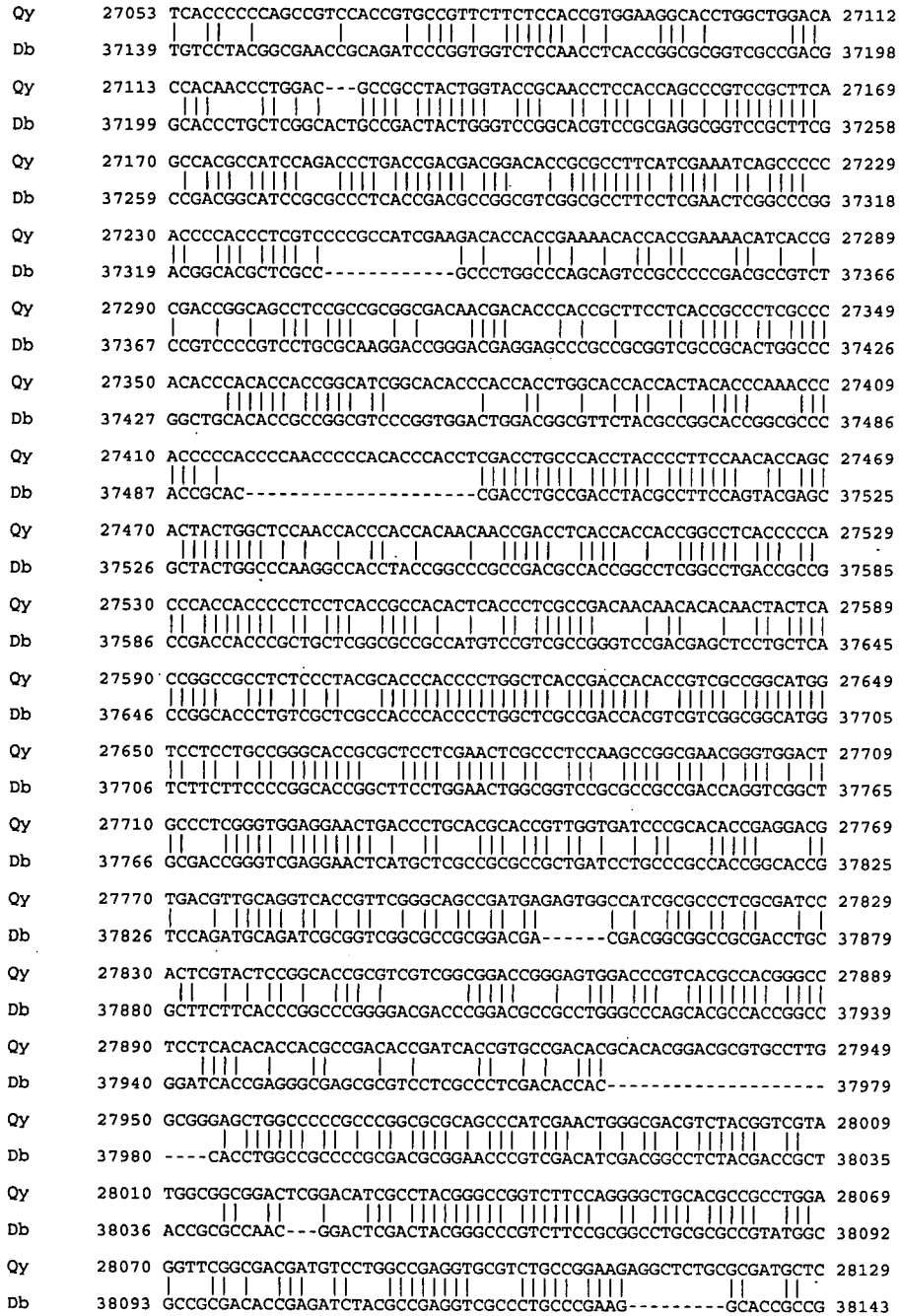
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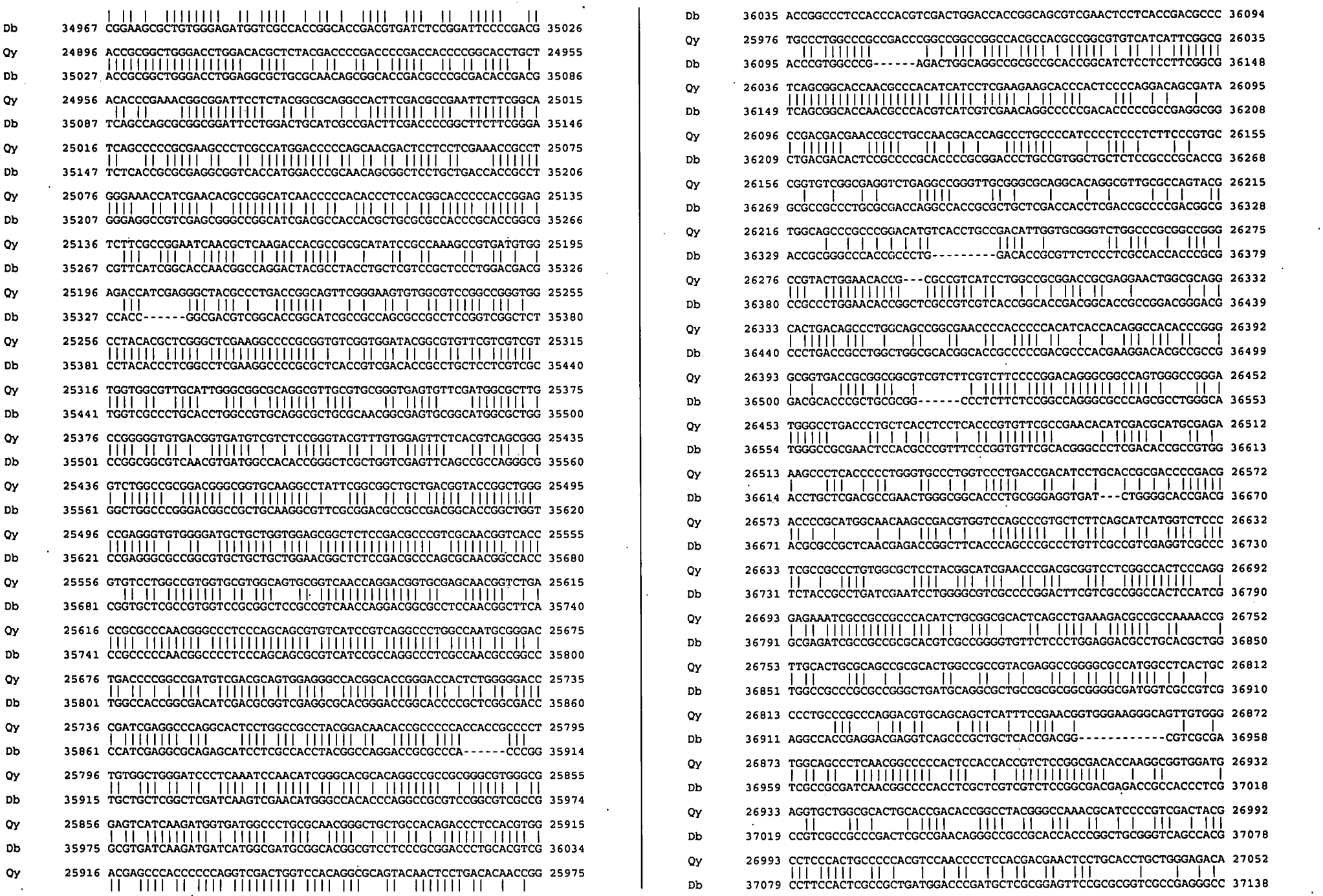
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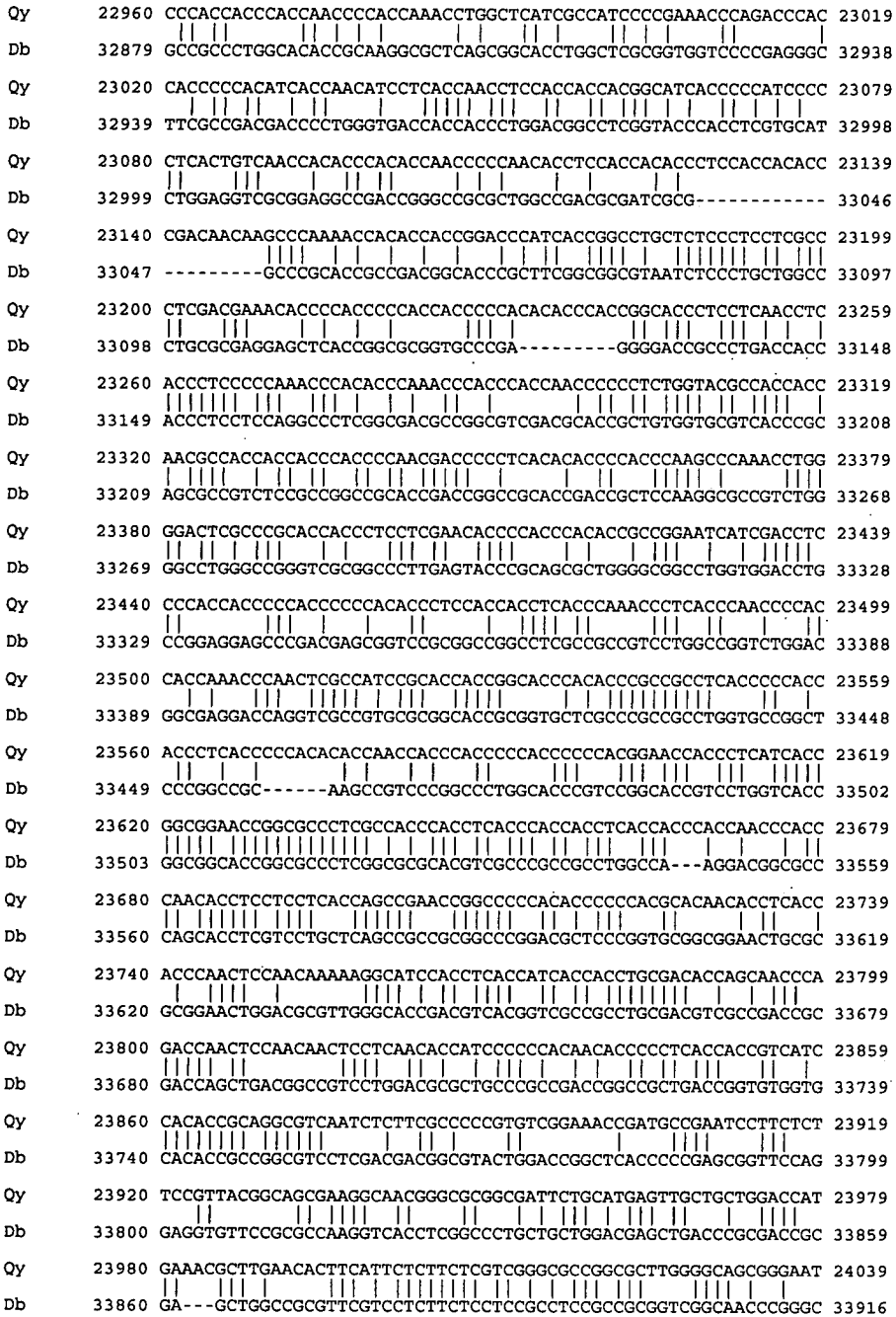
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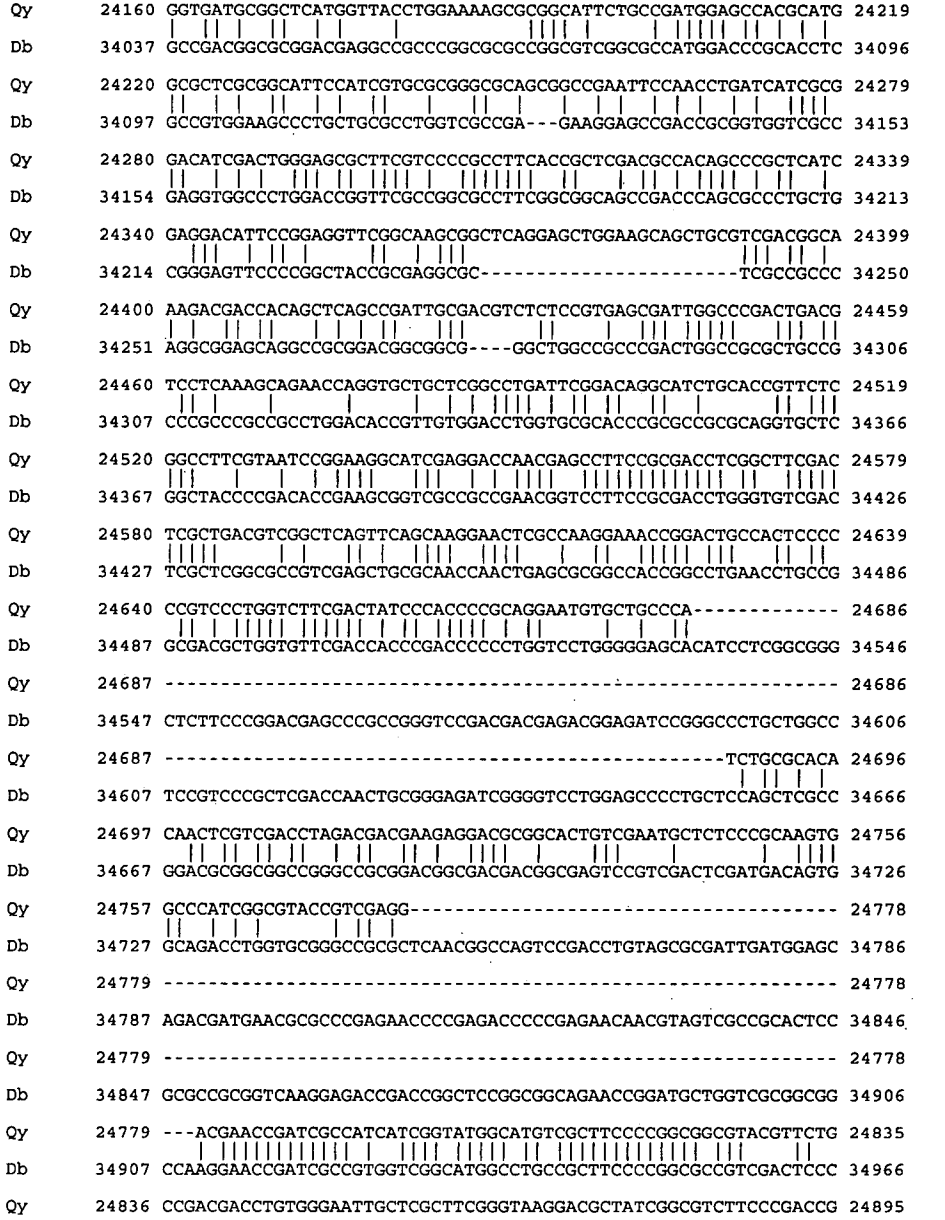
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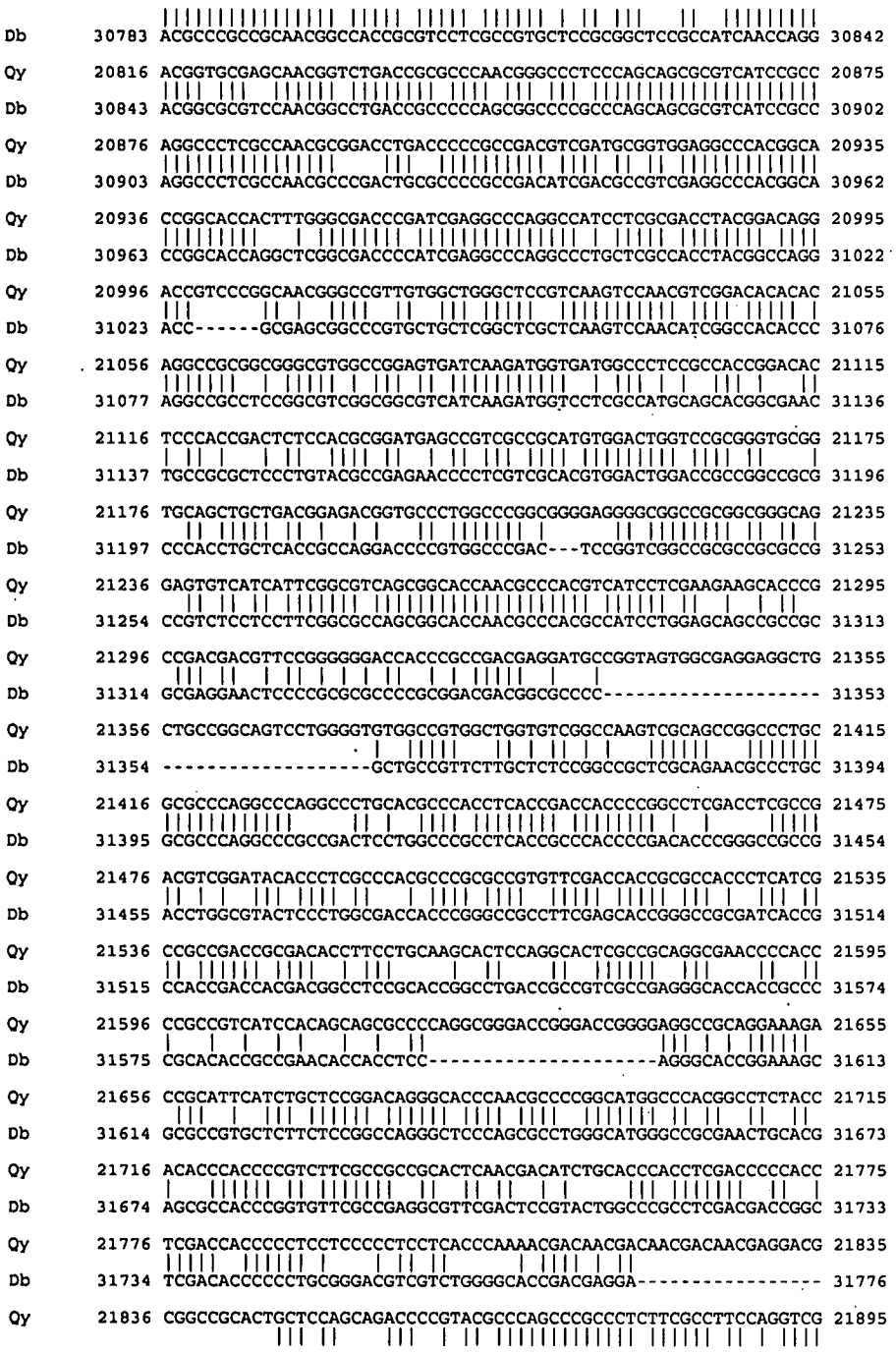

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XX
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XX
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PA   (SNTF ) SINTEF STIFTELSEN IND TEK FORSK.
PA   (ALPH-) ALPHARMA AS.
PA   (SINV-) SINVENT AS.
PA   (DZIE/) DZIEGLEWSKA H.
PA   (ZOTC/) ZOTCHEV S B.
PA   (SEKU/) SEKUROVA O N.
PA   (FJAE/) FJAERVIK E.
PA   (BRAU/) BRAUTASET T.
PA   (STRO/) STROM A R.
XX
PI   Zotchev SB,  Sekurova ON,  Fjaervik E,  Brautaset T,  Strom AR;
PI   Valla S,  Ellingsen TE,  Sletta H,  Gulliksen O;
XX
DR   WPI; 2001-557614/62.
DR   P-PSDB; AAE10125, AAE10126, AAE10127, AAE10128, AAE10129, AAE10130,
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PT   New nystatin polyketide synthase polynucleotides and polypeptides,
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PS   Claim 2; Page 116-151; 266pp; English.
XX
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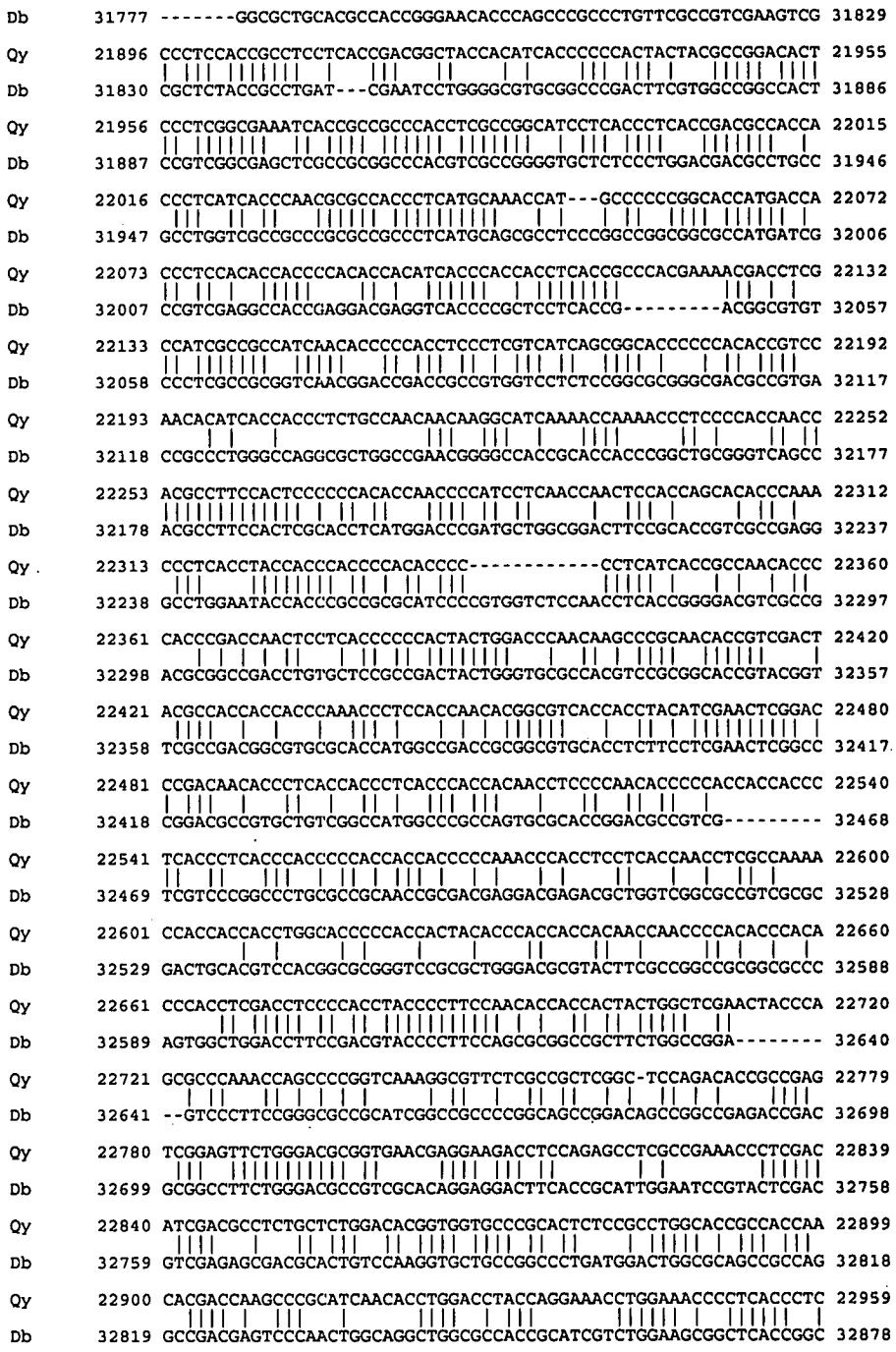

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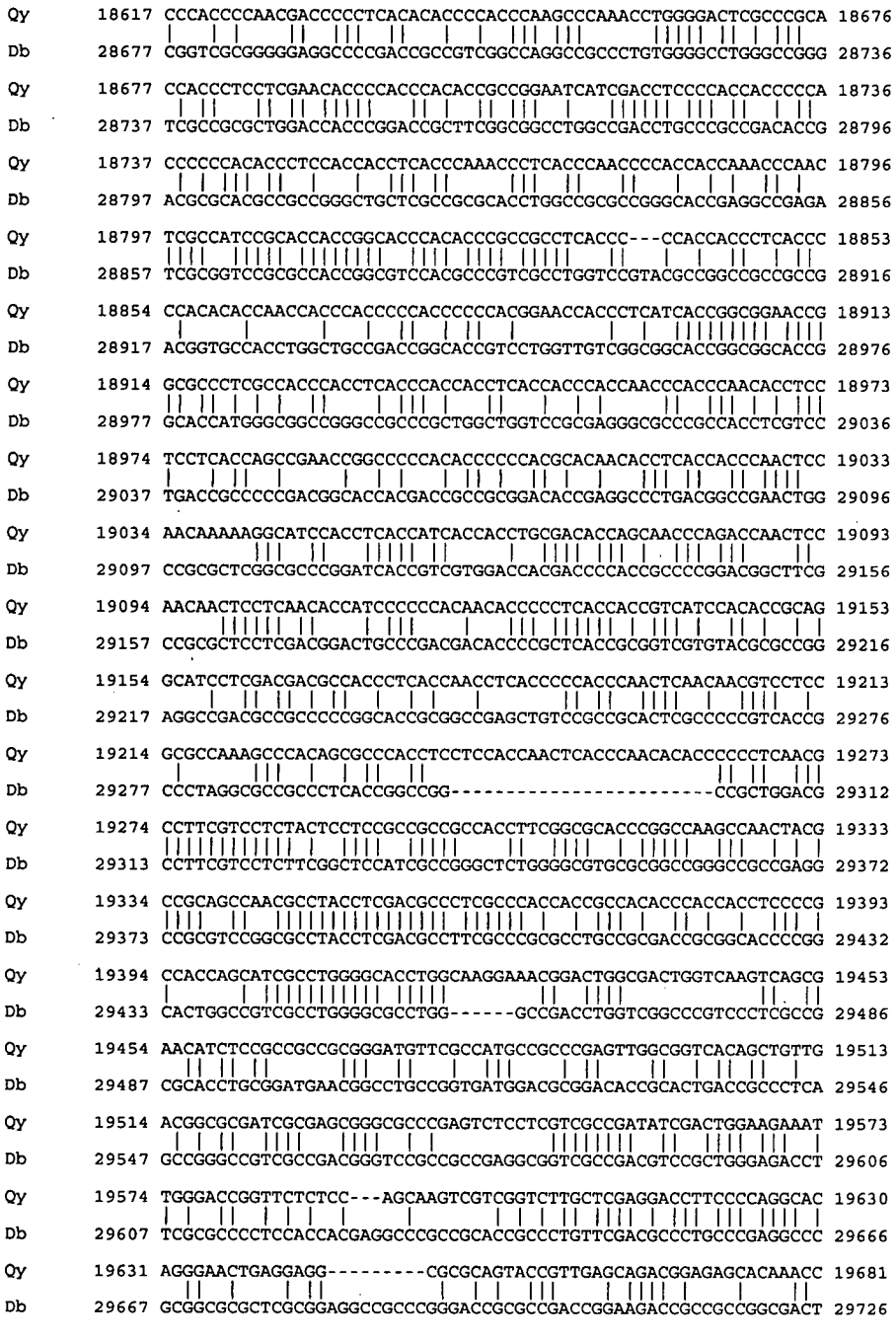


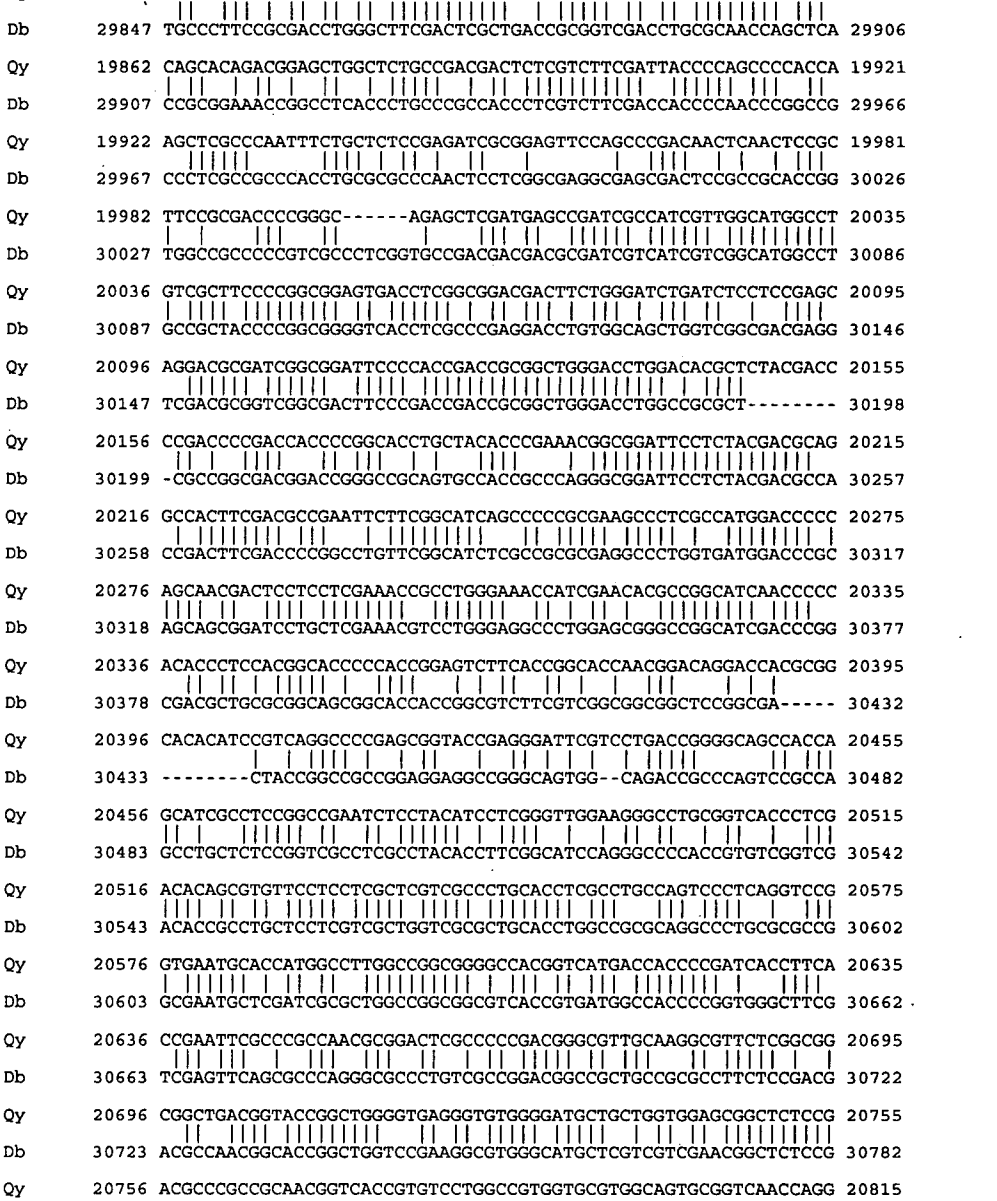


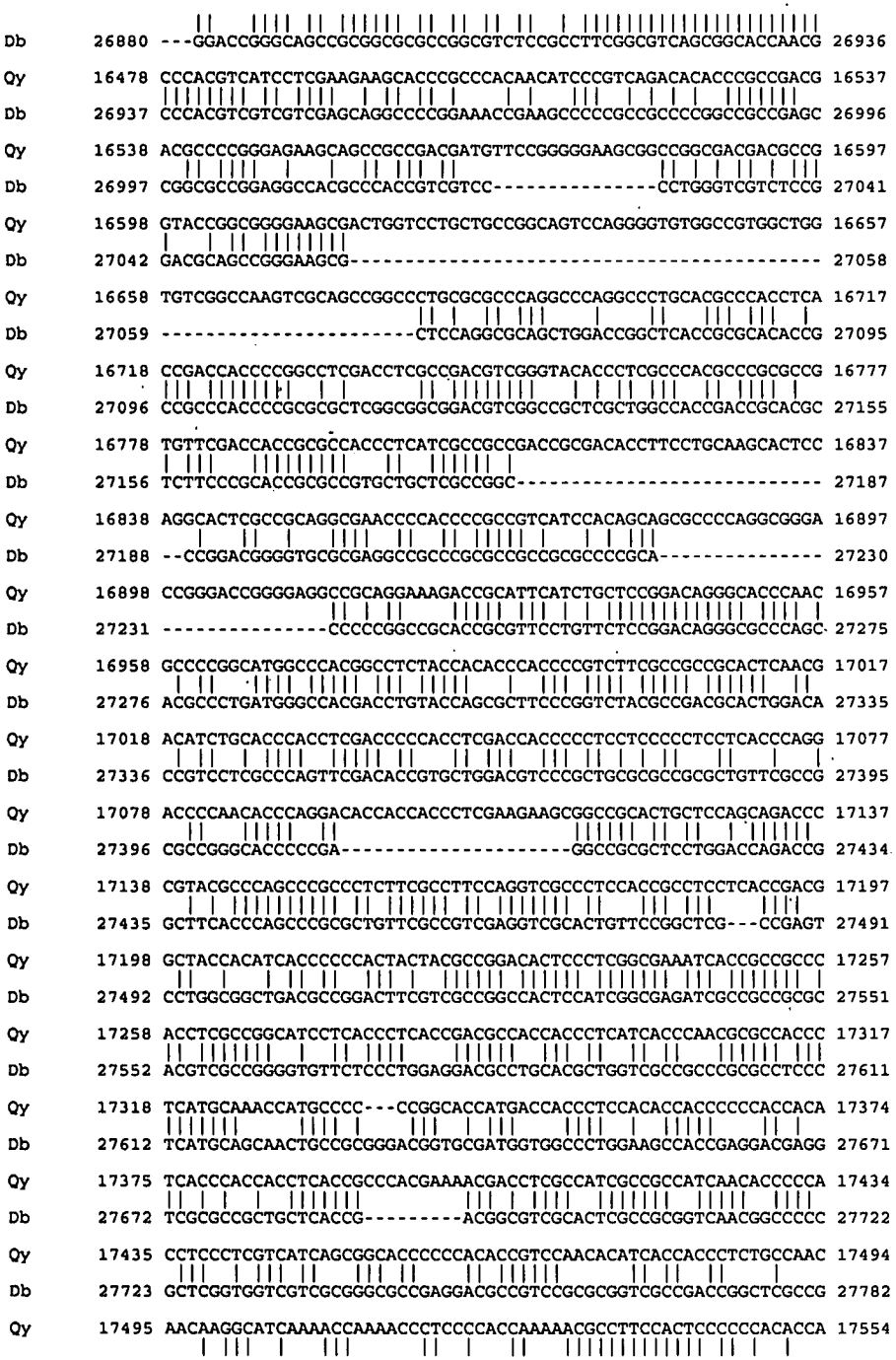


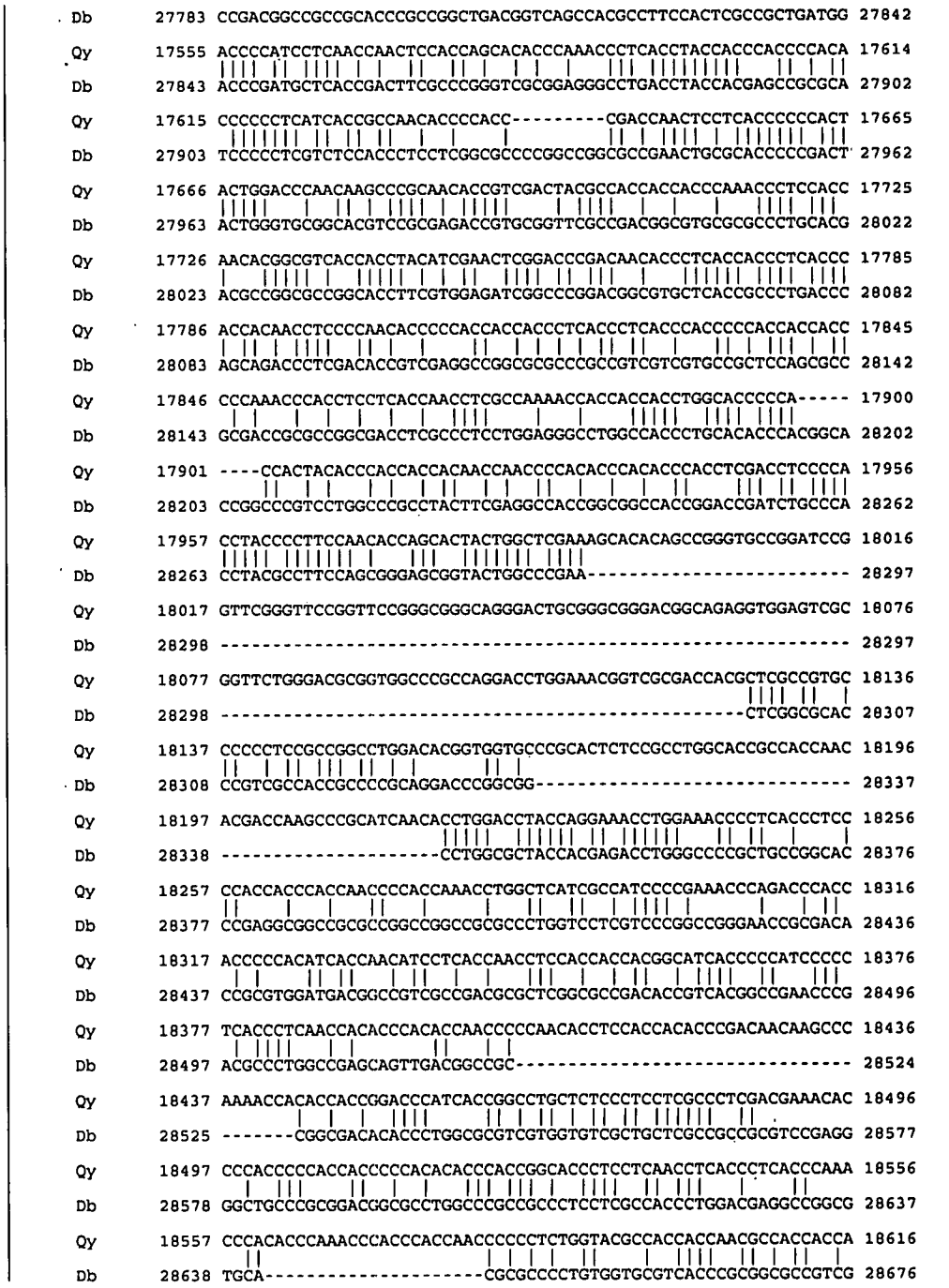

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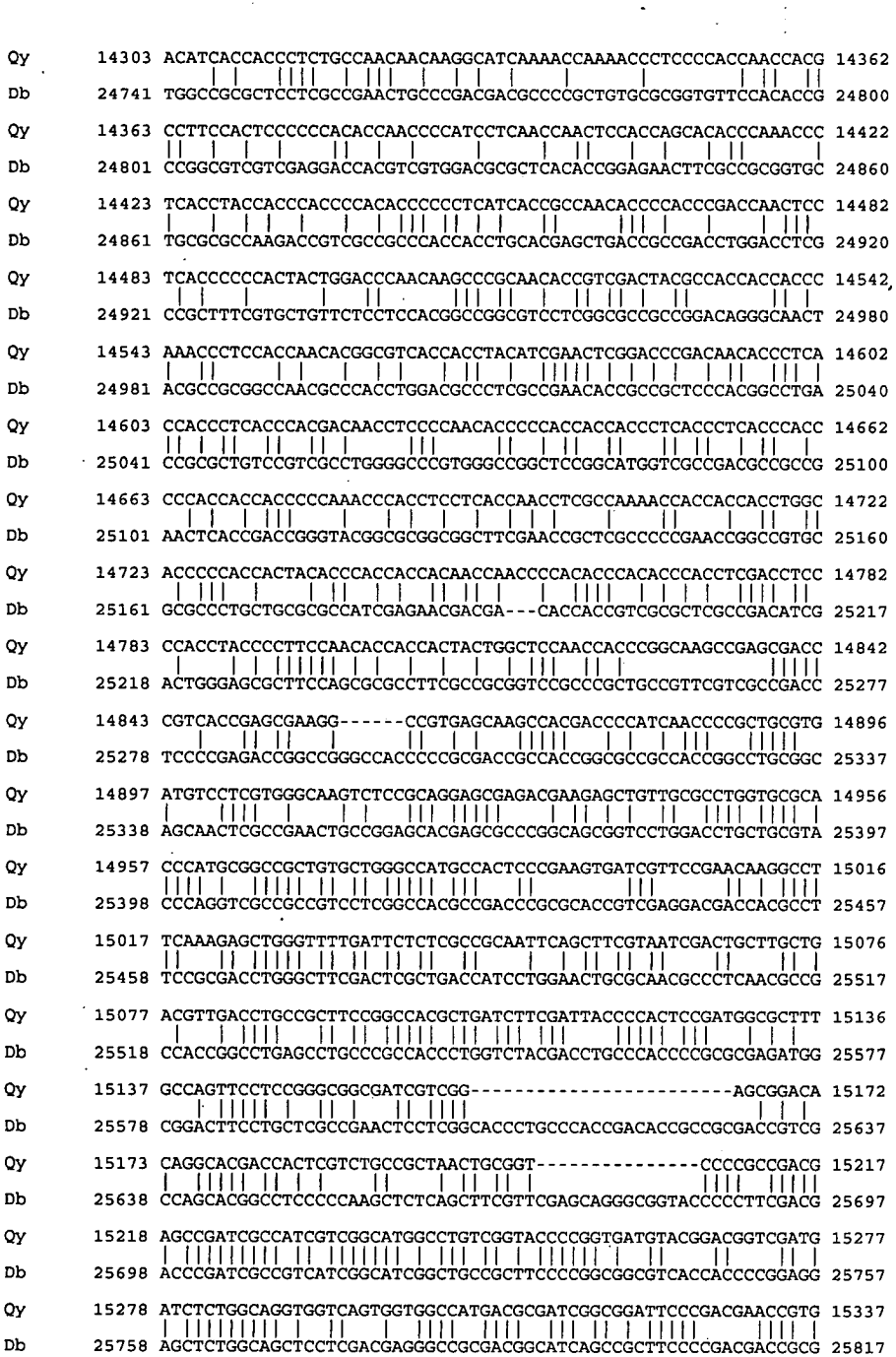

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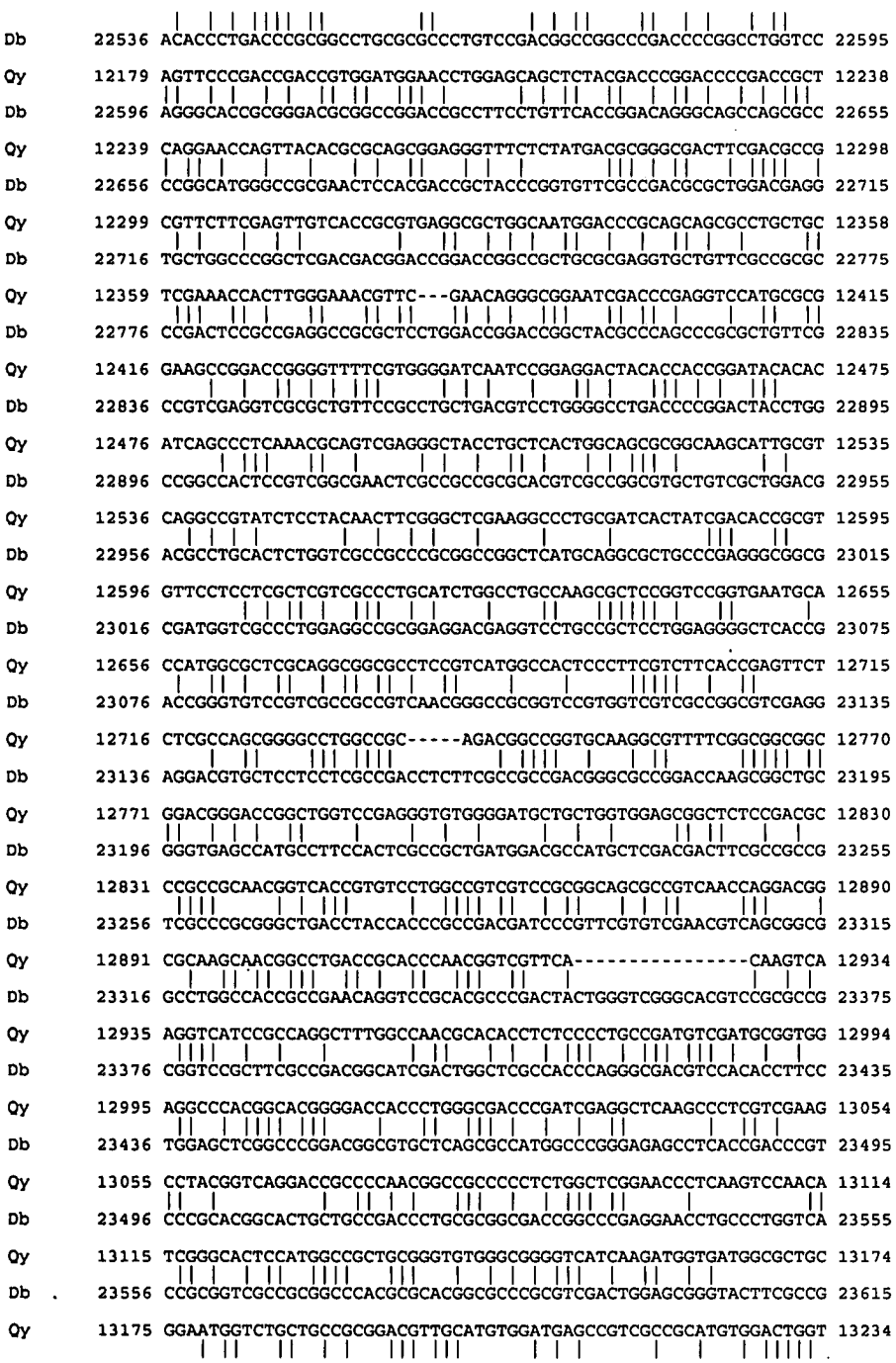


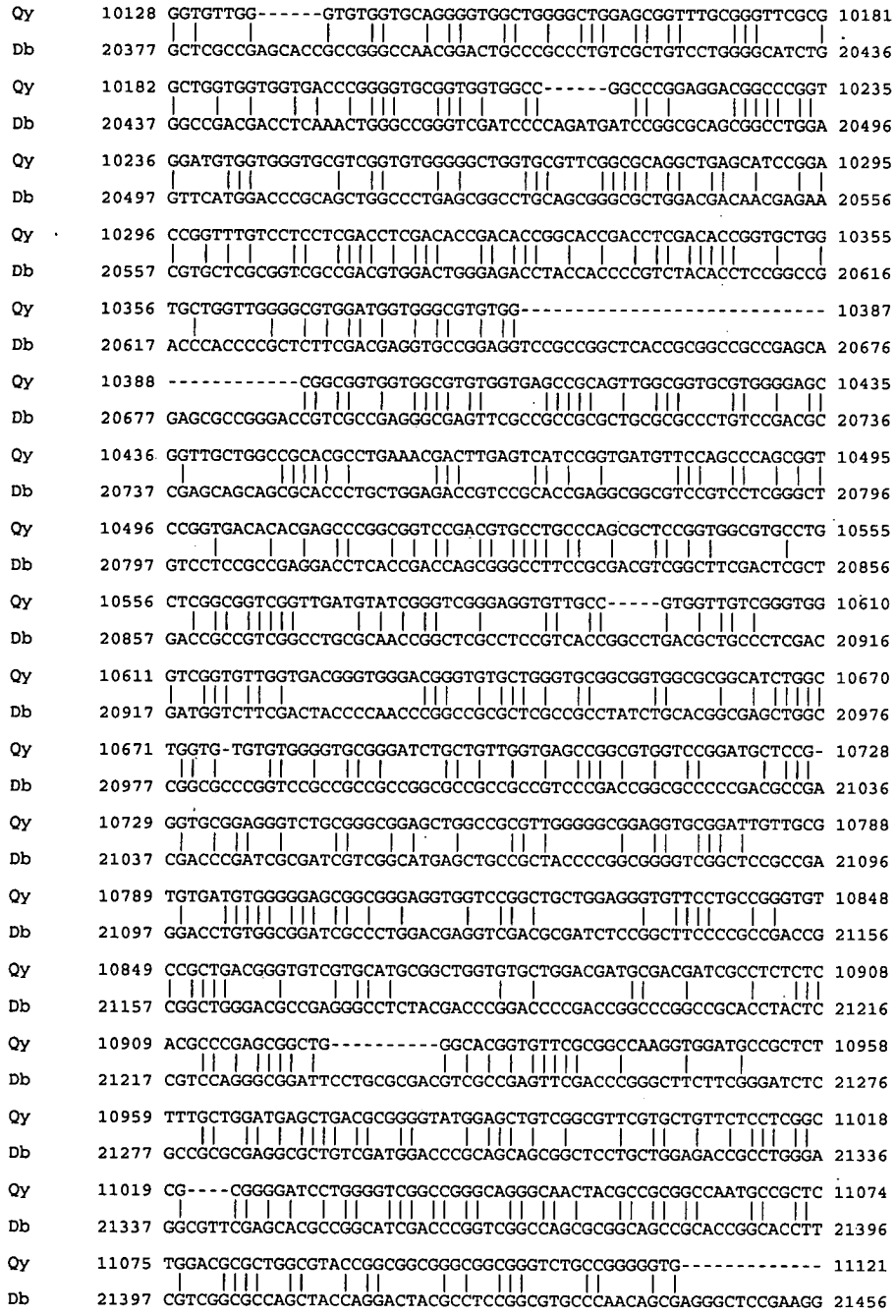


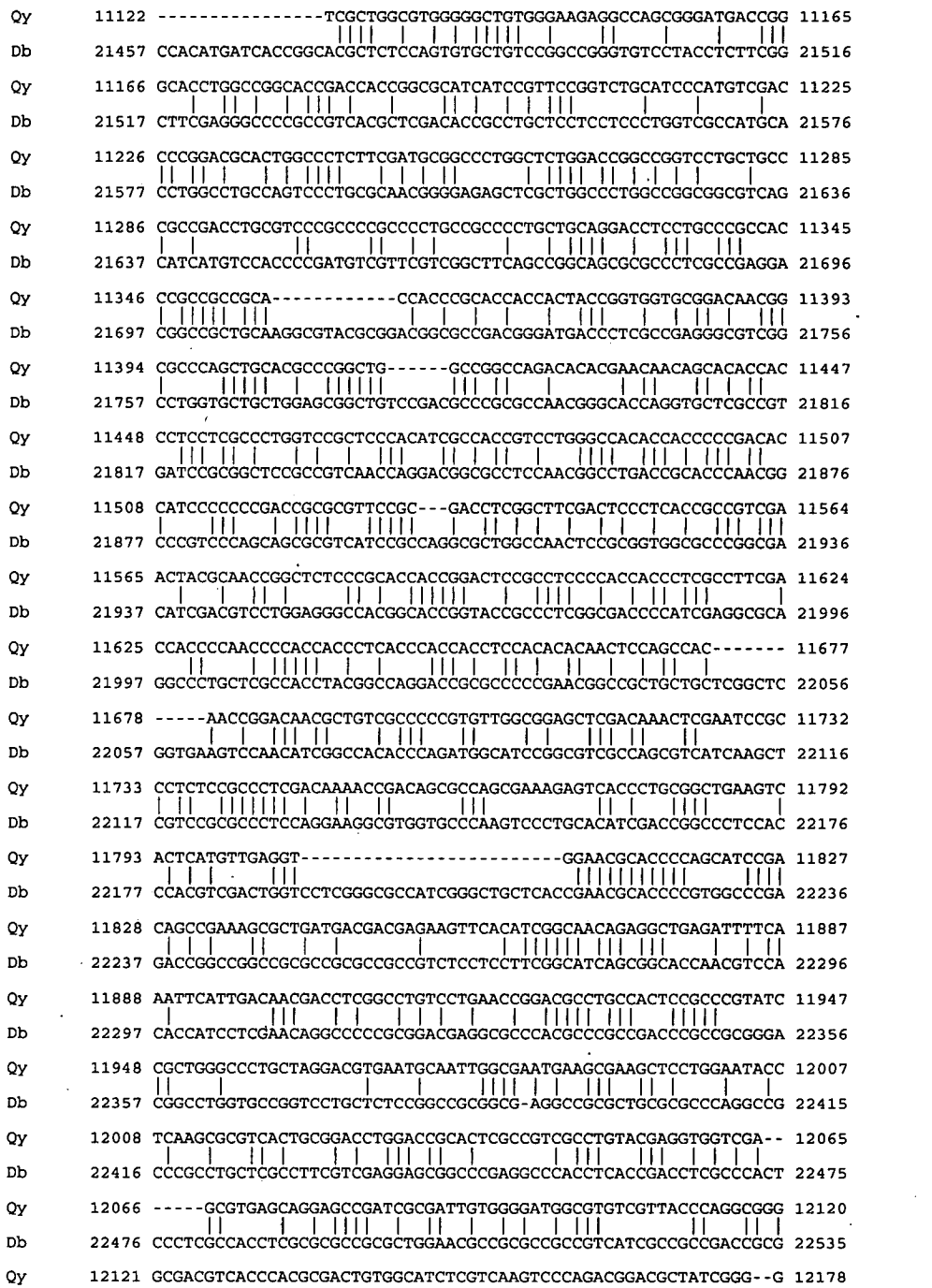


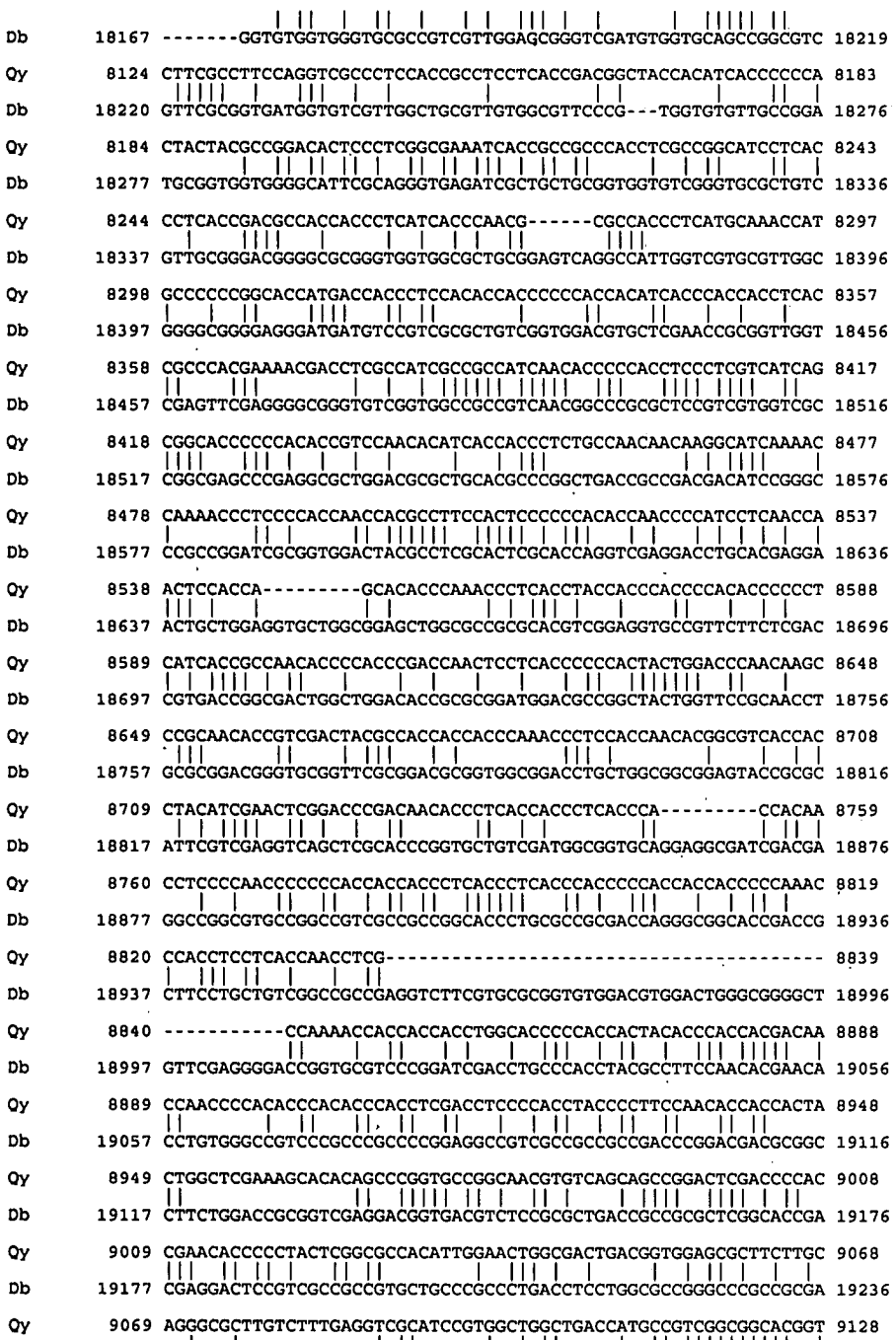


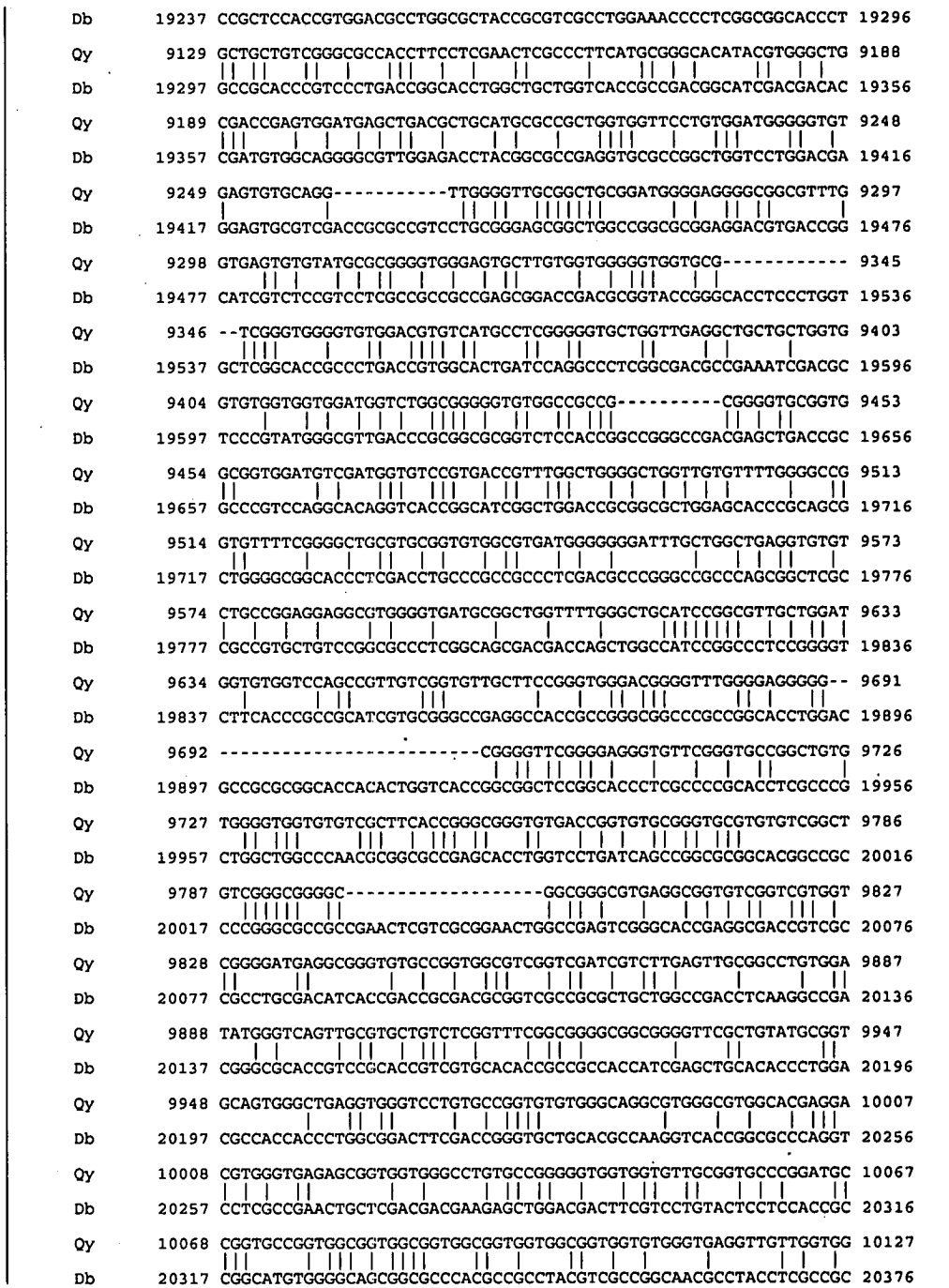

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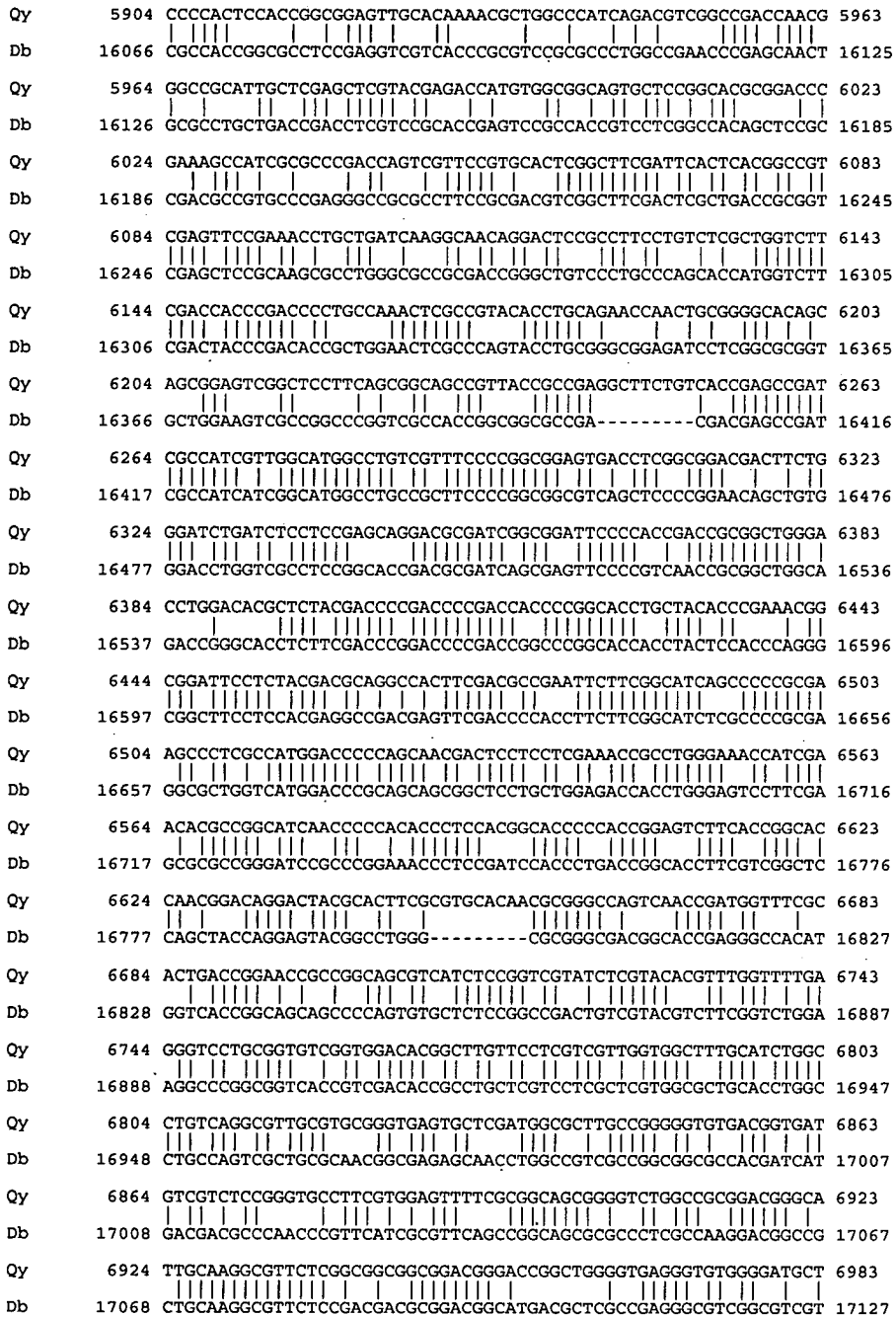

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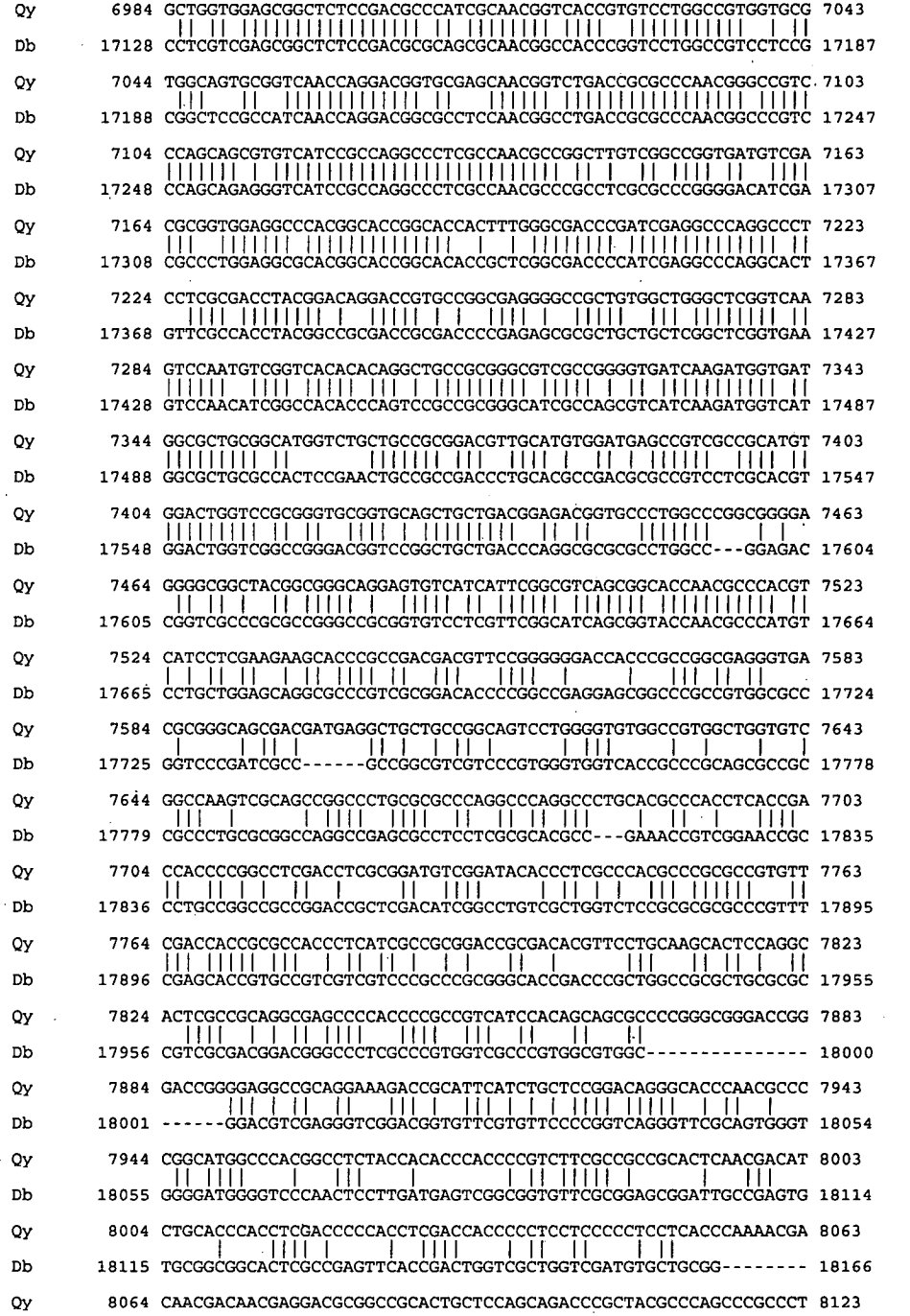


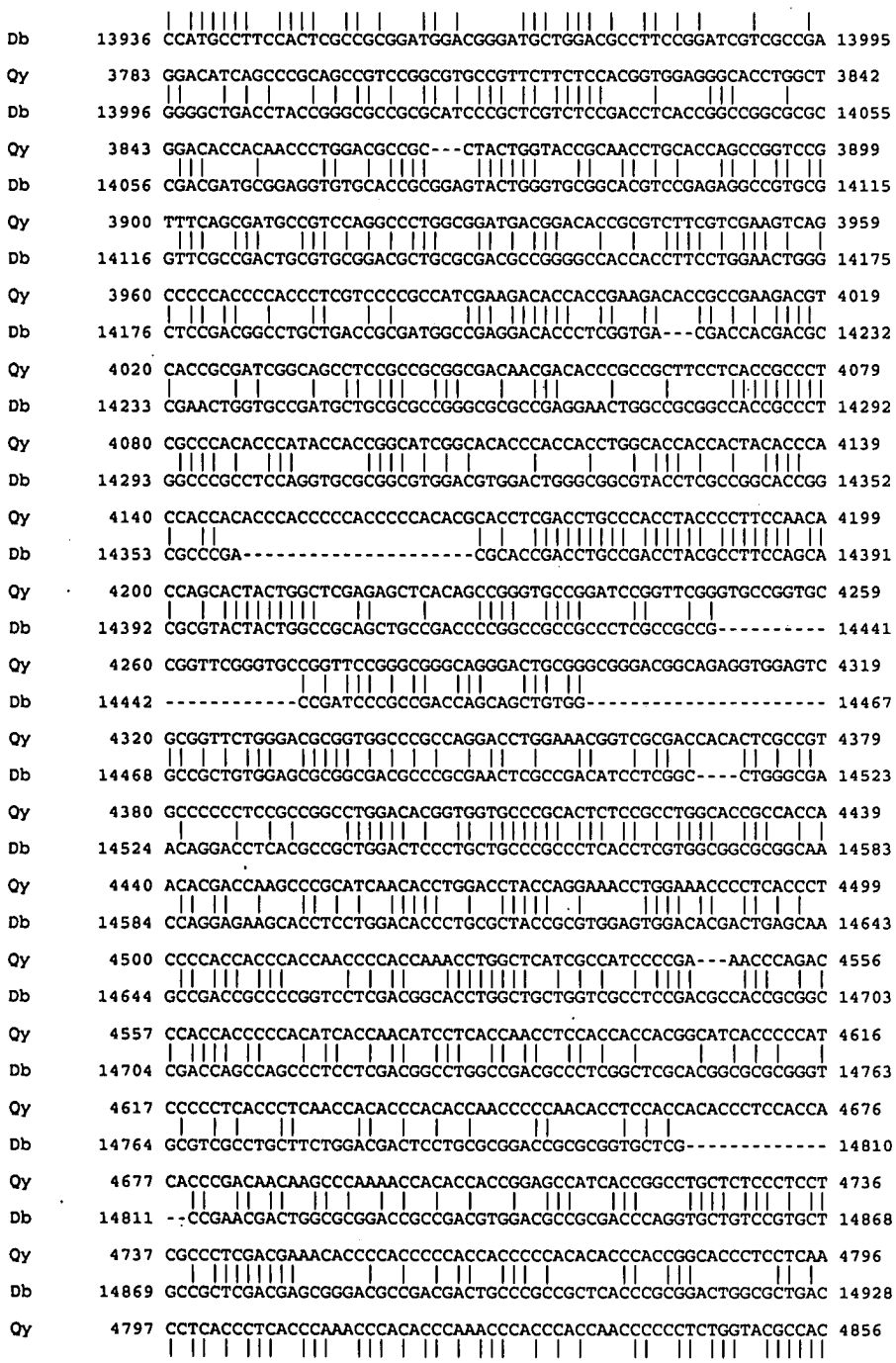


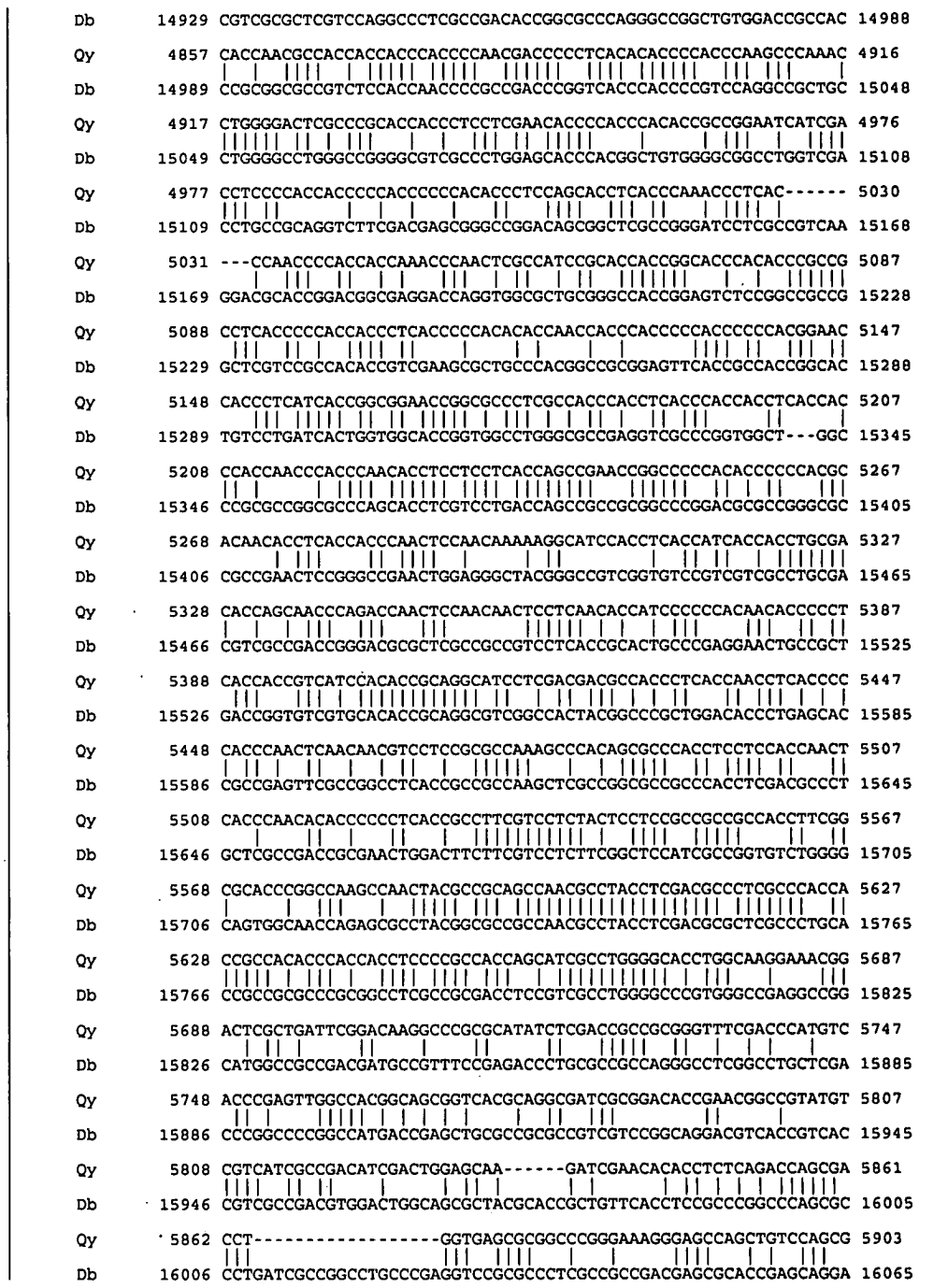


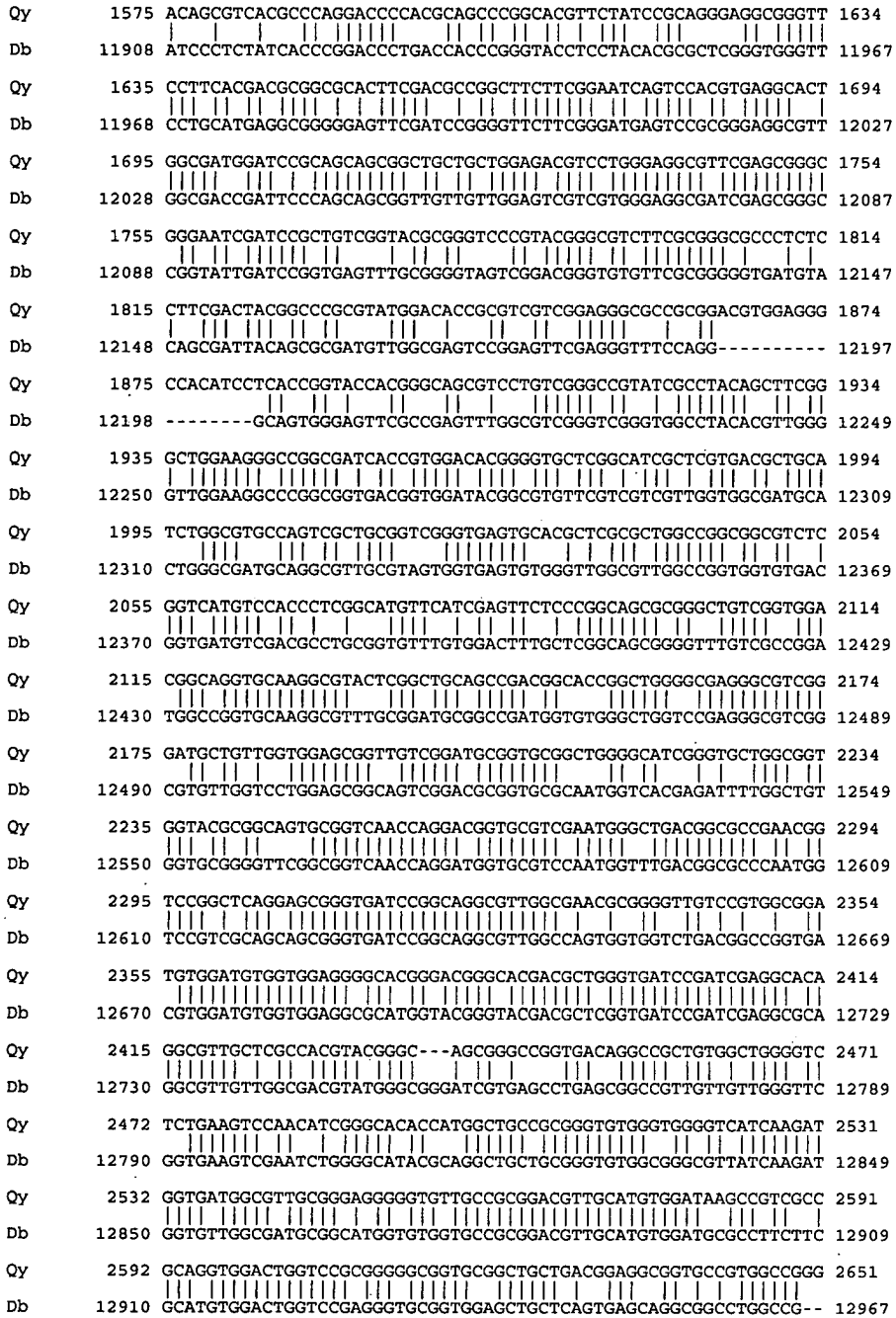



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Db      28507 CAGCACTACTGGCTCCAACCACCCACCACGACAACCGACCTCACCACCACCG 28558


RESULT 7
AAD17186
ID   AAD17186 standard; DNA; 125401 BP.
XX
AC   AAD17186;
XX
DT   29-NOV-2001  (first entry)
XX
DE   Streptomyces noursei nystatin PKS gene cluster DNA.
XX
KW   Polyketide synthase; PKS; macrolide; nystatin; PKS gene cluster;
KW   antifungal; antibiotic; ds.
XX
OS   Streptomyces noursei.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "NysI complete protein"
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FT                   /*tag= b
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XX
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XX
PD   16-AUG-2001.
XX
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XX
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PR   10-APR-2000; 2000GB-0008786.
PR   14-APR-2000; 2000GB-0009387.
XX
PA   (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA   (SNTF ) SINTEF STIFTELSEN IND TEK FORSK.
PA   (ALPH-) ALPHARMA AS.
PA   (SINV-) SINVENT AS.
PA   (DZIE/) DZIEGLEWSKA H.
PA   (ZOTC/) ZOTCHEV S B.
PA   (SEKU/) SEKUROVA O N.
PA   (FJAE/) FJAERVIK E.
PA   (BRAU/) BRAUTASET T.
PA   (STRO/) STROM A R.
XX
PI   Zotchev SB,  Sekurova ON,  Fjaervik E,  Brautaset T,  Strom AR;
PI   Valla S,  Ellingsen TE,  Sletta H,  Gulliksen O;
XX
DR   WPI; 2001-557614/62.
DR   P-PSDB; AAE10143, AAE10144, AAE10145, AAE10146, AAE10147, AAE10148,
DR   AAE10149, AAE10150.
XX
PT   New nystatin polyketide synthase polynucleotides and polypeptides,
PT   useful as antibiotics and antifungals -
XX
PS   Claim 1; Page 188-254; 266pp; English.
XX
CC   The present invention relates to the cloning and sequencing of the gene
CC   cluster encoding a modular type I polyketide synthase (PKS) enzyme
CC   involved in the biosynthesis of the macrolide antibiotic nystatin.
CC   The nystatin PKS is useful as antifungal antibiotics. The present
CC   sequence is a Streptomyces noursei nystatin PKS gene cluster DNA.
XX
SQ   Sequence 125401 BP; 15664 A; 49692 C; 42871 G; 17174 T; 0 other;

  Query Match             14.2%;  Score 4347.6;  DB 22;  Length 125401;
  Best Local Similarity   51.4%;  Pred. No. 0;
  Matches 15336;  Conservative    0;  Mismatches 12354;  Indels 2136;  Gaps  144;

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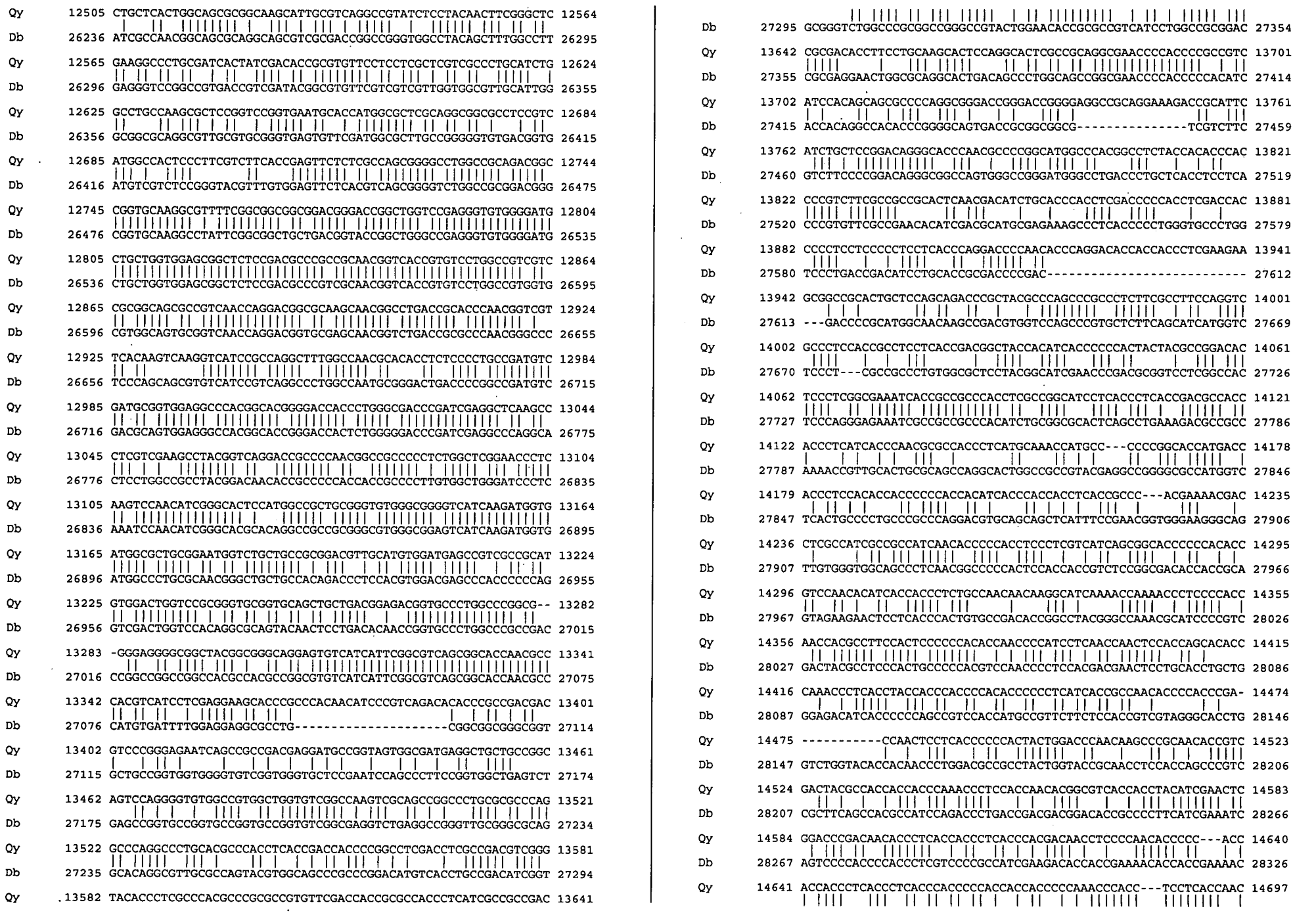
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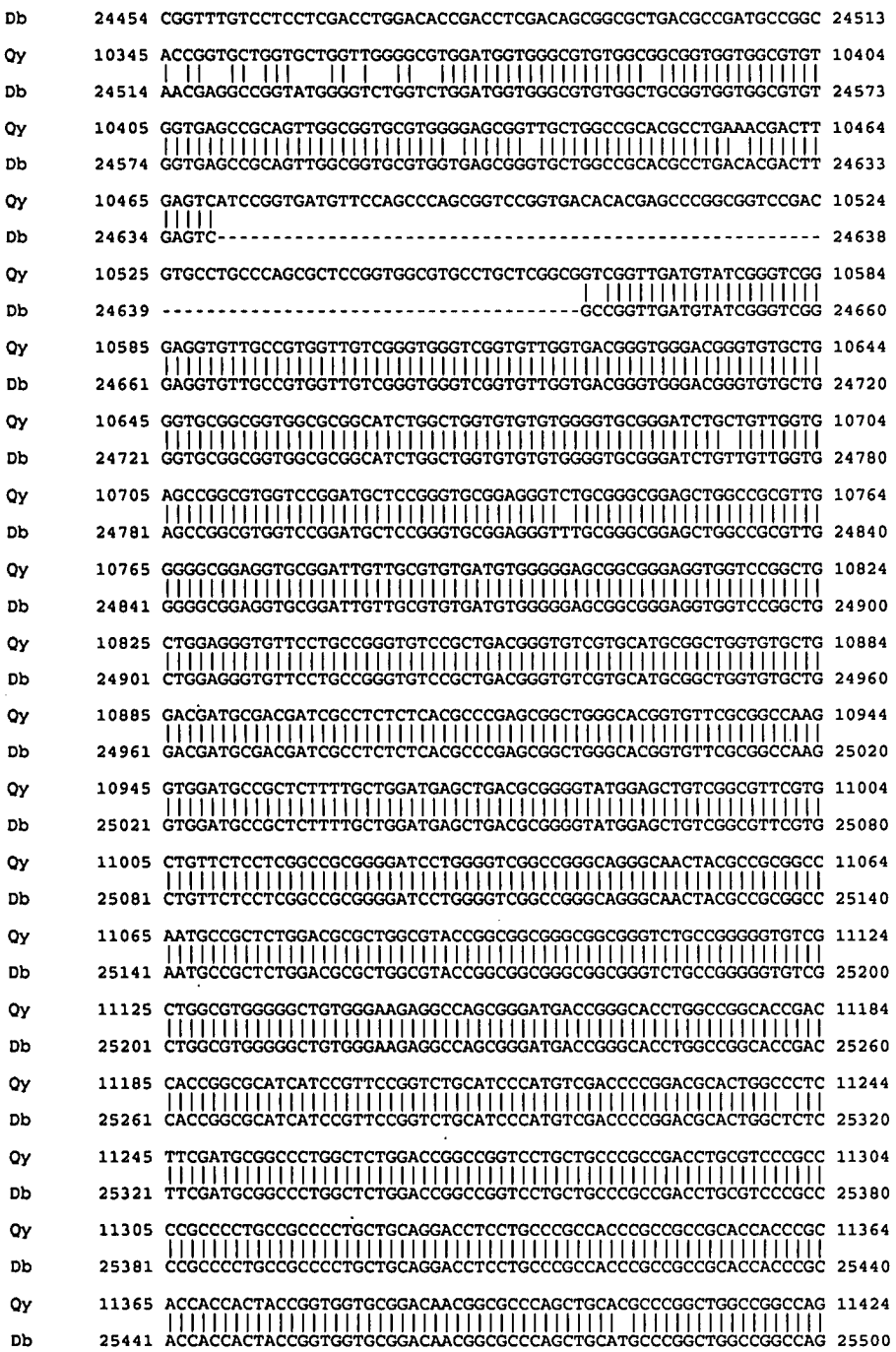
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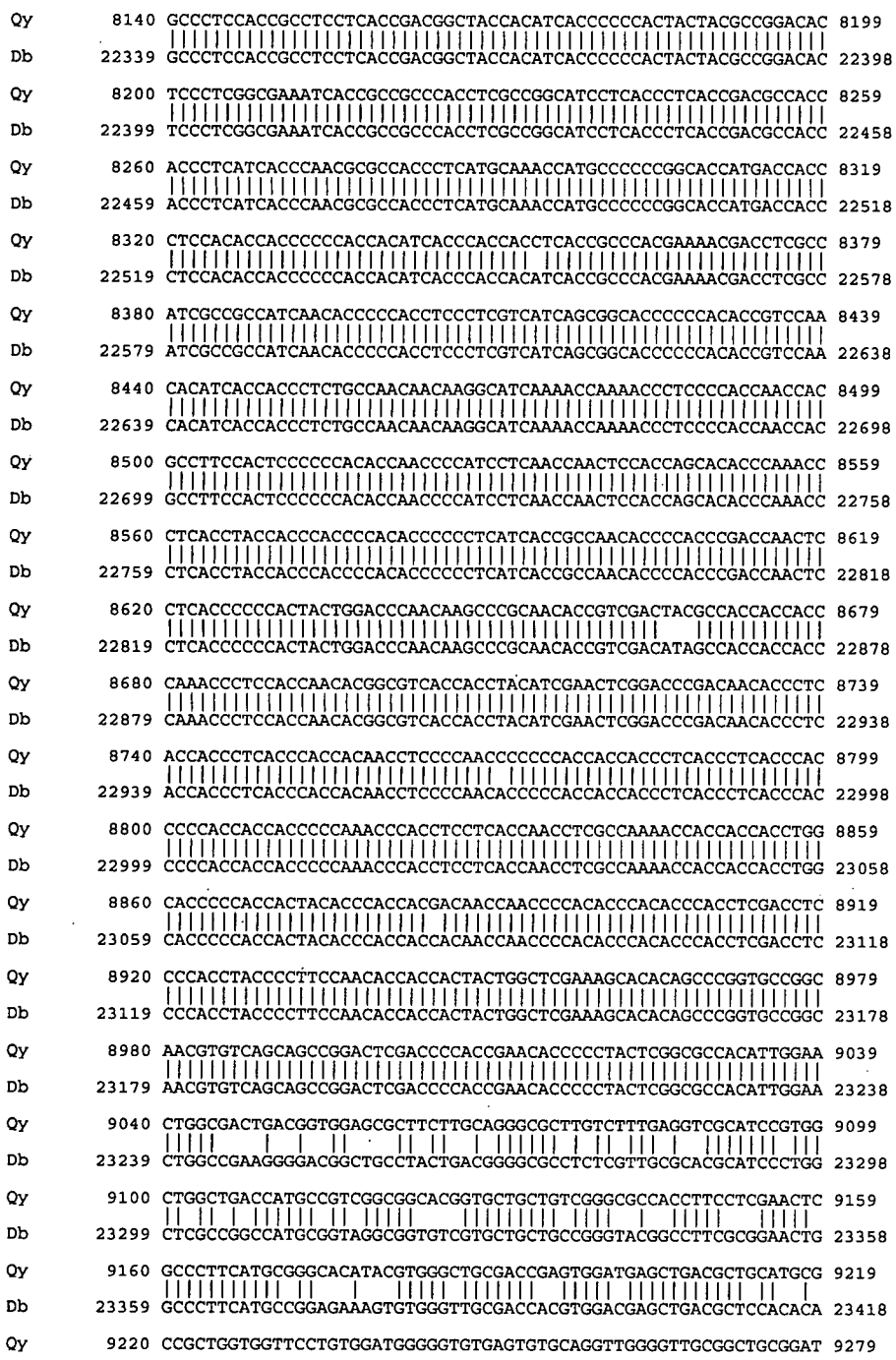
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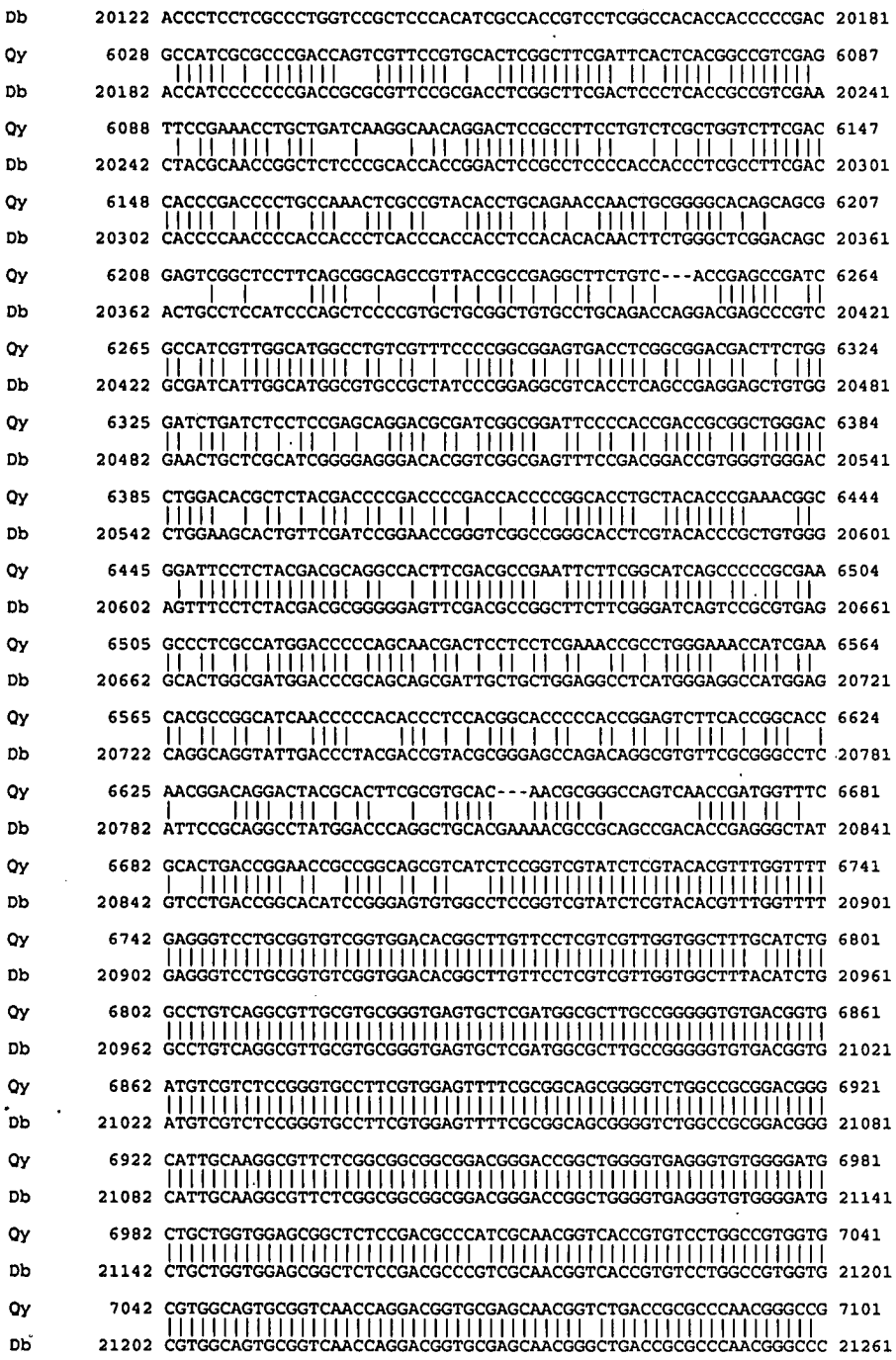
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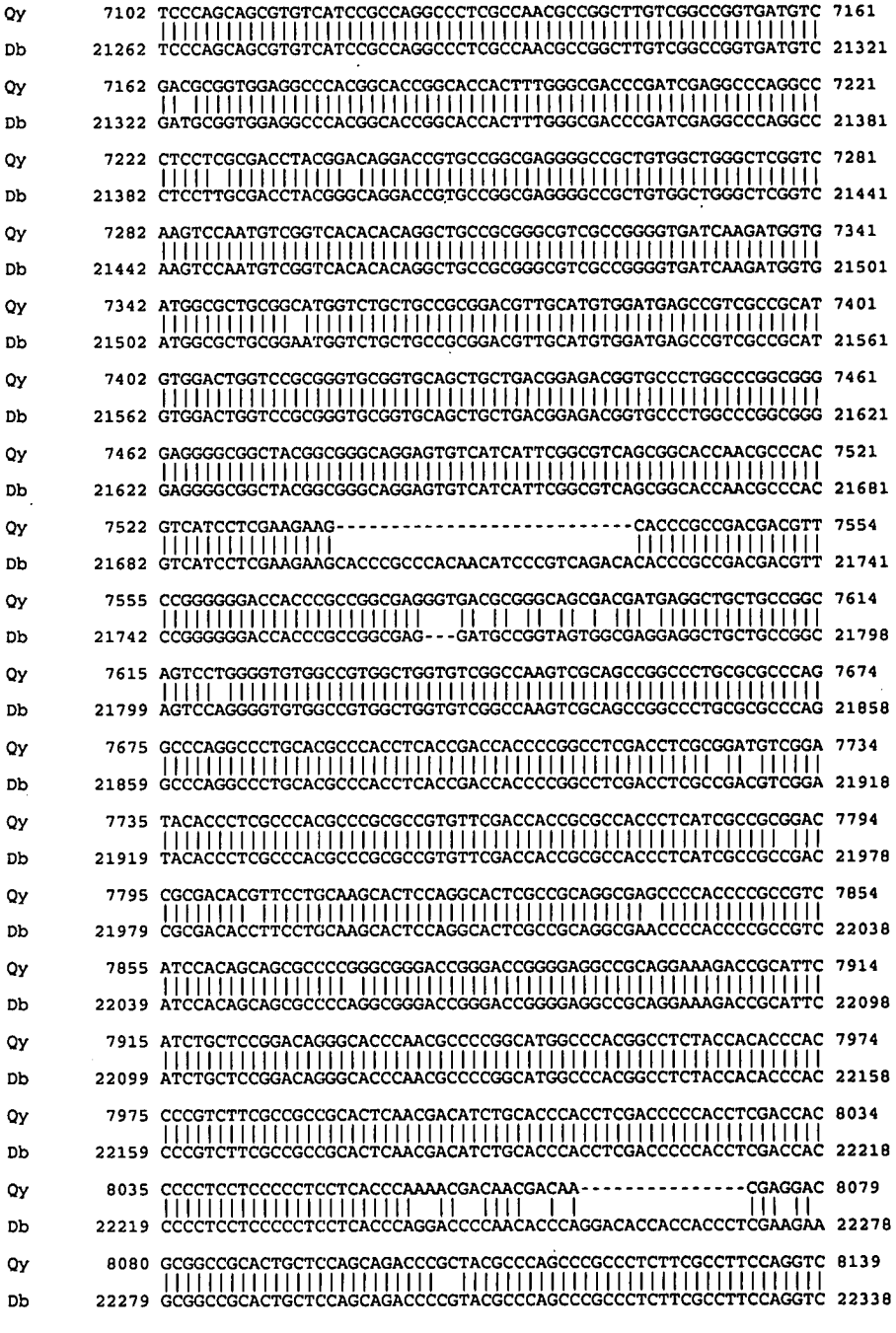
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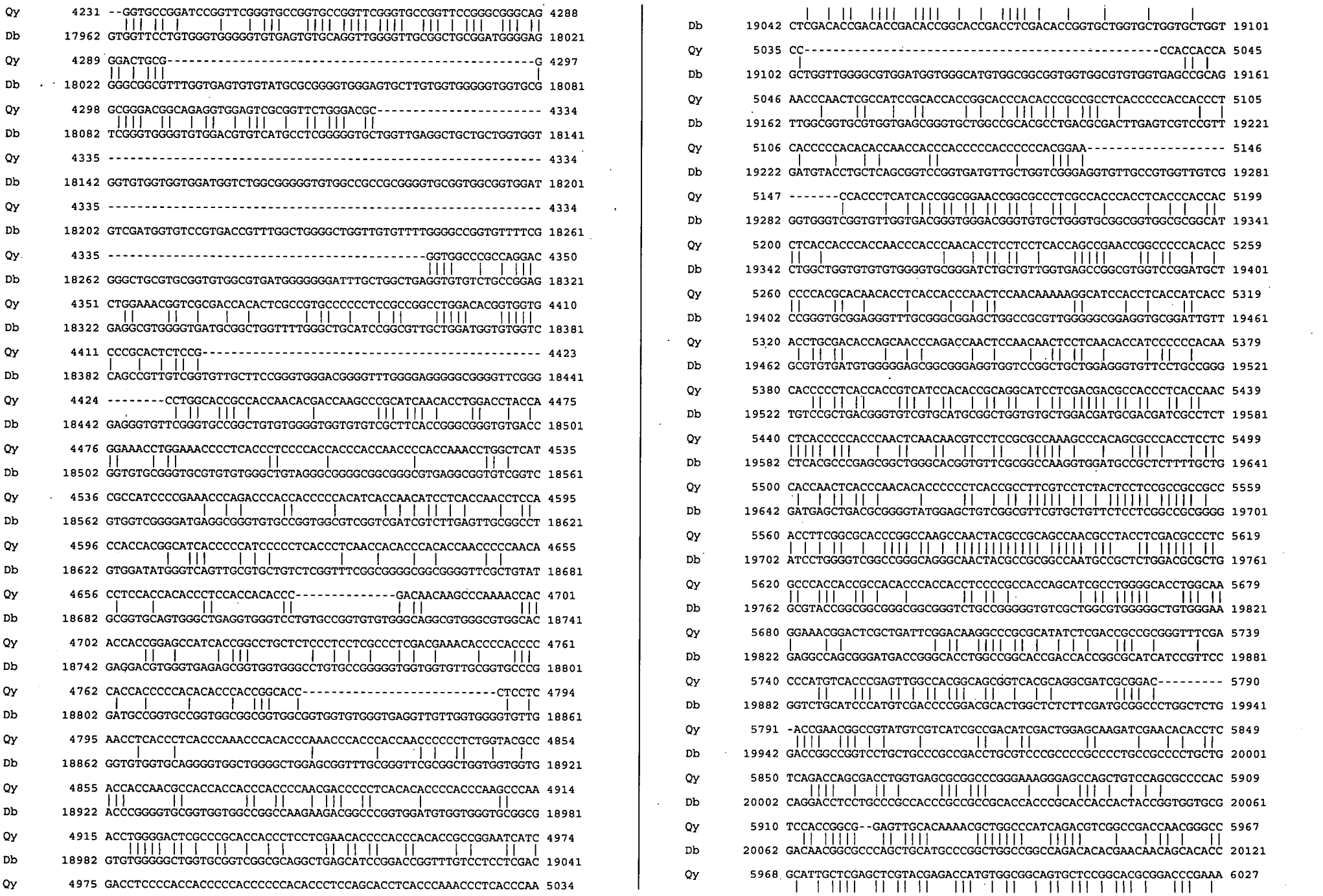


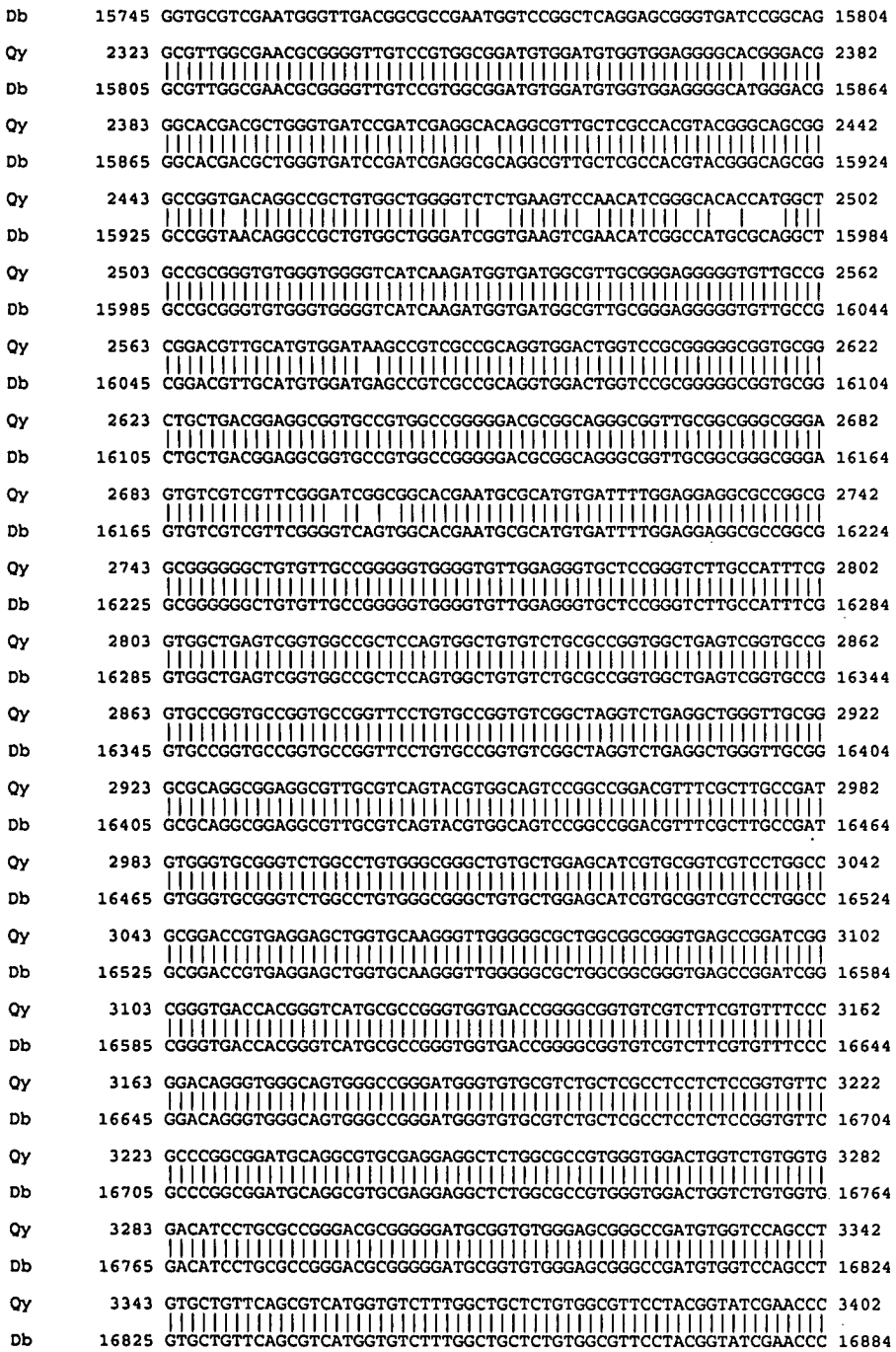

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Qy 10885 GACGATGCGACGATCGCCTCTCTCACGCCCGAGCGGCTGGGCACGGTGTTCGCGGCCAAG 10944
Db 24961 GACGATGCGACGATCGCCTCTCTCACGCCCGAGCGGCTGGGCACGGTGTTCGCGGCCAAG 25020
Qy 10945 GTGGATGCCGCTCTTTTGCTGGATGAGCTGACGCGGGGTATGGAGCTGTCGGCGTTCGTG 11004
Db 25021 GTGGATGCCGCTCTTTTGCTGGATGAGCTGACGCGGGGTATGGAGCTGTCGGCGTTCGTG 25080
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RESULT 6
AAH79278
ID AAH79278 standard; DNA; 31422 BP.
XX
AC AAH79278;
XX
DT 04-DEC-2001 (first entry)
XX
DE Streptomyces avermitilis coding sequences SEQ ID NO: 2.
XX
KW Avermectin aglycone synthase; AAS; avermectin derivative;
KW drug production; vetinary drug; pesticide; ds.
XX
OS Streptomyces avermitilis.
XX
FH Key Location/Qualifiers
FT CDS 1..14646
FT /*tag= a
FT /product= "AAG65266"
FT CDS 14824..31422
FT /*tag= b
FT /product= "AAG65267"
XX
PN WO200162939-A1.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-JP01381.
XX
PR 24-FEB-2000; 2000JP-0047405.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (KITA) KITASATO INST.
XX
PI Endo H, Yamaguchi H, Kanda Y, Hashimoto S, Omura S, Ikeda H;
XX
DR WPI; 2001-582053/65.
DR P-PSDB; AAG65266, AAG65267.
XX
PT New modified avermectin aglycone synthase derived from Streptomyces
PT avermectilis used in production of 22,23-dihydroavermectin B1a used in
PT drugs and pesticides -
XX
PS Disclosure; Page 103-149; 257pp; Japanese.
XX
CC The present invention relates to the production of modified derivatives
CC of avermectin aglycone synthase (AAS) derived from Streptomyces
CC avermitilis. The activity of an acyl carrier protein (ACP),
CC beta-ketoacyl carrier protein synthase (KS), acyltransferase (AT),
CC beta-ketoacyl carrier protein reductase (KR), dehydratase (DH), enoyl
CC reductase (ER) and/or thioesterase (TE) domain may be reduced or
CC suppressed. The process can be used in the production of drugs, vetinary
CC drugs and pesticides. The present sequence is a fragment of the S.
CC avermitilis genome.
XX
SQ Sequence 31422 BP; 4136 A; 10237 C; 11677 G; 5372 T; 0 other;

Query Match 21.0%; Score 6437.2; DB 22; Length 31422;
Best Local Similarity 69.9%; Pred. No. 0;
Matches 9934; Conservative 0; Mismatches 2928; Indels 1350; Gaps 39;

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Db      15277 TCCCGTACGGGTGTCTTCGCCGGGGTGATGTACCACGACTACGGATCCCGCCTGGGTACC 15336

Qy       1843 GCGTCGTCGGAGGGCGCCGCGGACGTGGAGGGCCACATCCTCACCGGTACCACGGGCAGC 1902

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Qy       1903 GTCCTGTCGGGCCGTATCGCCTACAGCTTCGGGCTGGAAGGGCCGGCGATCACCGTGGAC 1962

Db      15385 GTCGCGTCGGGCCGCGTCGCCTACACGCTCGGTCTCGAGGGCCCTGCCGTCTCGGTGGAC 15444

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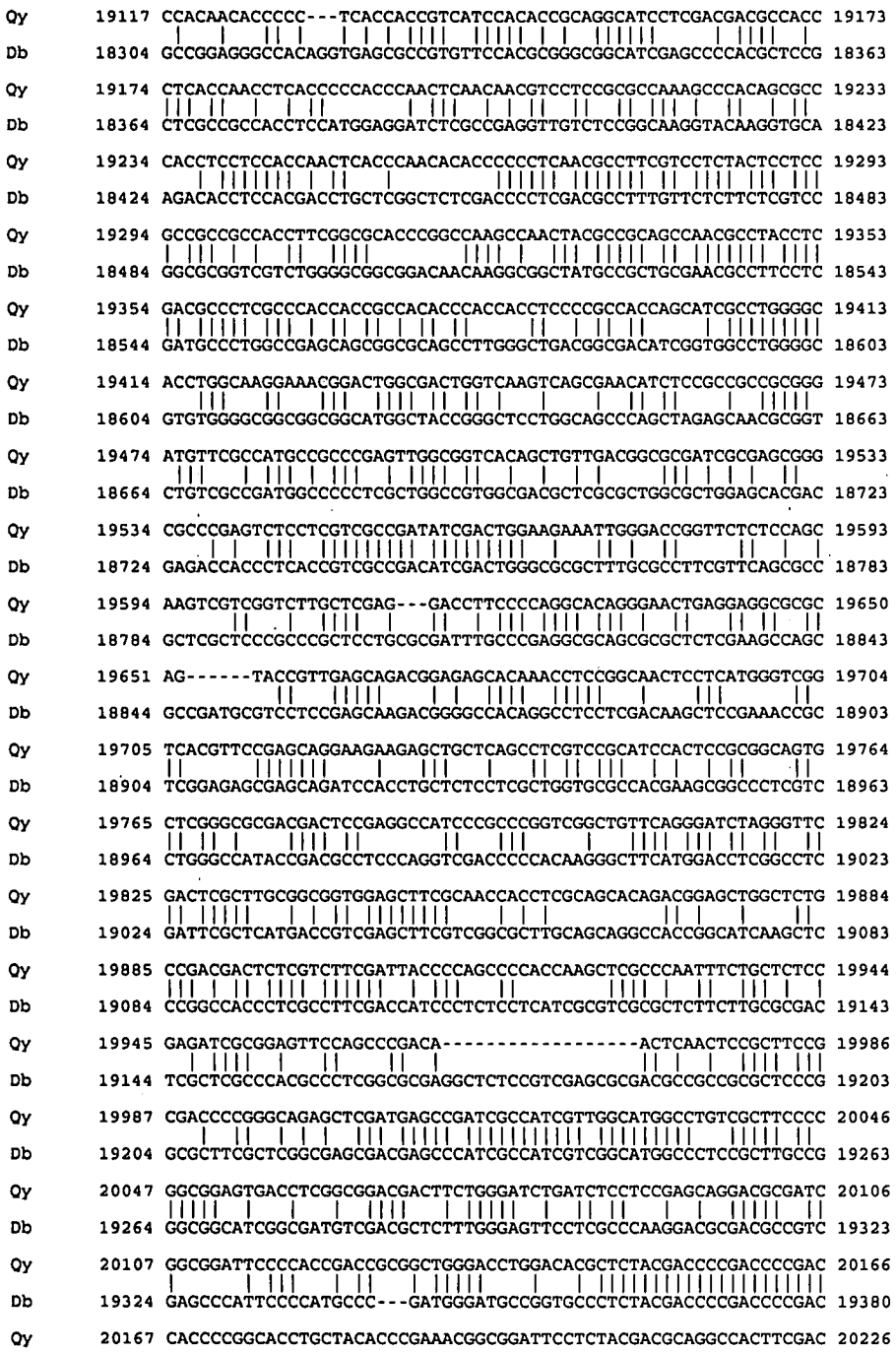
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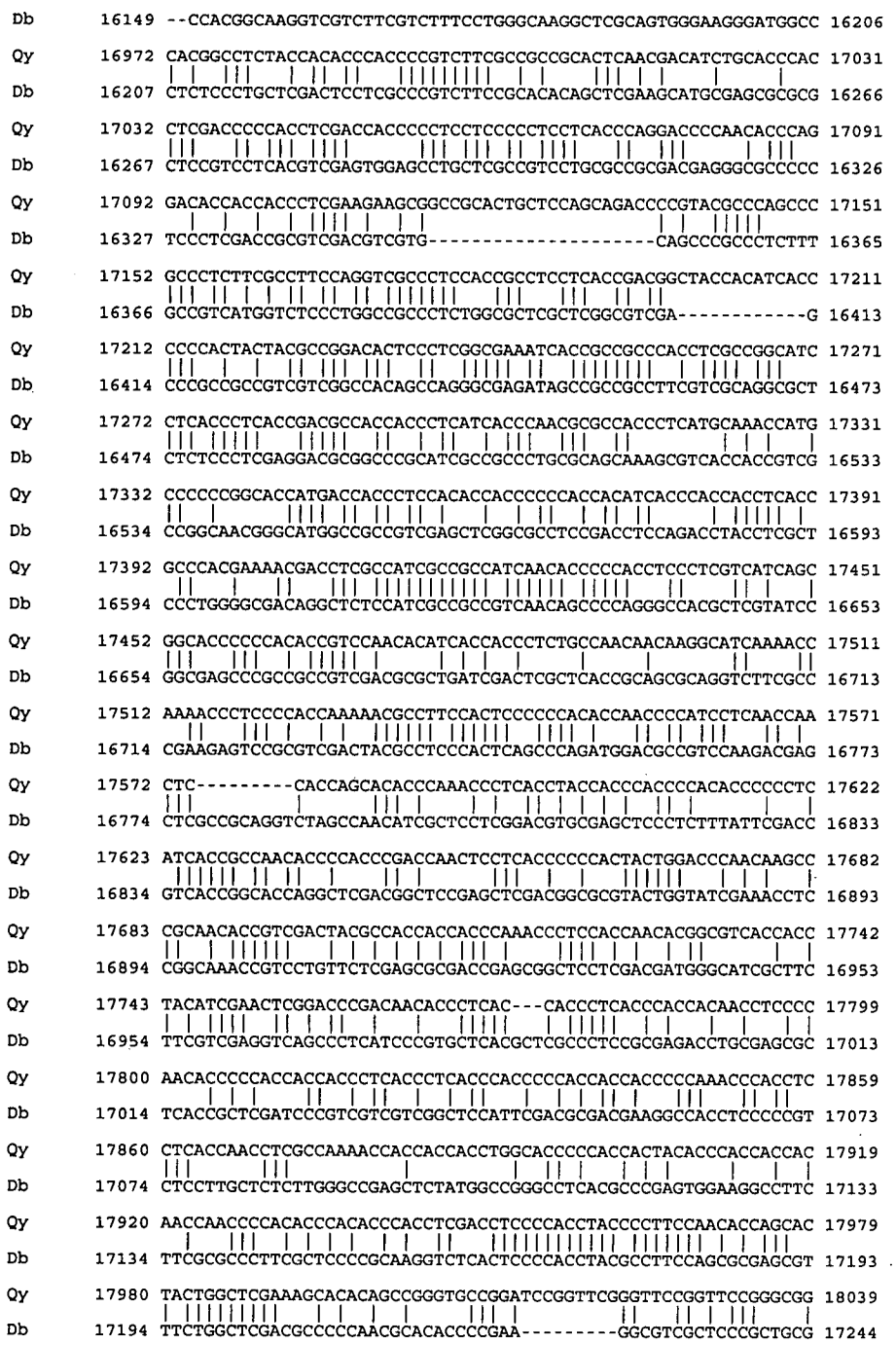
Db      15625 GCCGACGGCACCGGCATGGGCGAGGGCGTCGGGATGCTGTTGGTGGAGCGGTTGTCGGAT 15684

Qy       2203 GCGGTGCGGCTGGGGCATCGGGTGCTGGCGGTGGTACGCGGCAGTGCGGTCAACCAGGAC 2262

Db      15685 GCGGTGCGGCTGGGGCATCGGGTGCTGGCGGTGCTGCGCGGCAGTGCGGTCAATCAGGAC 15744

Qy       2263 GGTGCGTCGAATGGGCTGACGGCGCCGAACGGTCCGGCTCAGGAGCGGGTGATCCGGCAG 2322
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Qy 19117 CCACAACACCCCC---TCACCACCGTCATCCACACCGCAGGCATCCTCGACGACGCCACC 19173
Db 18304 GCCGGAGGGCCACAGGTGAGCGCCGTGTTCCACGCGGGCGGCATCGAGCCCCACGCTCCG 18363
Qy 19174 CTCACCAACCTCACCCCCACCCAACTCAACAACGTCCTCCGCGCCAAAGCCCACAGCGCC 19233
Db 18364 CTCGCCGCCACCTCCATGGAGGATCTCGCCGAGGTTGTCTCCGGCAAGGTACAAGGTGCA 18423
Qy 19234 CACCTCCTCCACCAACTCACCCAACACACCCCCCTCAACGCCTTCGTCCTCTACTCCTCC 19293
Db 18424 AGACACCTCCACGACCTGCTCGGCTCTCGACCCCTCGACGCCTTTGTTCTCTTCTCGTCC 18483
Qy 19294 GCCGCCGCCACCTTCGGCGCACCCGGCCAAGCCAACTACGCCGCAGCCAACGCCTACCTC 19353
Db 18484 GGCGCGGTCGTCTGGGGCGGCGGACAACAAGGCGGCTATGCCGCTGCGAACGCCTTCCTC 18543
Qy 19354 GACGCCCTCGCCCACCACCGCCACACCCACCACCTCCCCGCCACCAGCATCGCCTGGGGC 19413
Db 18544 GATGCCCTGGCCGAGCAGCGGCGCAGCCTTGGGCTGACGGCGACATCGGTGGCCTGGGGC 18603
Qy 19414 ACCTGGCAAGGAAACGGACTGGCGACTGGTCAAGTCAGCGAACATCTCCGCCGCCGCGGG 19473
Db 18604 GTGTGGGGCGGCGGCGGCATGGCTACCGGGCTCCTGGCAGCCCAGCTAGAGCAACGCGGT 18663
Qy 19474 ATGTTCGCCATGCCGCCCGAGTTGGCGGTCACAGCTGTTGACGGCGCGATCGCGAGCGGG 19533
Db 18664 CTGTCGCCGATGGCCCCCTCGCTGGCCGTGGCGACGCTCGCGCTGGCGCTGGAGCACGAC 18723
Qy 19534 CGCCCGAGTCTCCTCGTCGCCGATATCGACTGGAAGAAATTGGGACCGGTTCTCTCCAGC 19593
Db 18724 GAGACCACCCTCACCGTCGCCGACATCGACTGGGCGCGCTTTGCGCCTTCGTTCAGCGCC 18783
Qy 19594 AAGTCGTCGGTCTTGCTCGAG---GACCTTCCCCAGGCACAGGGAACTGAGGAGGCGCGC 19650
Db 18784 GCTCGCTCCCGCCCGCTCCTGCGCGATTTGCCCGAGGCGCAGCGCGCTCTCGAAGCCAGC 18843
Qy 19651 AG------TACCGTTGAGCAGACGGAGAGCACAAACCTCCGGCAACTCCTCATGGGTCGG 19704
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Db 18904 TCGGAGAGCGAGCAGATCCACCTGCTCTCCTCGCTGGTGCGCCACGAAGCGGCCCTCGTC 18963
Qy 19765 CTCGGGCGCGACGACTCCGAGGCCATCCCGCCCGGTCGGCTGTTCAGGGATCTAGGGTTC 19824
Db 18964 CTGGGCCATACCGACGCCTCCCAGGTCGACCCCCACAAGGGCTTCATGGACCTCGGCCTC 19023
Qy 19825 GACTCGCTTGCGGCGGTGGAGCTTCGCAACCACCTCGCAGCACAGACGGAGCTGGCTCTG 19884
Db 19024 GATTCGCTCATGACCGTCGAGCTTCGTCGGCGCTTGCAGCAGGCCACCGGCATCAAGCTC 19083
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Db 19084 CCGGCCACCCTCGCCTTCGACCATCCCTCTCCTCATCGCGTCGCGCTCTTCTTGCGCGAC 19143
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Qy 20107 GGCGGATTCCCCACCGACCGCGGCTGGGACCTGGACACGCTCTACGACCCCGACCCCGAC 20166
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Qy 20227 GCCGAATTCTTCGGCATCAGCCCCCGCGAAGCCCTCGCCATGGACCCCCAGCAACGACTC 20286
Db 19441 CCTGCCTTCTTTGGCATCAGCCCTCGCGAGGCCAAATACCTCGACCCCCAGCACCGCCTG 19500
Qy 20287 CTCCTCGAAACCGCCTGGGAAACCATCGAACACGCCGGCATCAACCCCCACACCCTCCAC 20346
Db 19501 CTCCTCGAATCTGCCTGGCTGGCCCTCGAGGACGCCGGCATCGTCCCCTCCACCCTCAAG 19560
Qy 20347 GGCACCCCCACCGGAGTCTTCACCGGCACCAACGGACAGGACCACGCGGCACACATCCGT 20406
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Db 19618 ACGAGCTCCGAAGAGGTCGAAGCGTATGCCCTCCAAGGCACCGCCGGGTCCTTTGCCGCG 19677
Qy 20467 GGCCGAATCTCCTACATCCTCGGGTTGGAAGGGCCTGCGGTCACCCTCGACACAGCGTGT 20526
Db 19678 GGGCGCTTGGCCTACACGCTCGGCCTGCAAGGGCCCGCGCTCTCGGTCGACACCGCCTGC 19737
Qy 20527 TCCTCCTCGCTCGTCGCCCTGCACCTCGCCTGCCAGTCCCTCAGGTCCGGTGAATGCACC 20586
Db 19738 TCCTCCTCGCTCGTCGCCCTCCACCTCGCCTGCCAAGCCCTCCGACAGGGCGAGTGCAAC 19797
Qy 20587 ATGGCCTTGGCCGGCGGGGCCACGGTCATGACCACCCCGATCACCTTCACCGAATTCGCC 20646
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Qy 20767 AACGGTCACCGTGTCCTGGCCGTGGTGCGTGGCAGTGCGGTCAACCAGGACGGTGCGAGC 20826
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Qy 20827 AACGGTCTGACCGCGCCCAACGGGCCCTCCCAGCAGCGCGTCATCCGCCAGGCCCTCGCC 20886
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Db 18184 CAGGCCGAAGGCGCCGTGGAGCTCCACGCCGAGCTCACCGCCCTCGGCGCGCGCGTCACC 18243
Qy 19057 ATCACCACCTGCGACACCAGCAACCCAGACCAACTCCAACAACTCCTCAACACCATCCCC 19116
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CC   attack by phytopathogens.
XX
SQ   Sequence 28958 BP; 4084 A; 11863 C; 8356 G; 4655 T; 0 other;

  Query Match           10.2%;  Score 3140.6;  DB 18;  Length 28958;
  Best Local Similarity  54.1%;  Pred. No. 0;
  Matches 8239;  Conservative    0;  Mismatches 6284;  Indels  698;  Gaps   63;

Qy      14872 ACGACCCCATCAACCCCGCTGCGTGATGTCCTCGTGGGCAAGTCTCCGCAGGAGCGAGAC 14931
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Qy      14932 GAAGAGCTGTTGCGCCTGGTGCGCACCCATGCGGCCGCTGTGCTGGGCCATGCCACTCCC 14991
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Qy      14992 GAAGTGATCGTTCCGAACAAGGCCTTCAAAGAGCTGGGTTTTGATTCTCTCGCCGCAATT 15051
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Qy      15052 CAGCTTCGTAATCGACTGCTTGCTGACGTTGACCTGCCGCTTCCGGCCACGCTGATCTTC 15111
               |||| || ||||||||     || | ||  |  |||| ||| | ||| || ||  |||||
Db      14416 GAGCTCCGAAATCGACTCGCCGCCGCCGCCGGGCTGCGGCTCCAGGCTACTCTCCTCTTC 14475

Qy      15112 GATTACCCCACTCCGATGGCGCTTTGCCAGTTCCTCCGGGCGGCGATCGTCGGAGCGGAC 15171
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Db      14476 GACTATCCAACCCCGACTGCGCTCTCACGCTTTTTCACGACGCATCTCTTCGG---GGGA 14532

Qy      15172 ACAGGCACGACCACTCGTCTGCCGCTAACTGCGGTCCCCGCCGACGAGCCGATCGCCATC 15231
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Qy      15232 GTCGGCATGGCCTGTCGGTACCCCGGTGATGTACGGACGGTCGATGATCTCTGGCAGGTG 15291
              || |  |||  ||| || | ||| || || || || |||  ||| |||||||||| || |
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Qy      15292 GTCAGTGGTGGCCATGACGCGATCGGCGGATTCCCGACGAACCGTGGGTGGGACCTCGAC 15351
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Db      14653 TTGCTCGACGGACAAGATGCCATCTCCGGCTTTCCCCAAAATCGCGGCTGGAGTCTCGAT 14712

Qy      15352 ACGCTGTACAACCCGGACCCGGACCACCACGGAACCAGCTACACCCGGAGCGGCGGATTC 15411
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Qy      15592 CACGACTACGCCGCGCGCTTTCCCACAGCTCCGGCAGGGTTCGAGGGGTATCTCGGGCAC 15651
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Qy      15652 GGAAGCGCAGGCAGTATCGCCTCGGGTCGTGTCGCCTACGCTCTCGGCCTGGAAGGTCCG 15711
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Qy      15712 GCCCTCACAGTCGACACTGCCTGCTCTTCGTCCCTGGTCGCTCTGCACCTGGCCTGTCAG 15771
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Db      15055 GCCATCAGCGTGGAGACGGCGTGC---AGCTTCCTCGTCGCGGTTCACCTCGCCTGCCAG 15111

Qy      15772 GCGCTGCGGTCCGGCGAGTGTTCCATGGCCCTCGCGGGTGGCGTCACGGTGATGTCAACC 15831
              || |  |    |||||| |  ||| |||| ||||| || |||||  ||  | |||  | ||
Db      15112 GCCCCCCCCCACGGCGAATACTCCCTGGCGCTCGCTGGCGGCGTGACCATCATGGCCACG 15171

Qy      15832 CCGGCCGGGTTCGTGGAGTTTTCGCGGCAGCGGGGCCTGGCCGTGGACGGGCGGTGCAAG 15891
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Db      15172 CCAGCCATATTCATCGCGTTCGACTCCGAGAGCGCGGGTGCCCCCGACGGTCGCTGCAAG 15231

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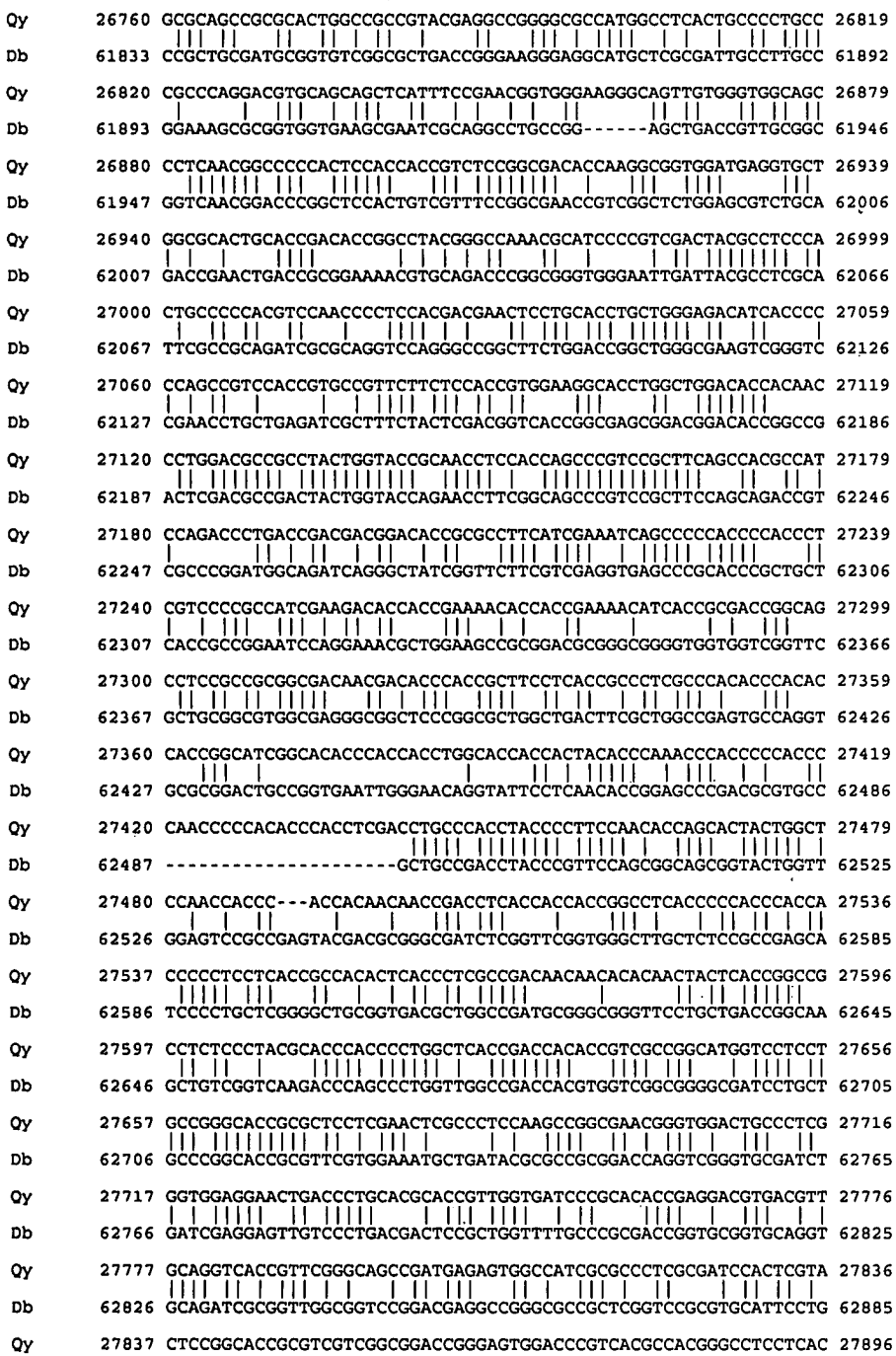
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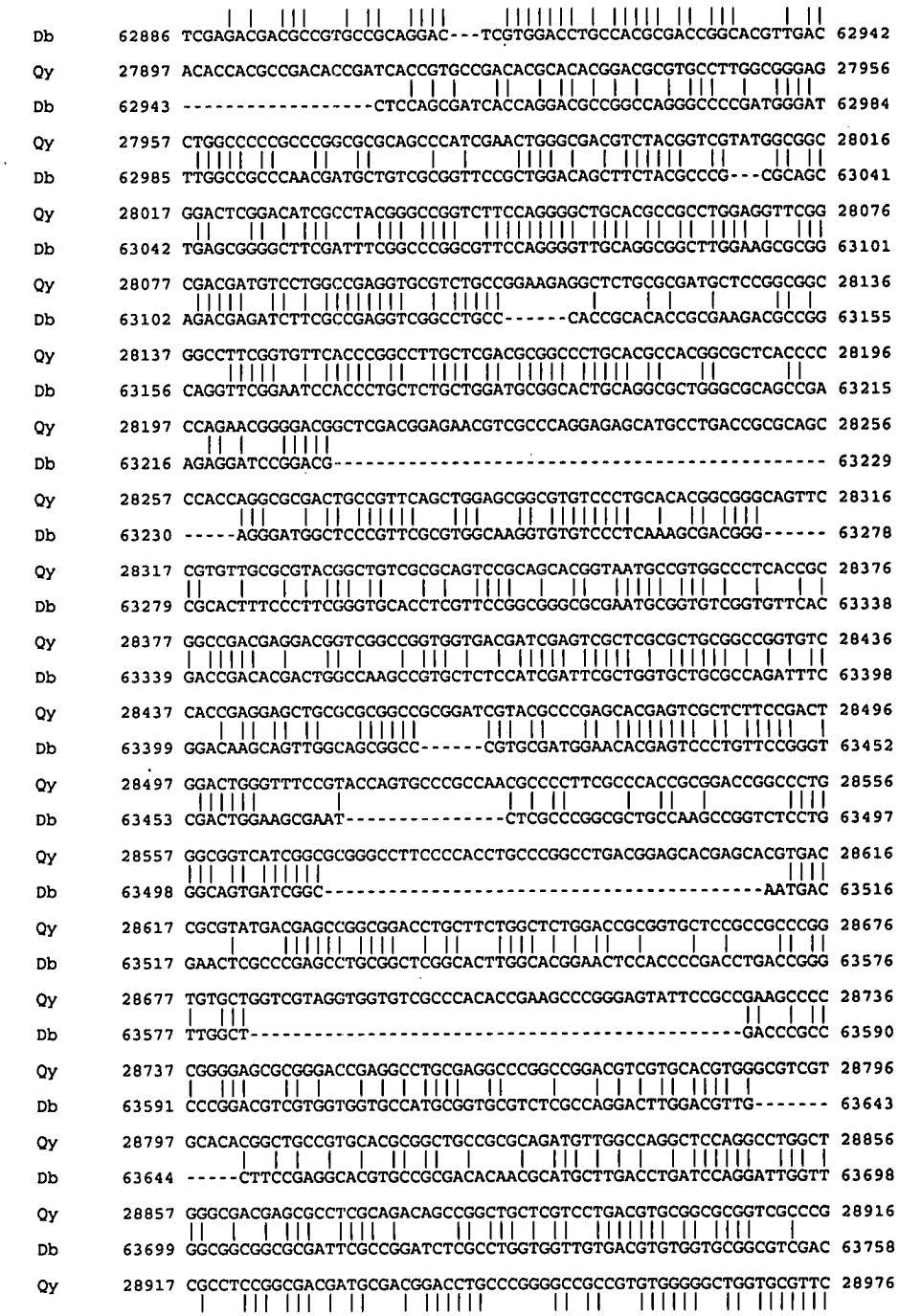
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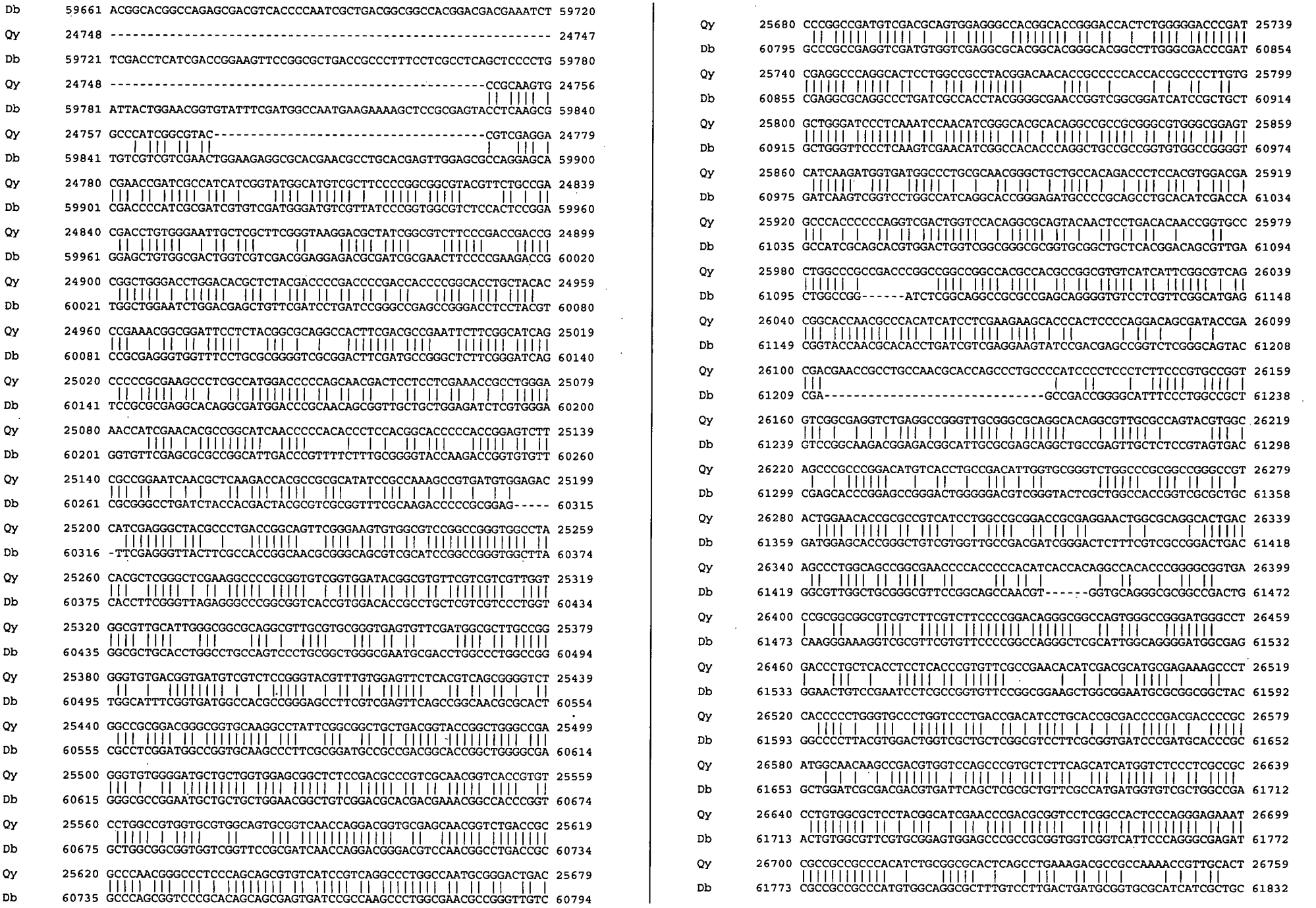
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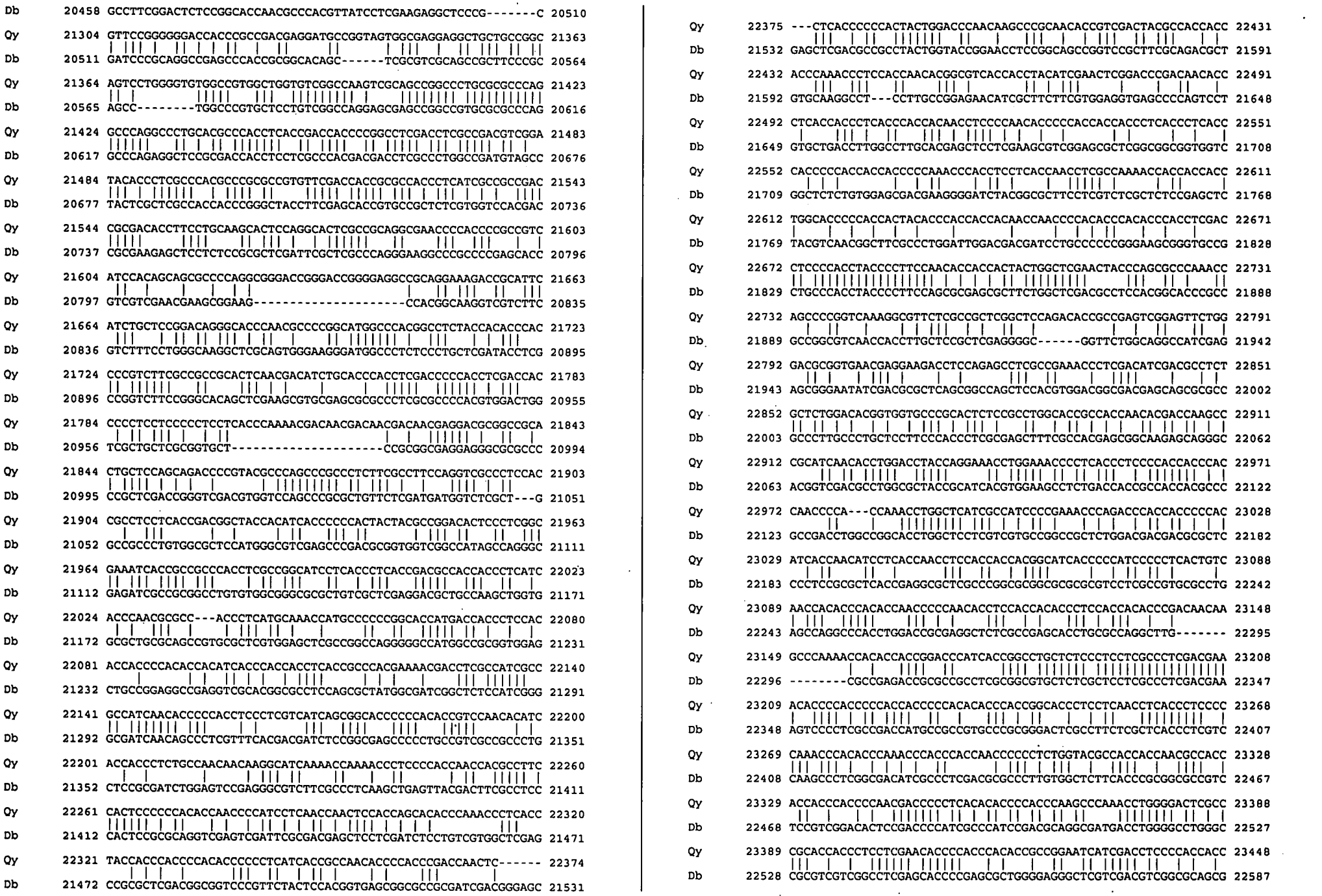
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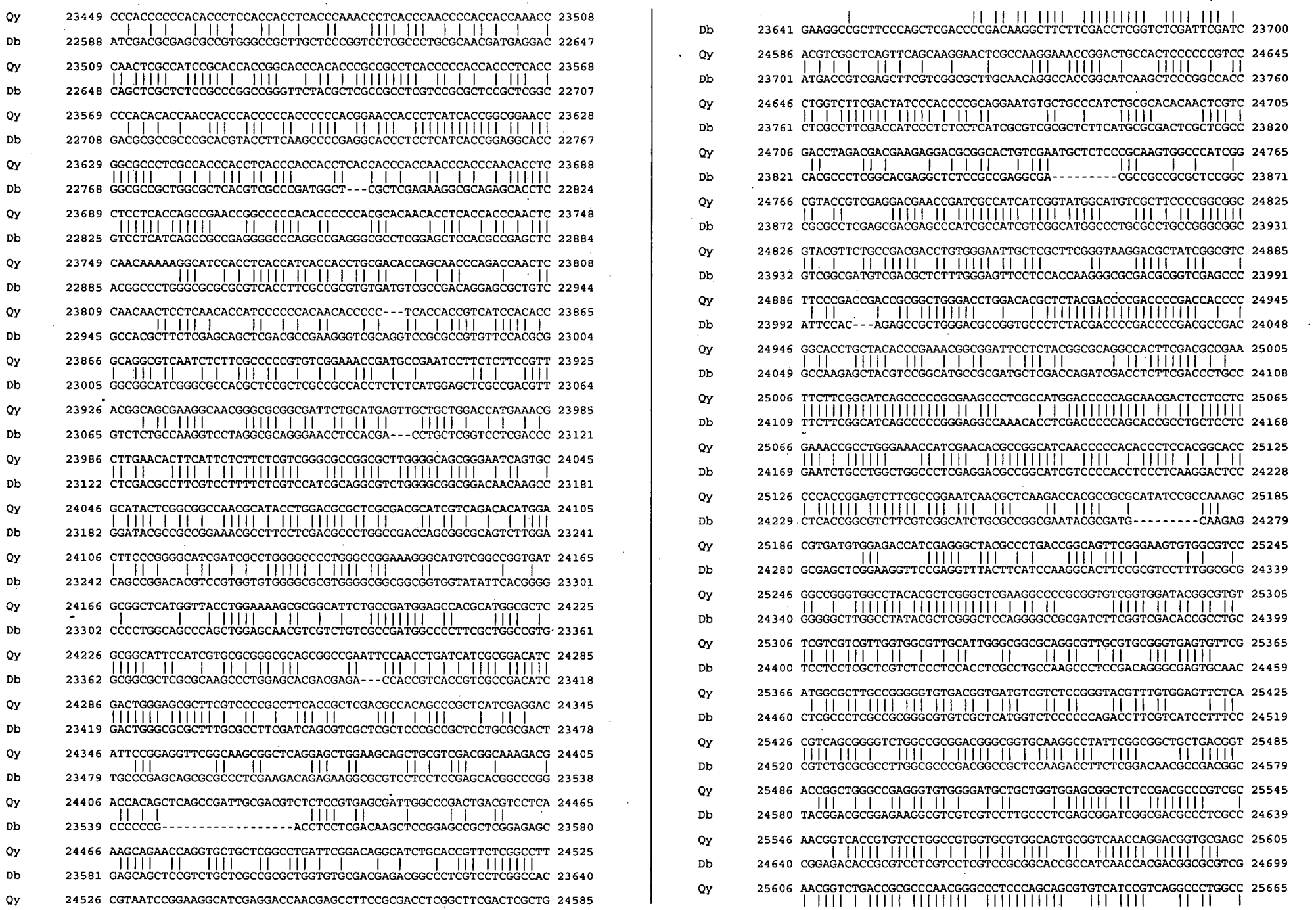

RESULT 15
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AC   AAT89956;
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DT   12-MAR-1998  (first entry)
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DE   Sorangium cellulosum soraphen gene cluster genomic DNA.
XX
KW   Soraphen; polyketide synthase; PKS; antipathogenic; antibiotic;
KW   transgenic plant; phytopathogen; resistance; ss.
XX
OS   Sorangium cellulosum.
XX
PN   US5662898-A.
XX
PD   02-SEP-1997.
XX
PF   01-JUN-1995;   95US-0457342.
XX
PR   20-AUG-1990;   90US-0570184.
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PR   08-JUN-1994;   94US-0258261.
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PA   (CIBA ) CIBA GEIGY CORP.
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PI   Beck JJ,  Gaffney TD,  Hammer PE,  Hill DS,  Lam ST;
PI   Ligon JM,  Ryals JA,  Schupp T,  Uknes SJ;
XX
DR   WPI; 1997-447901/41.
XX
PT   Protecting plants against pathogens with genetically transformed
PT   biological control agent - which expresses all polypeptide(s)
PT   involved in pyrrolnitrin biosynthetic pathway
XX
PS   Ex 16; Column 104-128; 88pp; English.
XX
CC   This genomic DNA sequence encodes the Soraphen gene cluster. This
CC   sequence encodes two open reading frames (ORF's), the positions of which
CC   are not given in the specification. ORF1 is approximately 25.5 kb in
CC   size and encodes 5 biosynthetic modules homologous to the erythromycin
CC   genes of Saccharopolyspora erythraea. Each module contains a
CC   beta-ketoacylsynthase (KS), an acyltransferase (AT), a ketoreductase
CC   (KR) and an acyl carrier protein (ACP) domain. ORF2 is immediately
CC   adjacent to ORF1 and is thought to contain 3 modules. Soraphen is a
CC   type I polyketide synthase (PKS) which has antibiotic activity.
CC   Transgenic plants containing such antipathogenic genes like those
CC   encoded in the Soraphen cluster should have enhanced resistance to
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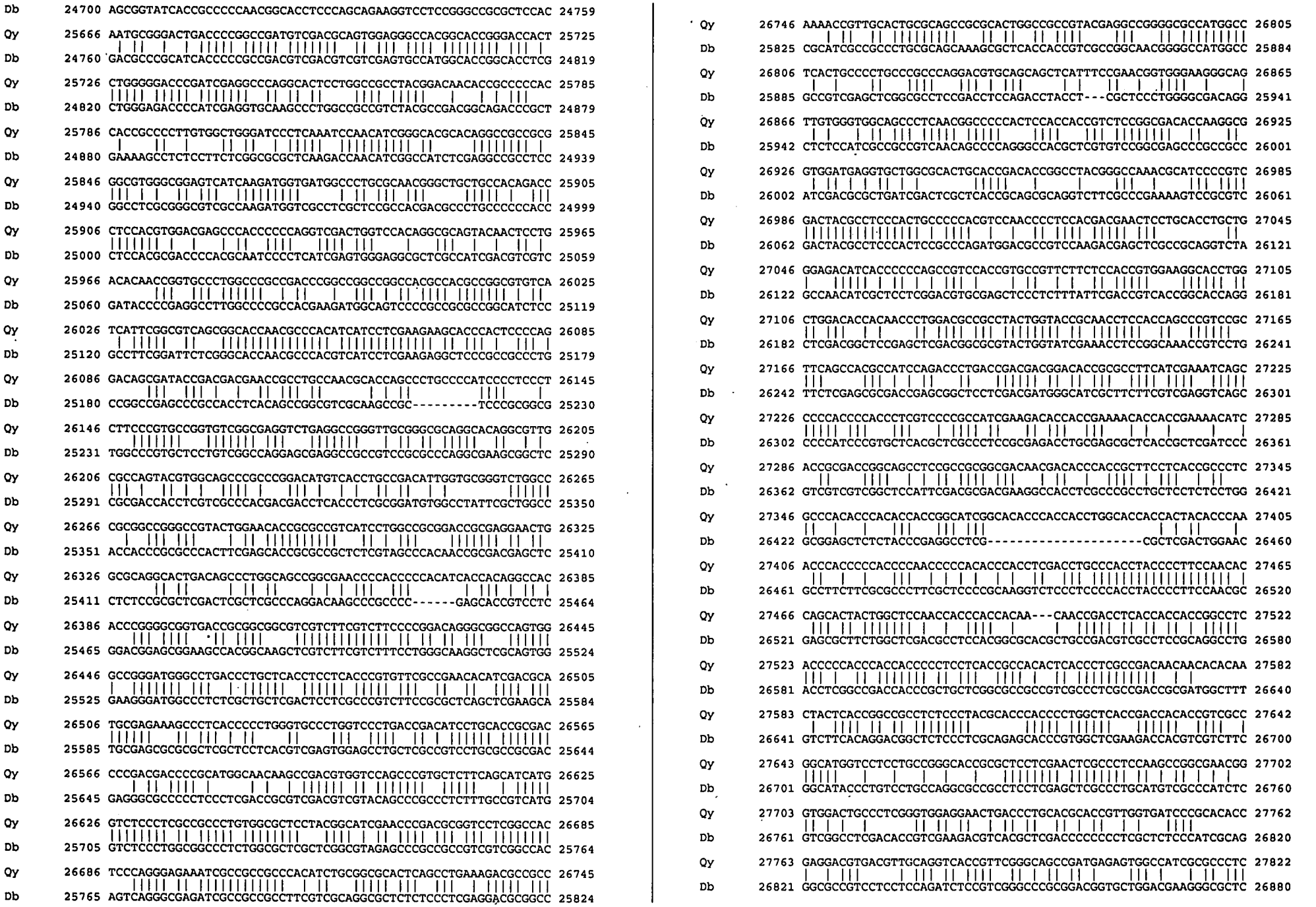


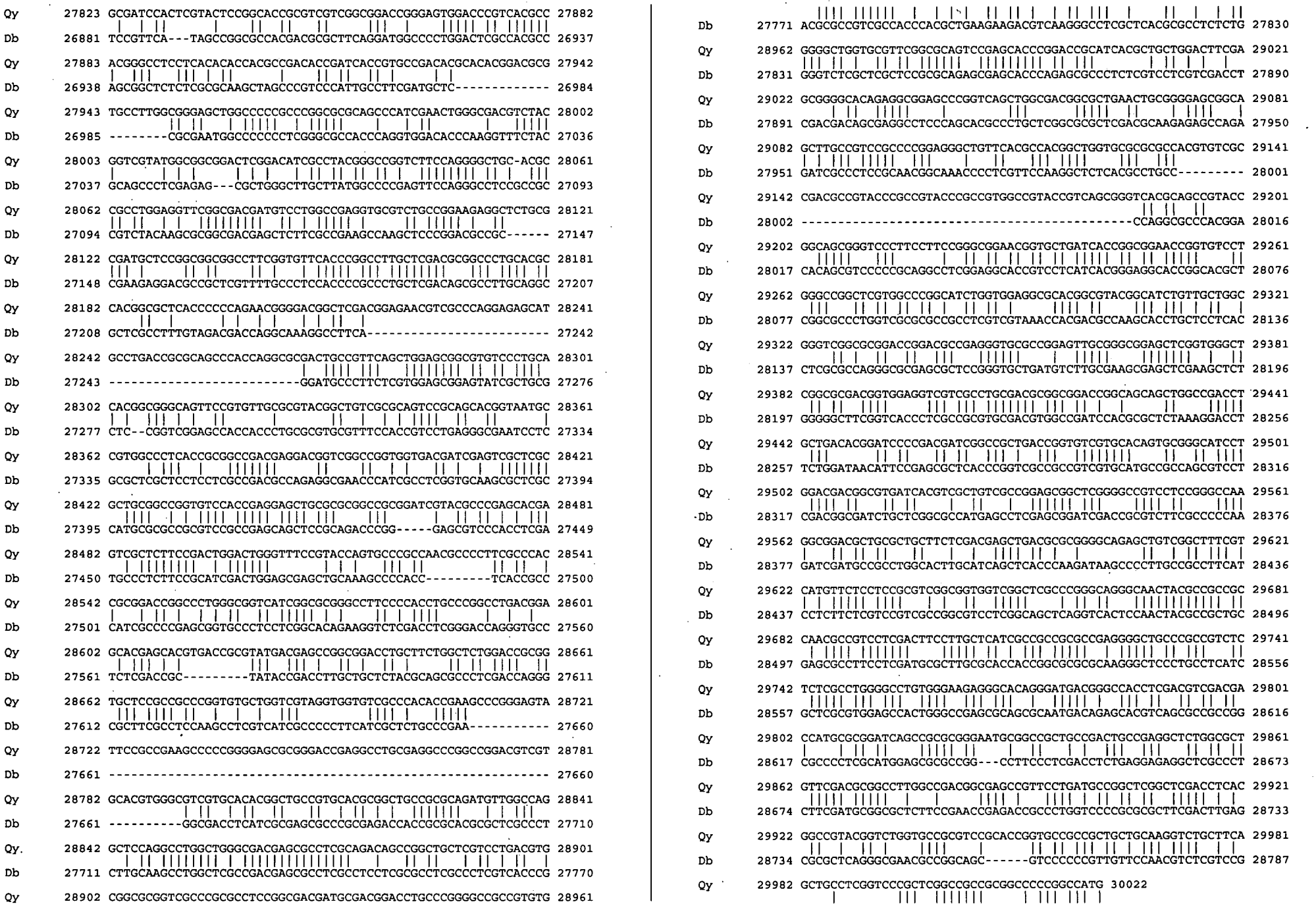












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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
US-08-764-233A-1
; Sequence 1, Application US/08764233A
; Patent No. 5716849
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Schupp, Thomas
; APPLICANT: Beck, James J.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Neff, Snezanna
; APPLICANT: Ryals, John A.
; TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,233A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/729,214
; FILING DATE: 09-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 1506/CIP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:

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;       ORGANISM:  Sorangium cellulosum
;     IMMEDIATE SOURCE:
;       CLONE:  p98/1, pJL3, and pVKM15
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;       OTHER INFORMATION:  Saccharopolyspora erythraea."
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;       OTHER INFORMATION:  compounds."
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;       LOCATION:  942..7115
;       OTHER INFORMATION:  /product= "Module 1 of SorA"
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;       OTHER INFORMATION:  /product= "SorM"
;       OTHER INFORMATION:  /note= "The protein encoded by the sorM gene is highly
;       OTHER INFORMATION:  homologous to the methyltransferase from Streptomyces
;       OTHER INFORMATION:  hygroscopicus that is involved in the synthesis of the
;       OTHER INFORMATION:  polyketide rappamicin."
US-08-764-233A-1

  Query Match             10.4%;  Score 3194.8;  DB 1;  Length 49377;
  Best Local Similarity   54.1%;  Pred. No. 0;
  Matches 8389;  Conservative    0;  Mismatches 6392;  Indels  719;  Gaps   64;

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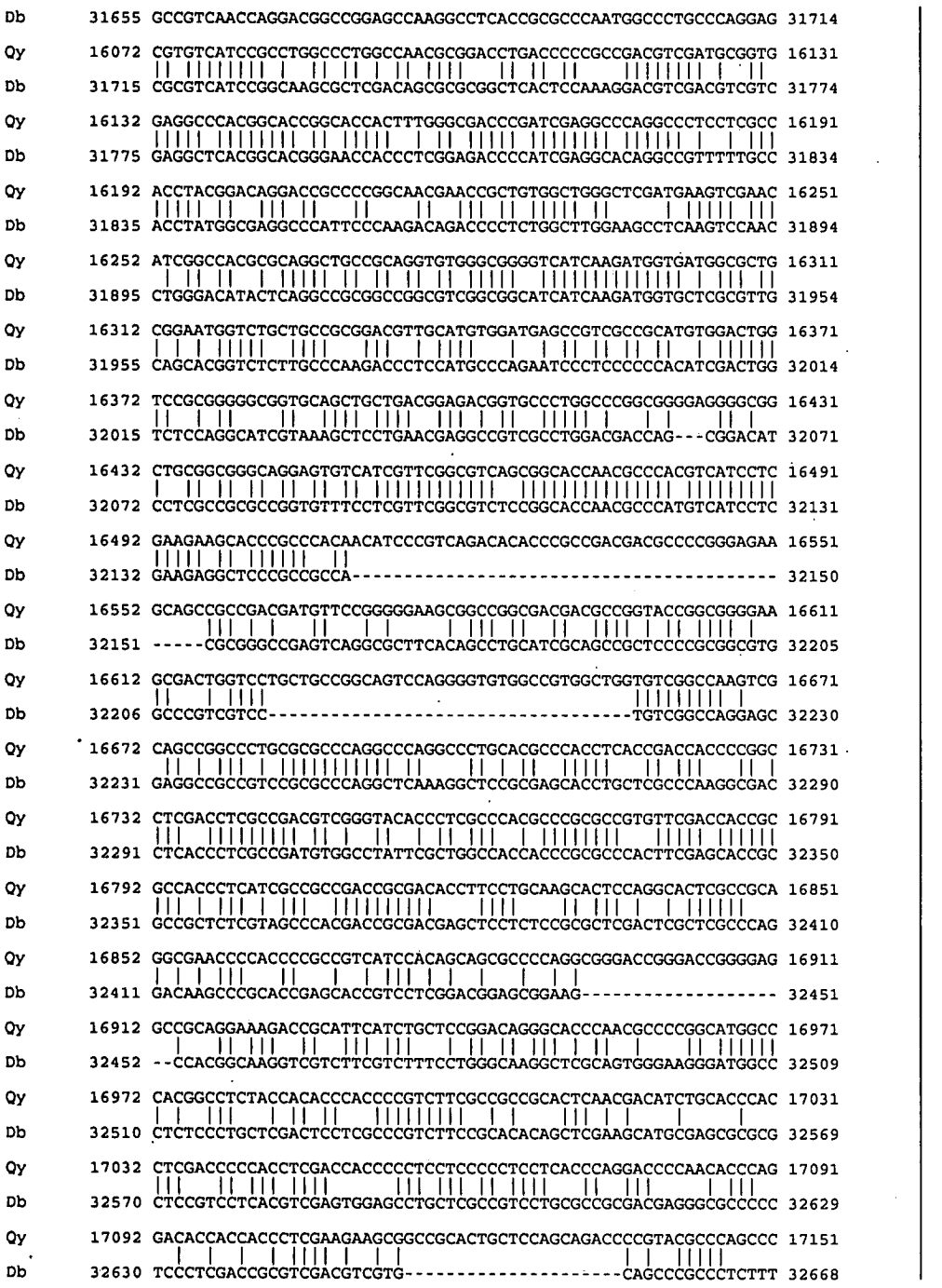
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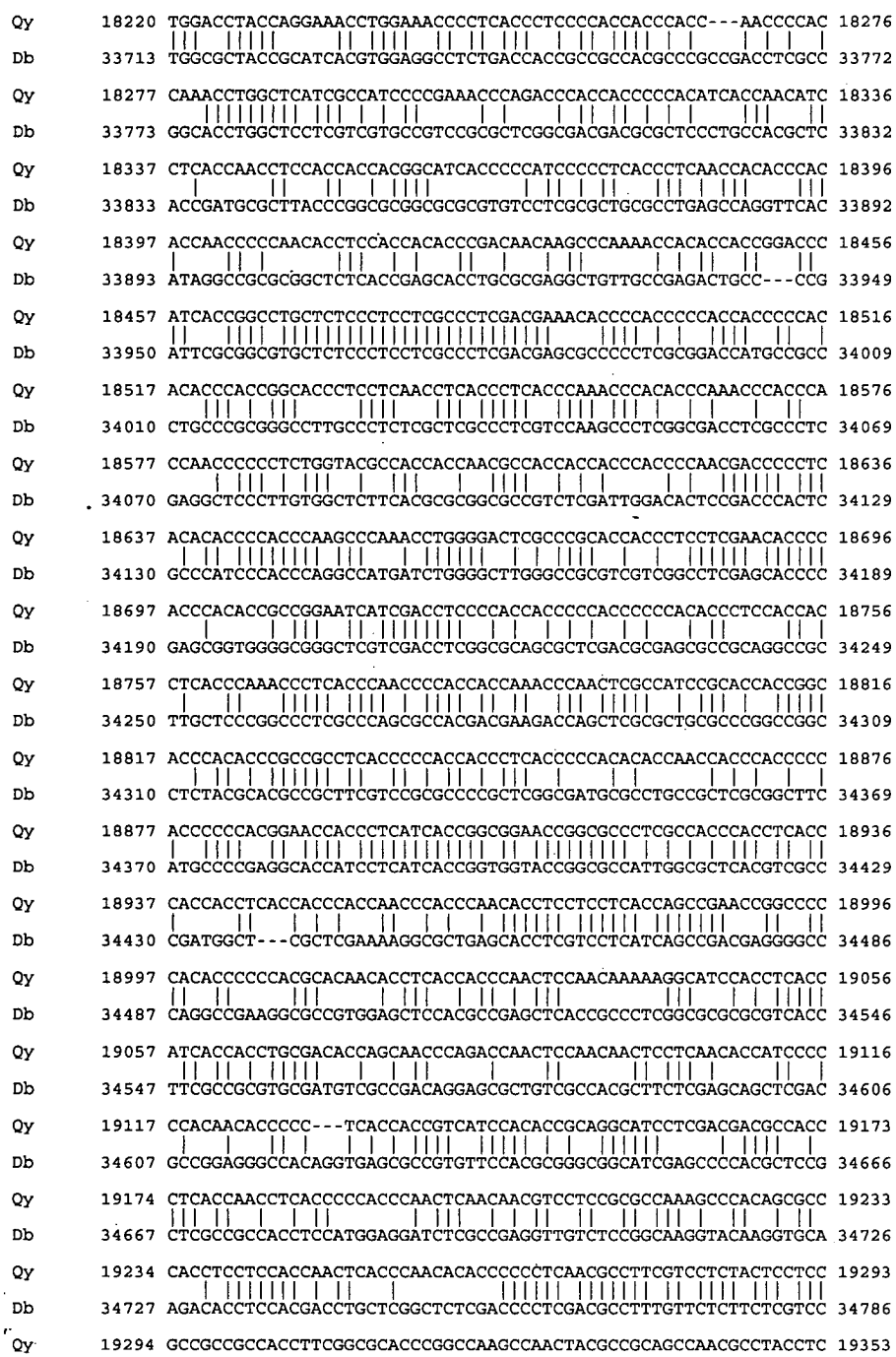
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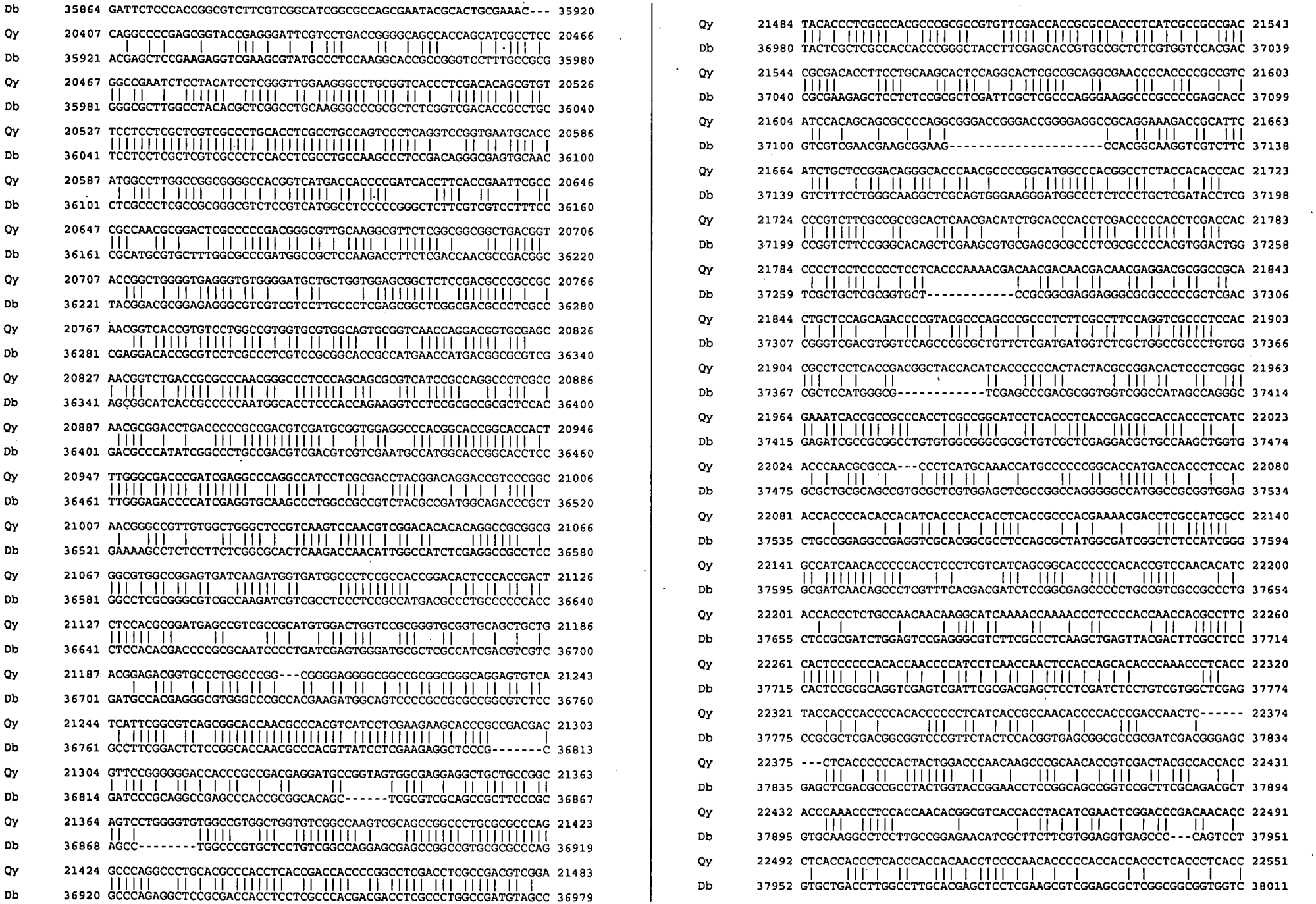
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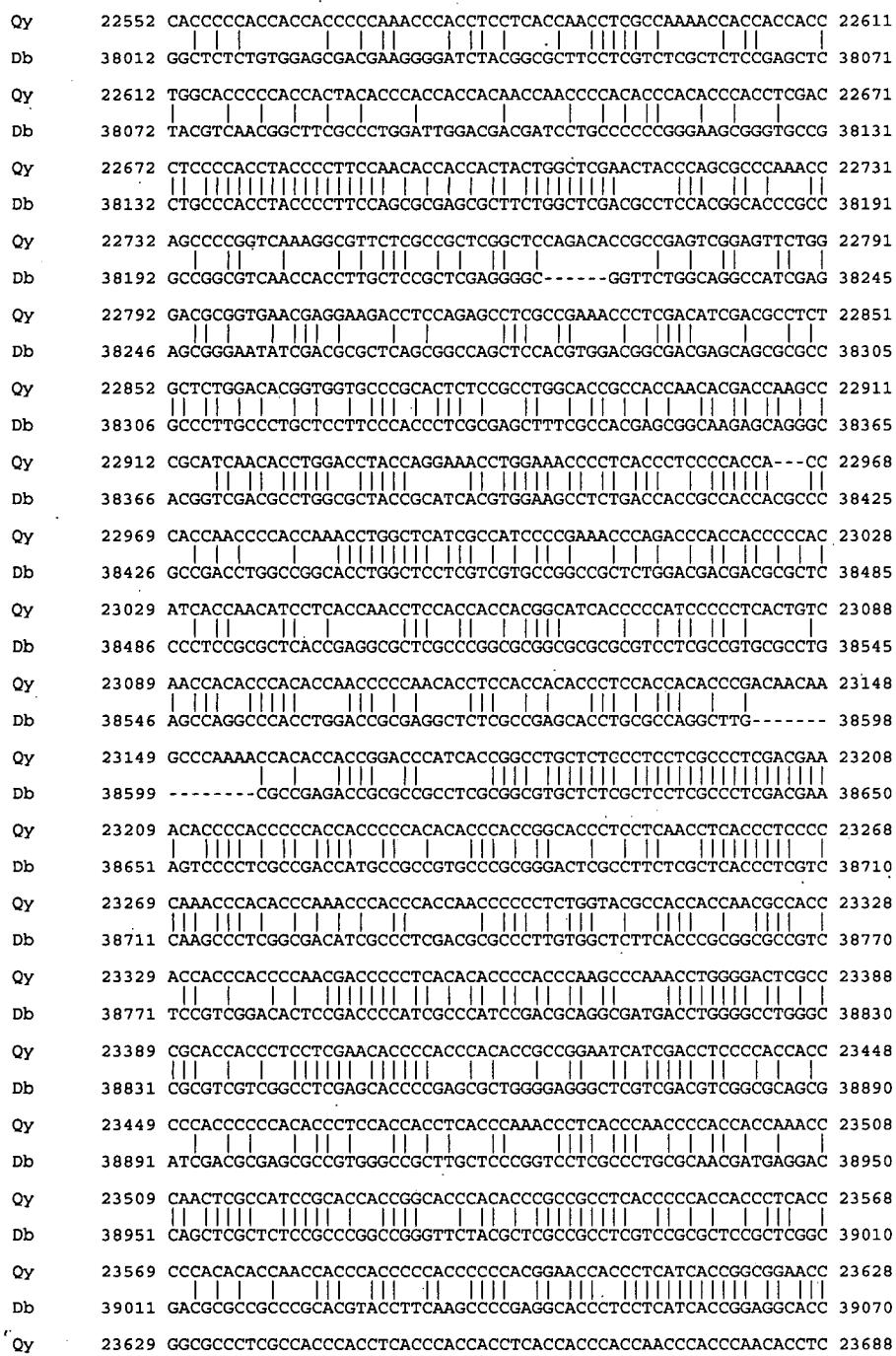
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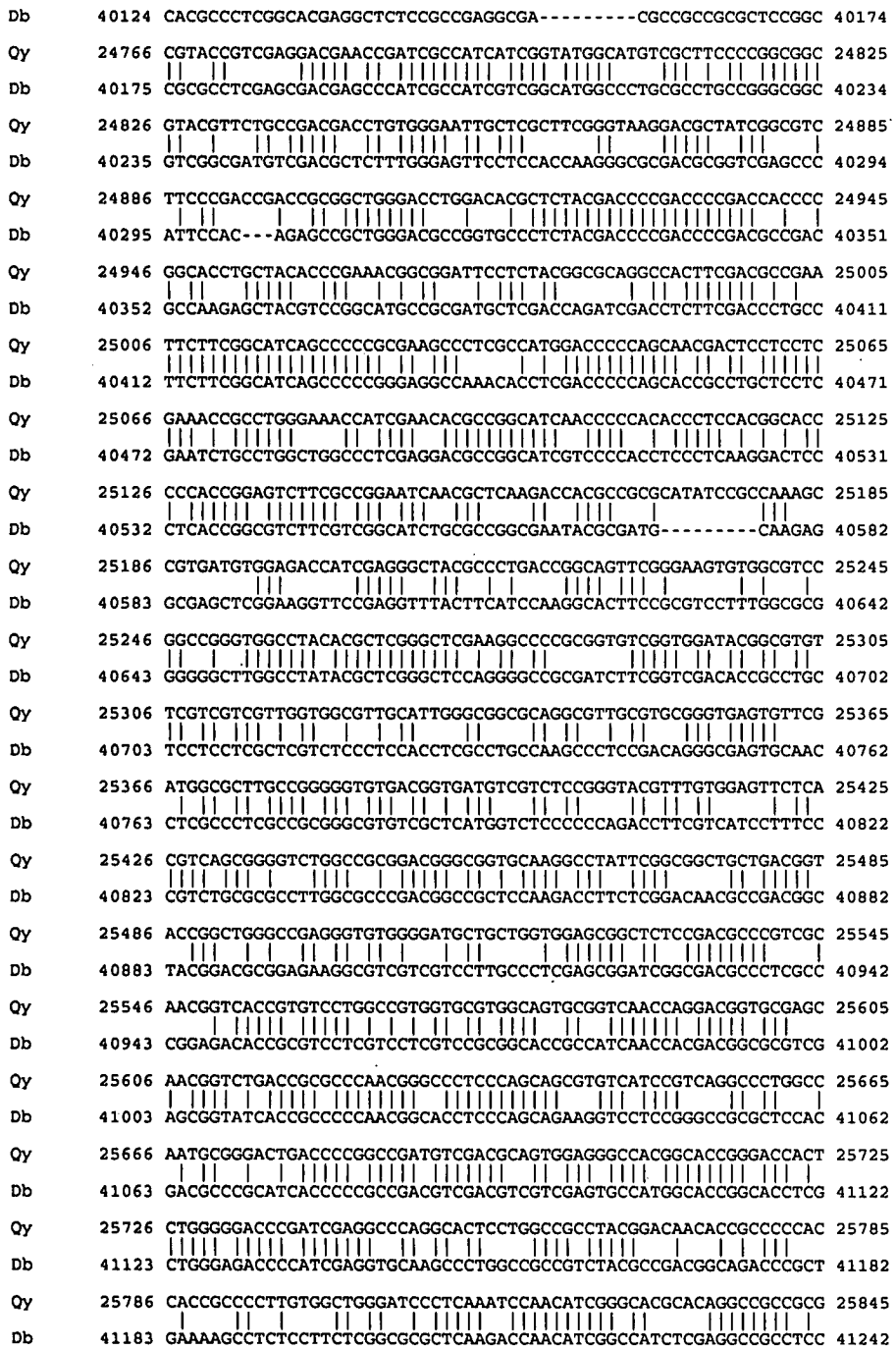
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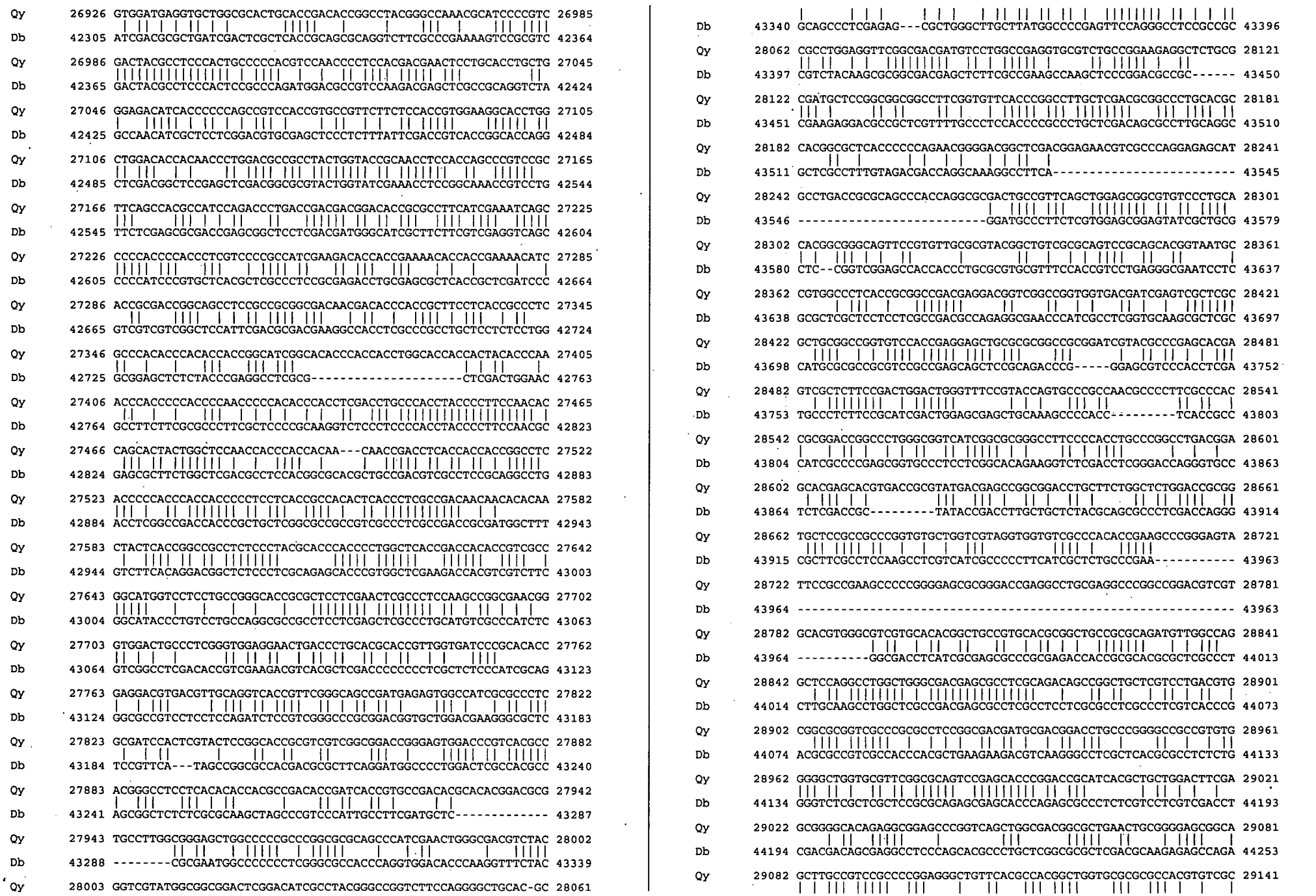

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Qy 19885 CCGACGACTCTCGTCTTCGATTACCCCAGCCCCACCAAGCTCGCCCAATTTCTGCTCTCC 19944
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Qy 22672 CTCCCCACCTACCCCTTCCAACACCACCACTACTGGCTCGAACTACCCAGCGCCCAAACC 22731
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Qy 22732 AGCCCCGGTCAAAGGCGTTCTCGCCGCTCGGCTCCAGACACCGCCGAGTCGGAGTTCTGG 22791
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Qy 24226 GCGGCATTCCATCGTGCGCGGGCGCAGCGGCCGAATTCCAACCTGATCATCGCGGACATC 24285
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Qy 24586 ACGTCGGCTCAGTTCAGCAAGGAACTCGCCAAGGAAACCGGACTGCCACTCCCCCCGTCC 24645
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Qy 25726 CTGGGGGACCCGATCGAGGCCCAGGCACTCCTGGCCGCCTACGGACAACACCGCCCCCAC 25785
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Qy      29622 CATGTTCTCCTCCGCGTCGGCGGTGGTCGGCTCGCCCGGGCAGGGCAACTACGCCGCCGC 29681

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Qy      29682 CAACGCCGTCCTCGACTTCCTTGCTCATCGCCGCCGCGCCGAGGGGCTGCCCGCCGTCTC 29741

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Db      45370 AACCCCAGCTGCGCTCGCAG 45389


RESULT 2
US-09-036-987A-1
; Sequence 1, Application US/09036987A
; Patent No. 6143526
;  GENERAL INFORMATION:
;    APPLICANT:  Baltz, Richard H.
;    APPLICANT:  Broughton, Mary C.
;    APPLICANT:  Crawford, Kathryn P.
;    APPLICANT:  Madduri, Krishnamurthy
;    APPLICANT:  Merlo, Donald J.
;    APPLICANT:  Treadway, Patti J.
;    APPLICANT:  Turner, Jan R.
;    APPLICANT:  Waldron, Clive
;    TITLE OF INVENTION:  Biosynthetic Genes For Spinosyn Insecticide
;    TITLE OF INVENTION:  Production
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dow AgroSciences LLC Patent Department
;      STREET:  9330 Zionsville Road
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  USA
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/036,987A
;      FILING DATE:  09-MAR-1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stuart, Donald R
;      REGISTRATION NUMBER:  28,479
;      REFERENCE/DOCKET NUMBER:  50,608
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317)337-4816
;      TELEFAX:  (317)337-4847
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  80161 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-036-987A-1

  Query Match             10.2%;  Score 3142;  DB 3;  Length 80161;
  Best Local Similarity   49.2%;  Pred. No. 0;
  Matches 15063;  Conservative    0;  Mismatches 12830;  Indels 2753;  Gaps  147;

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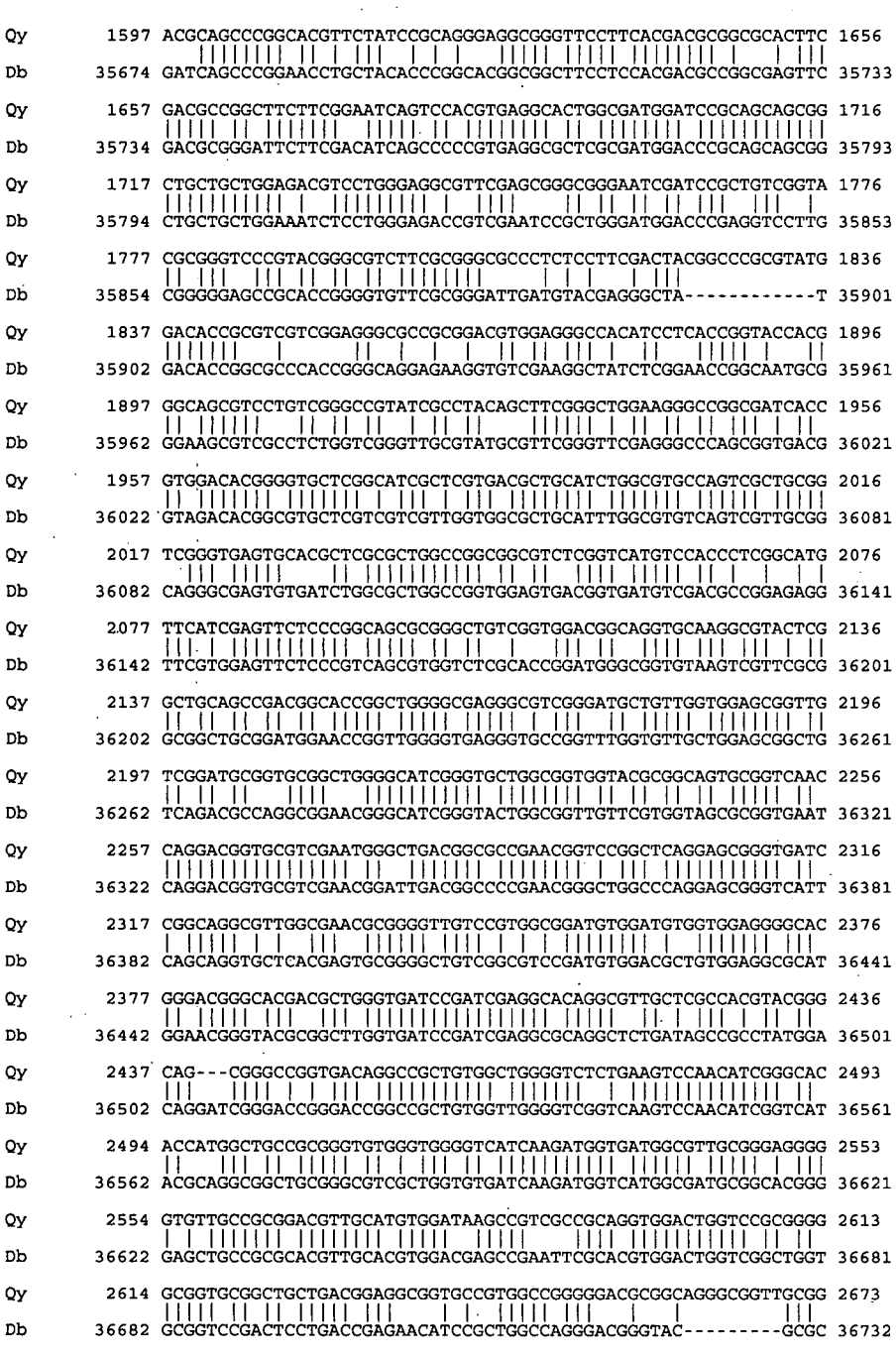
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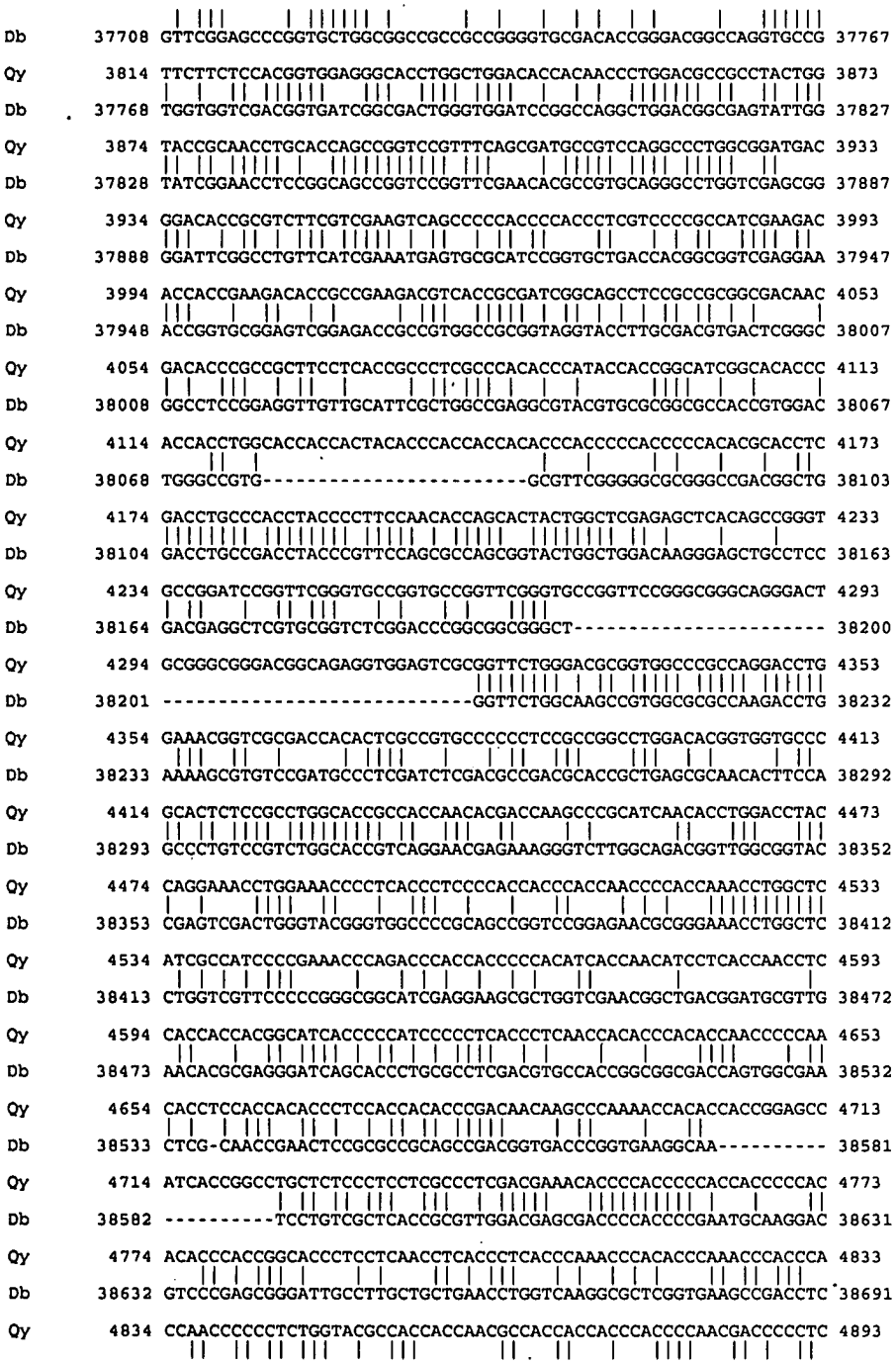
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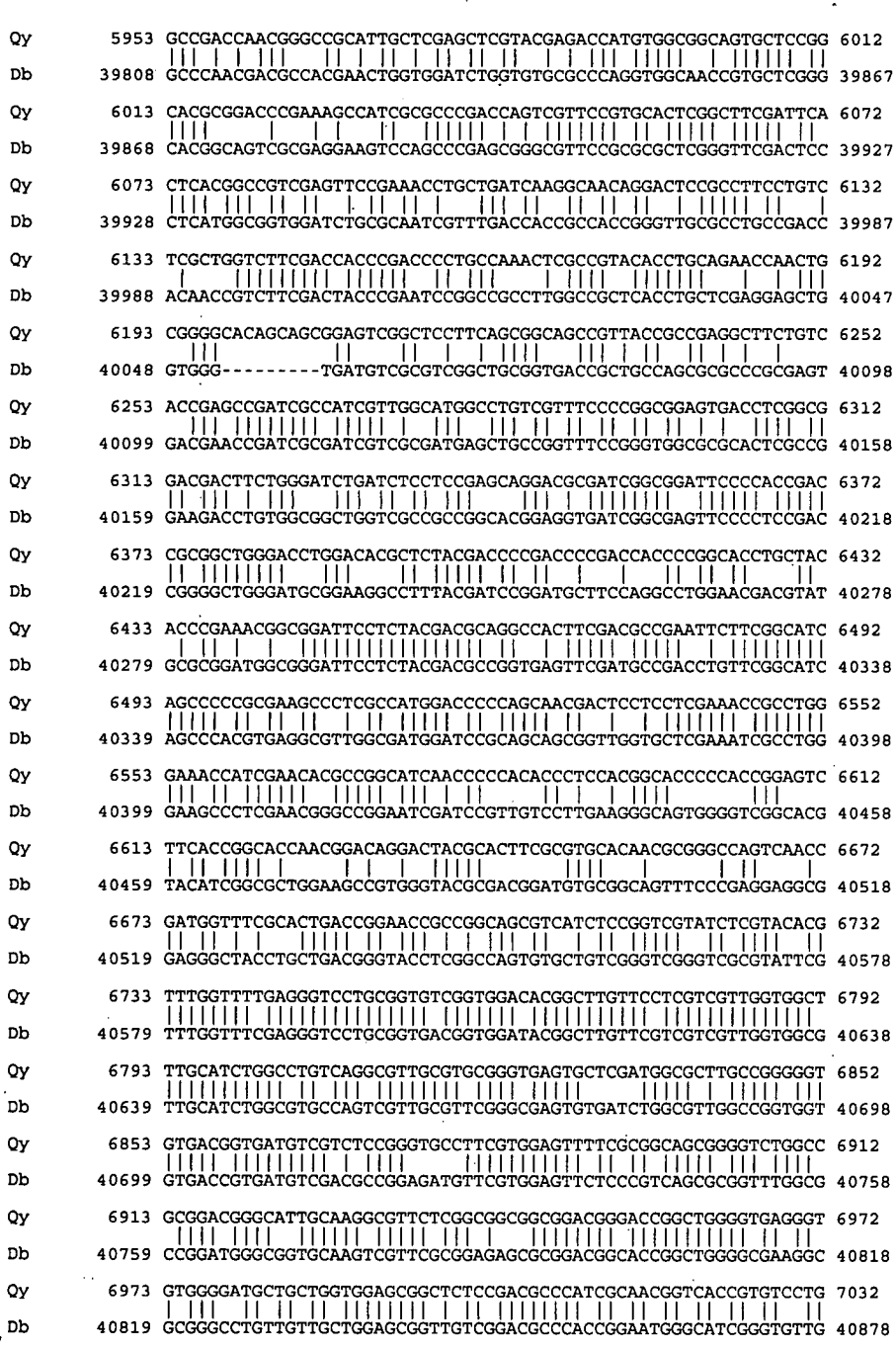
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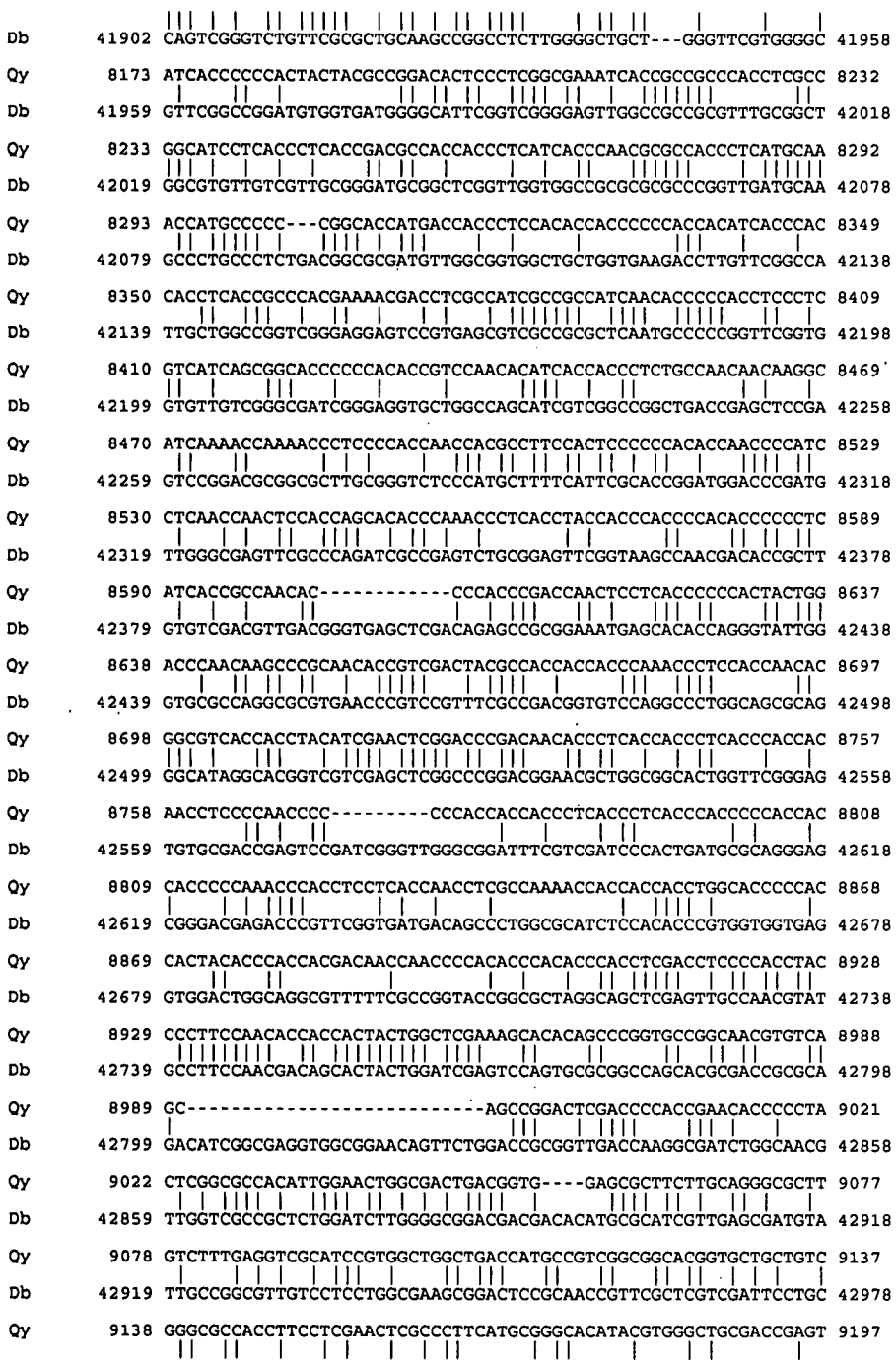
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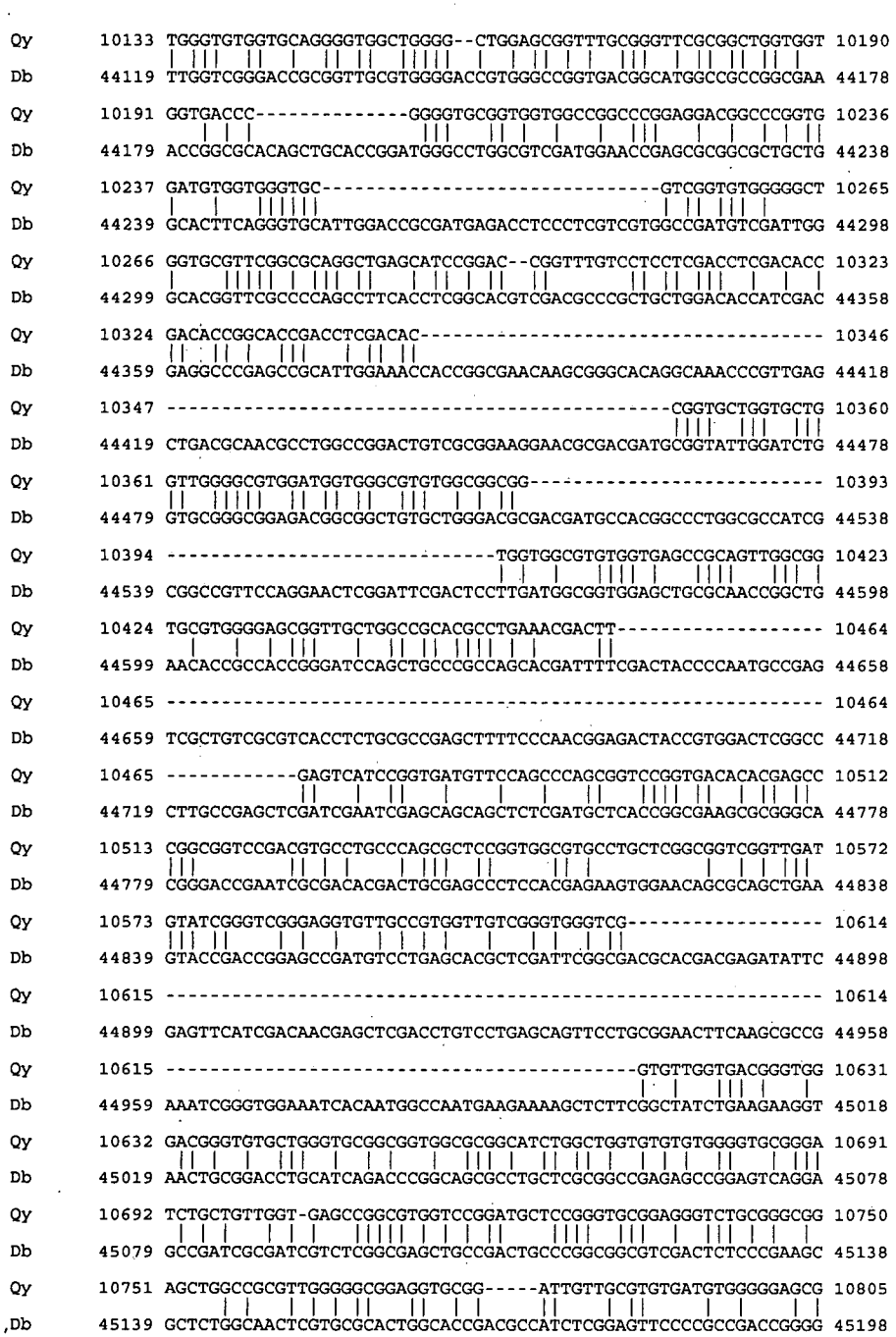
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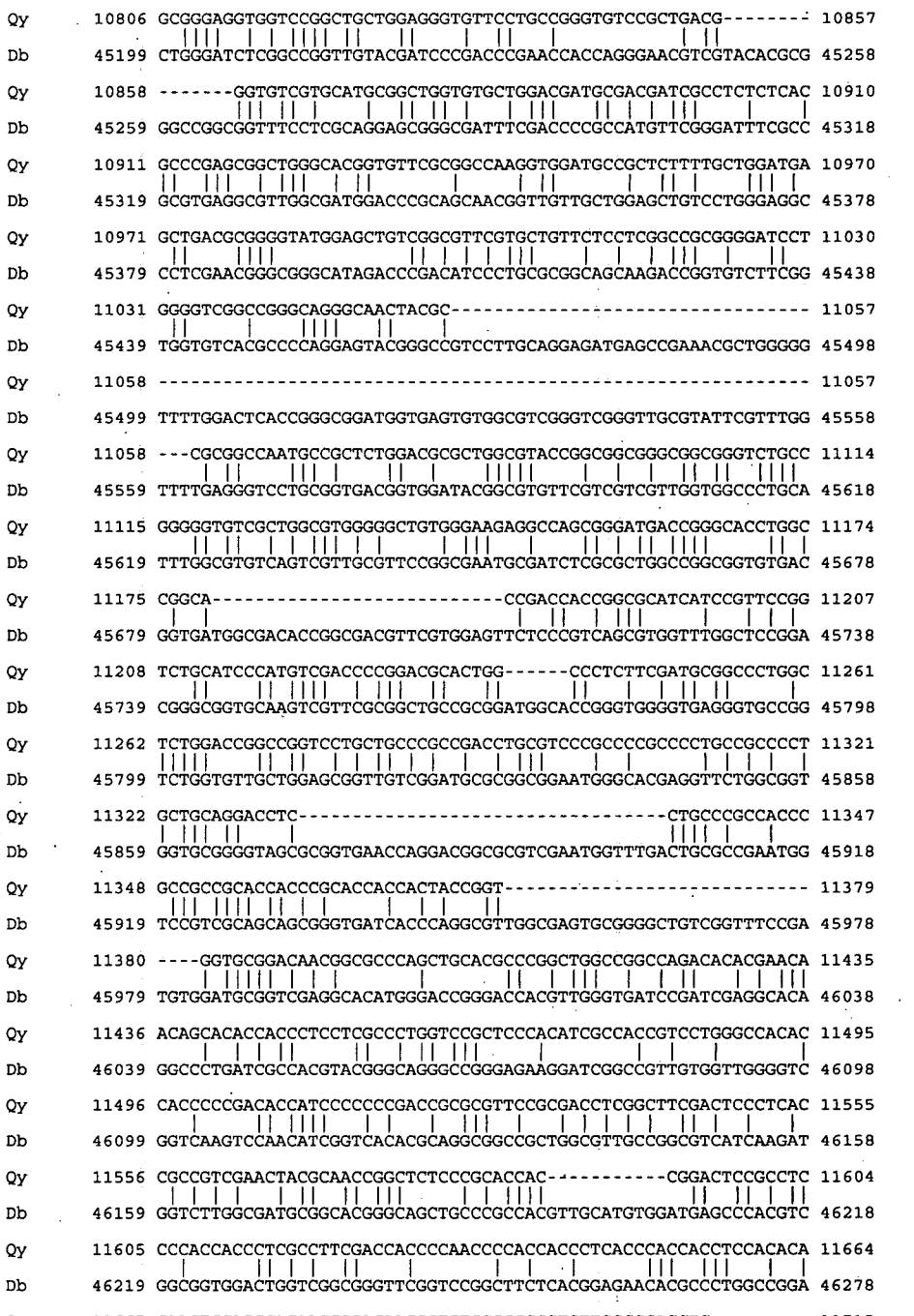

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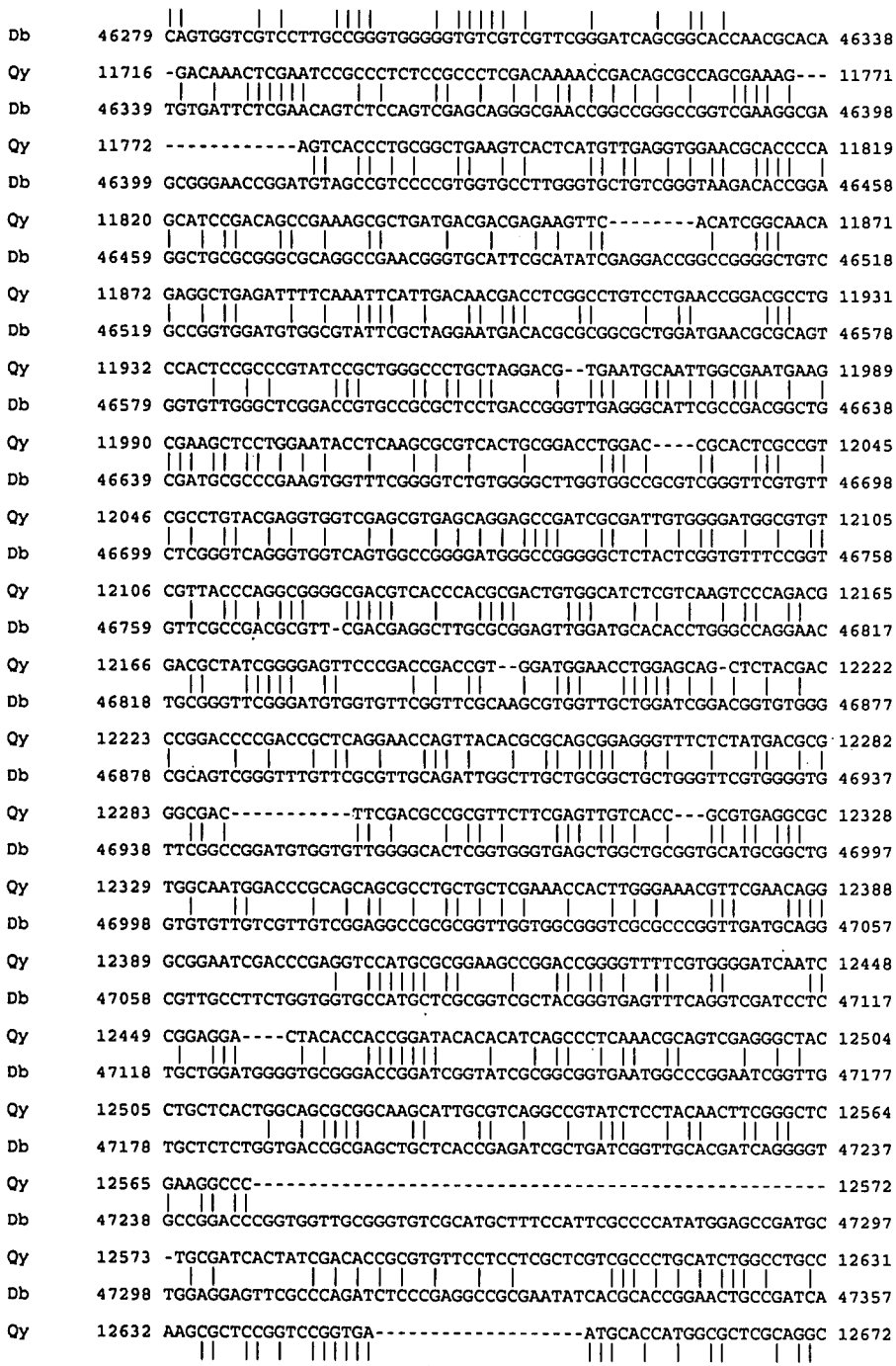

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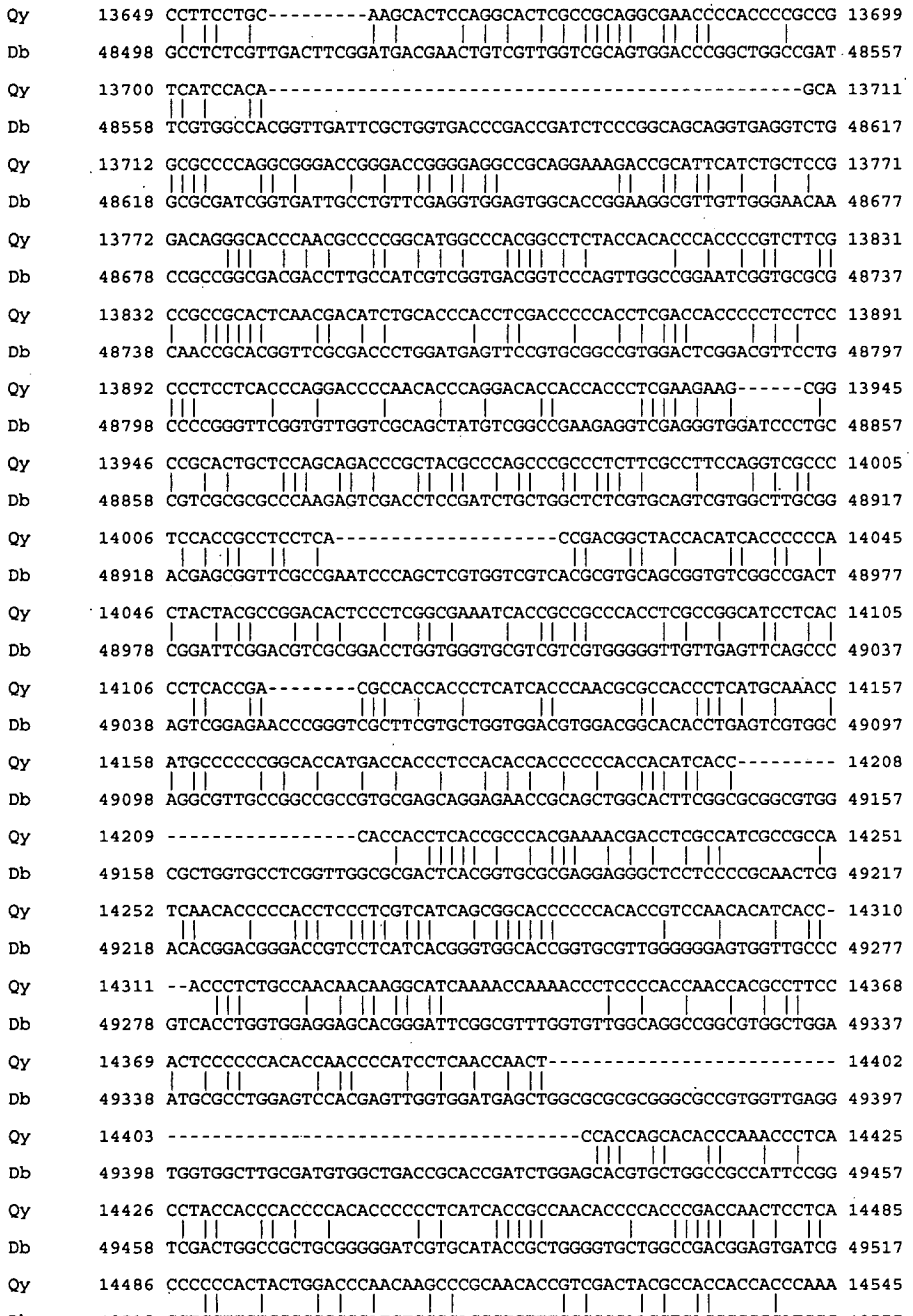

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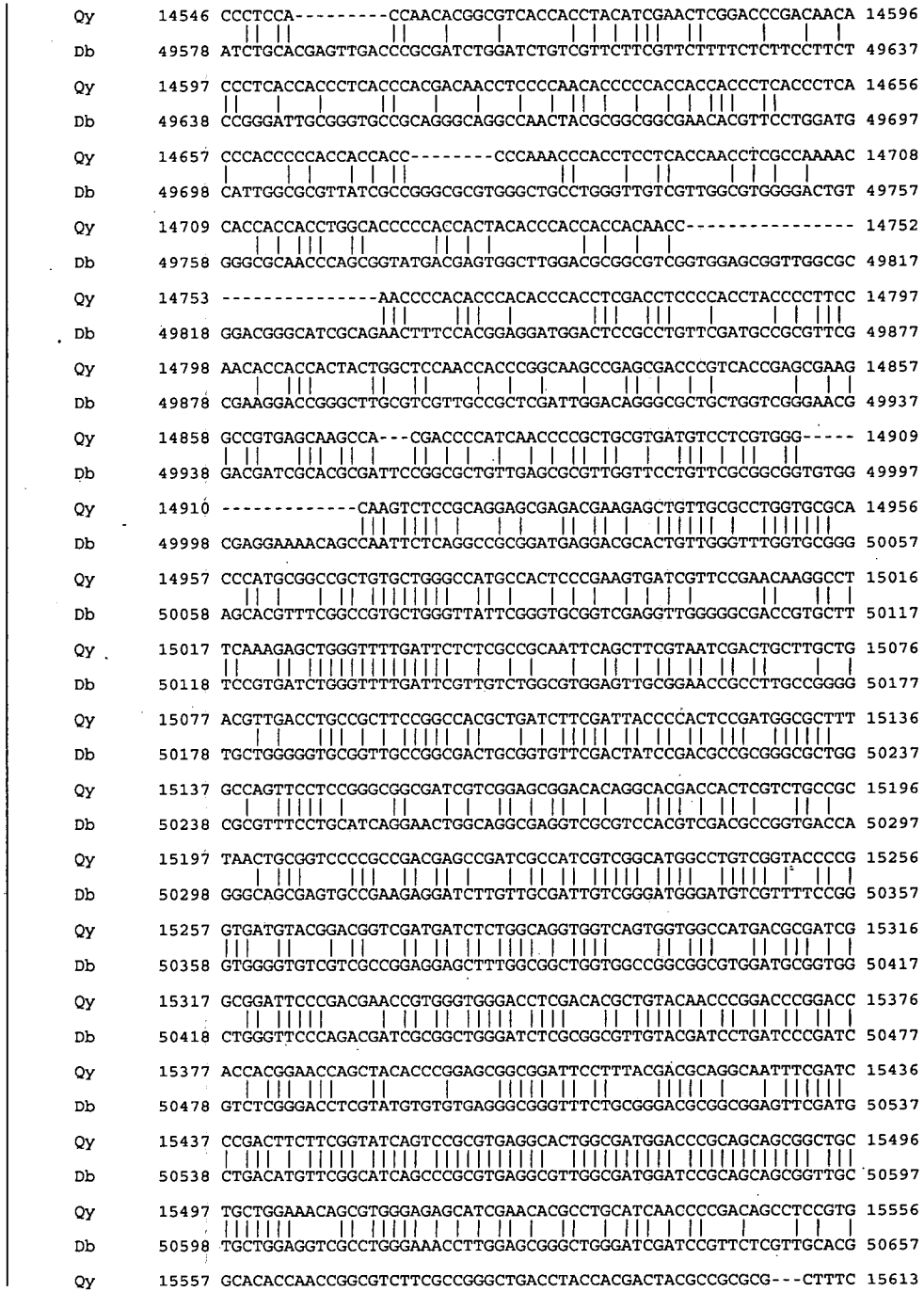

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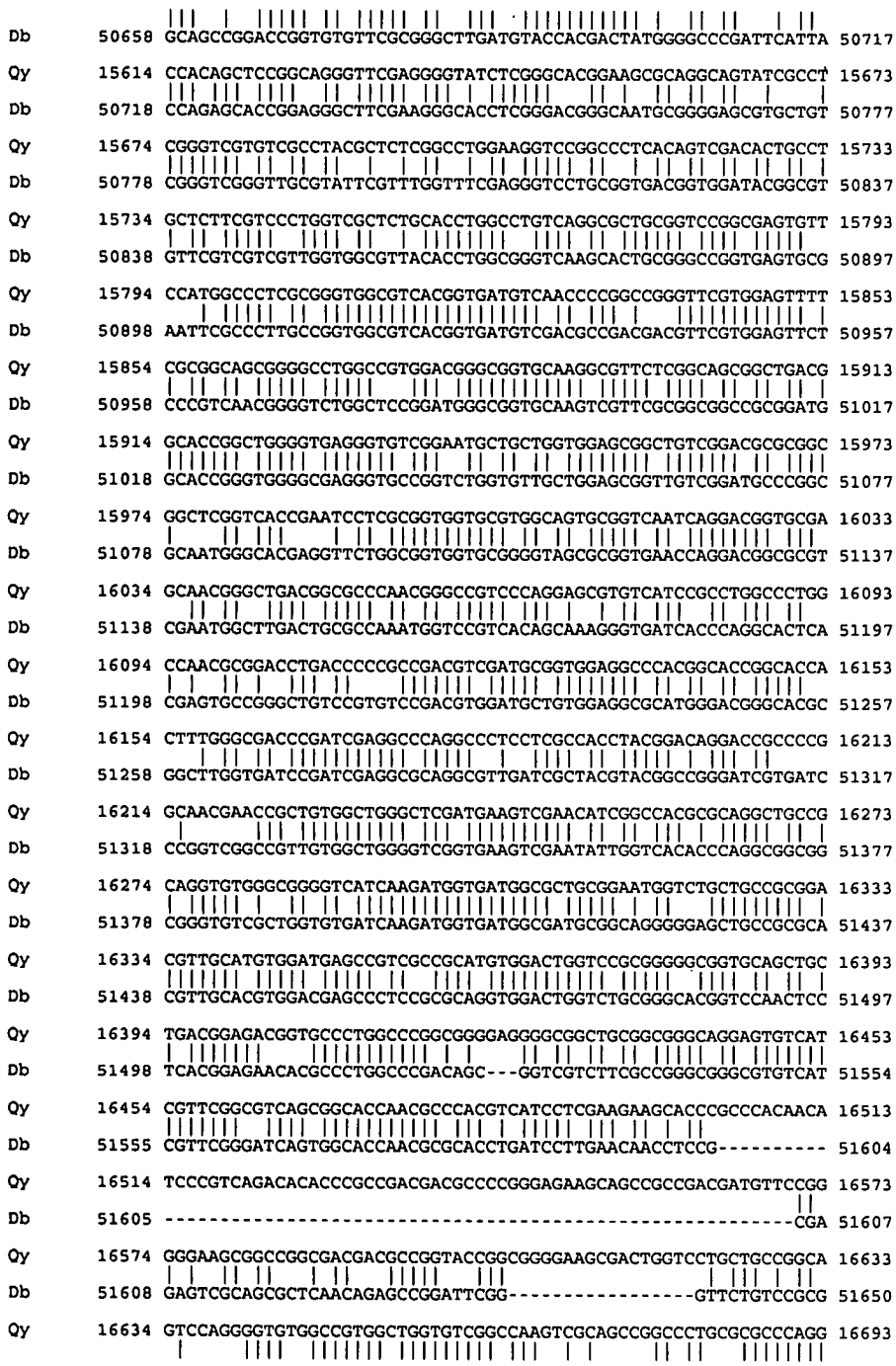


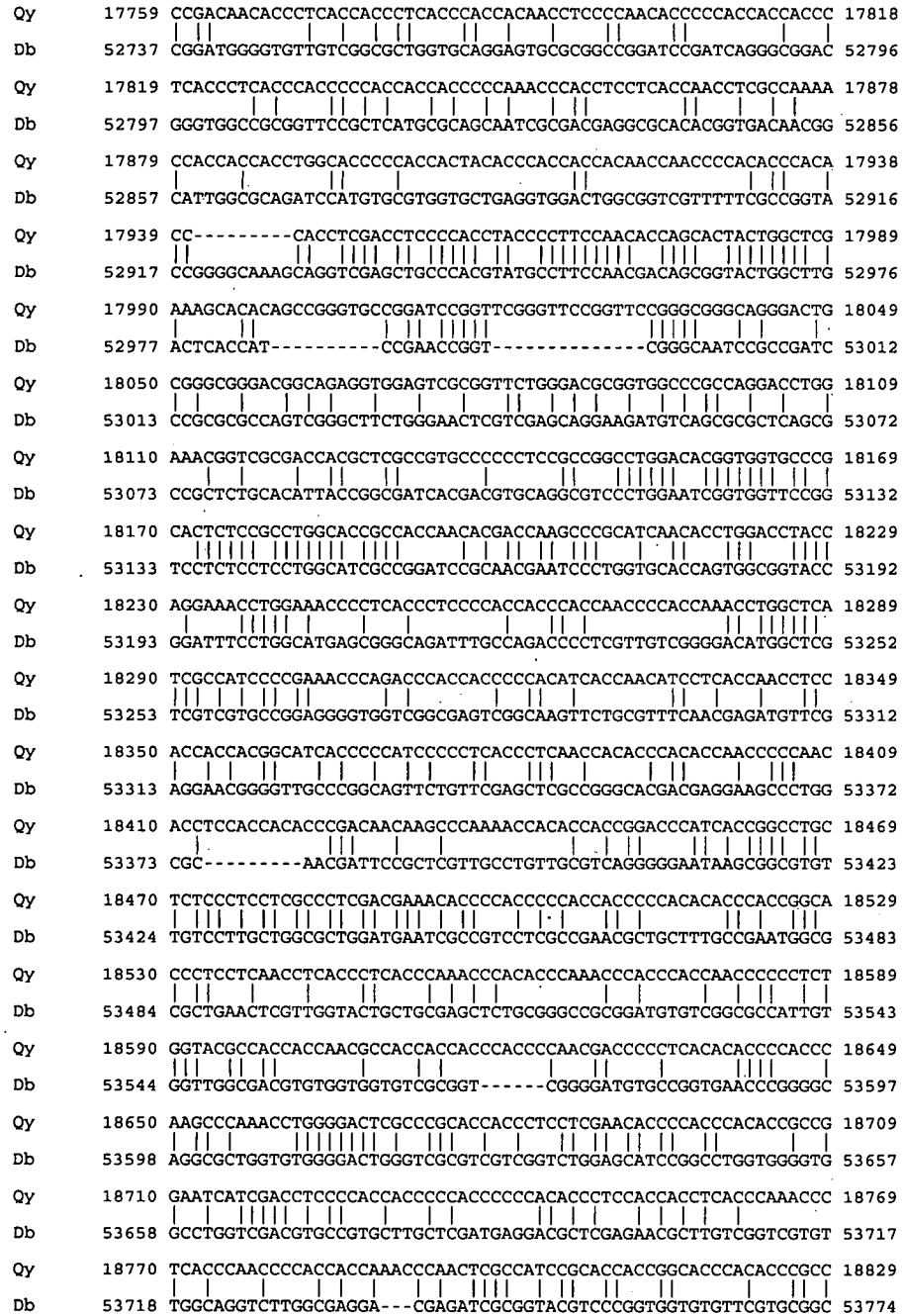


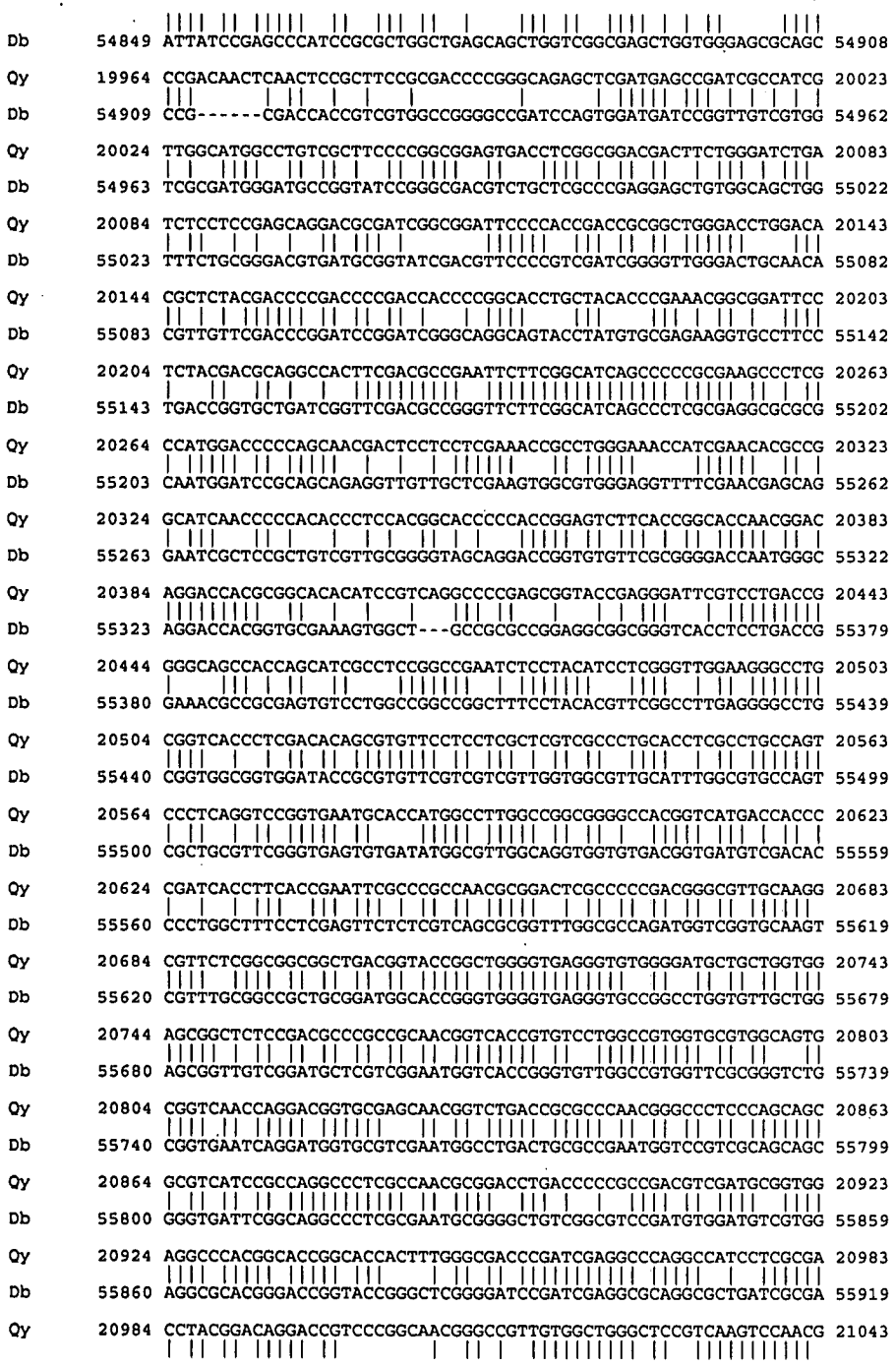

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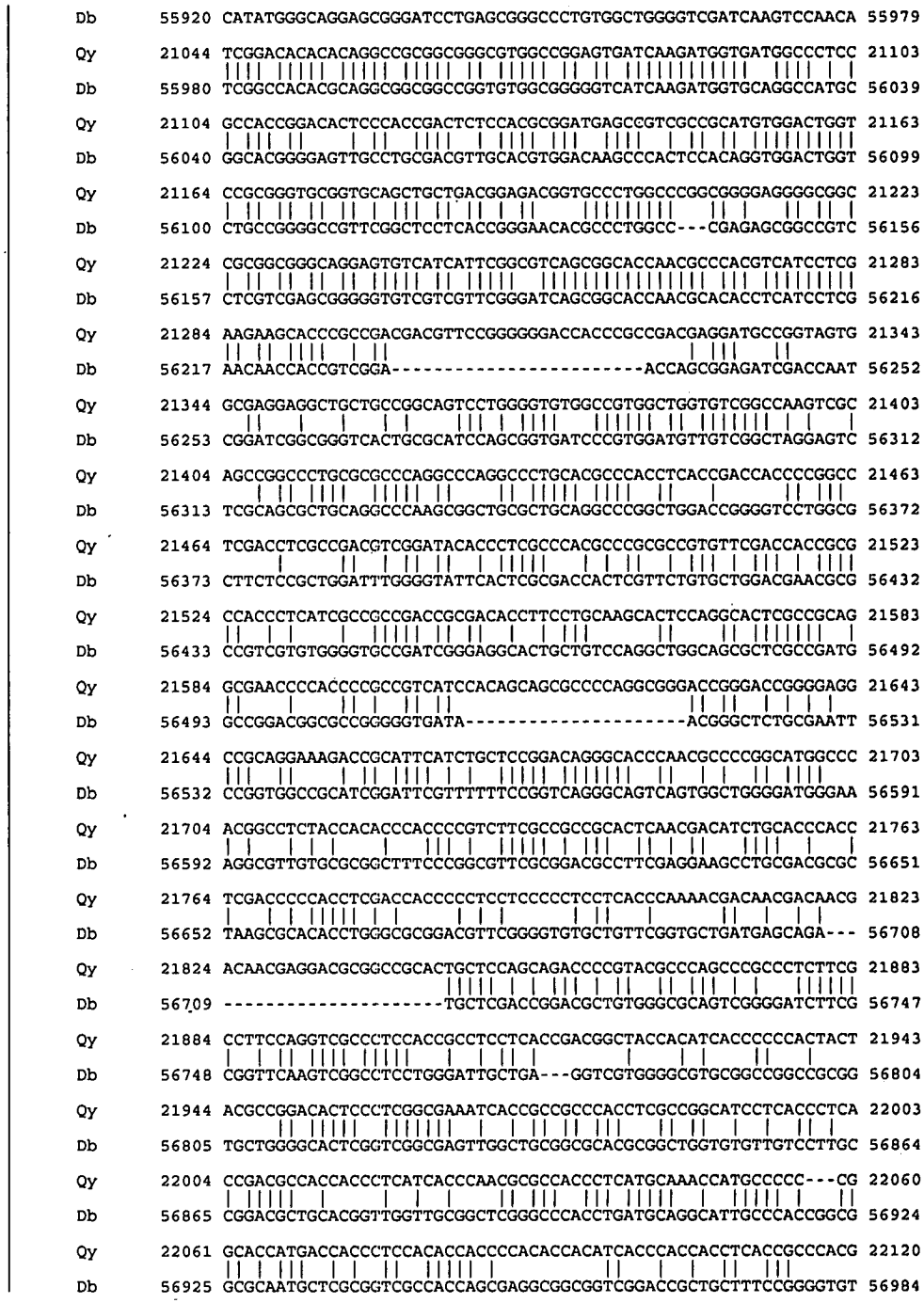


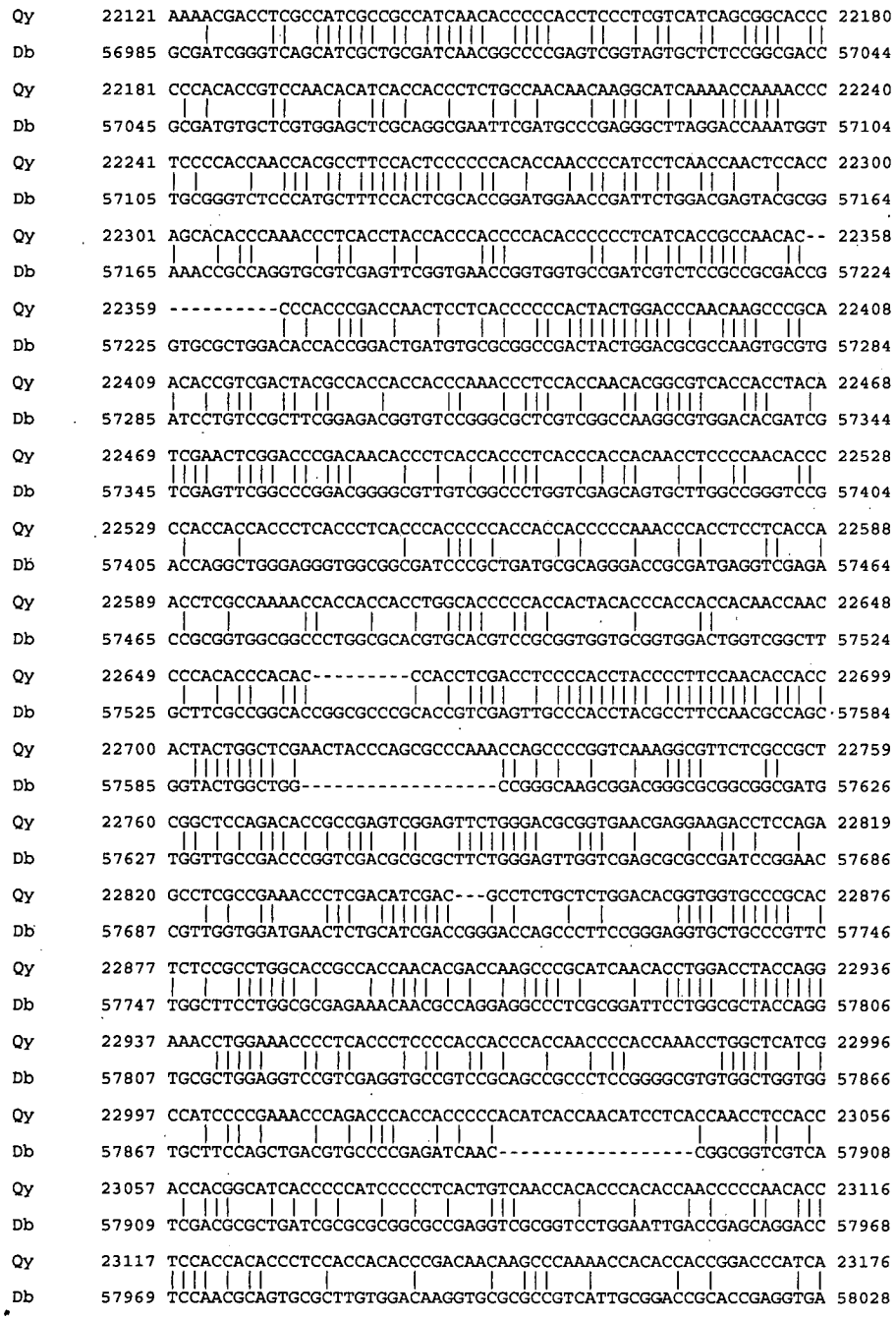


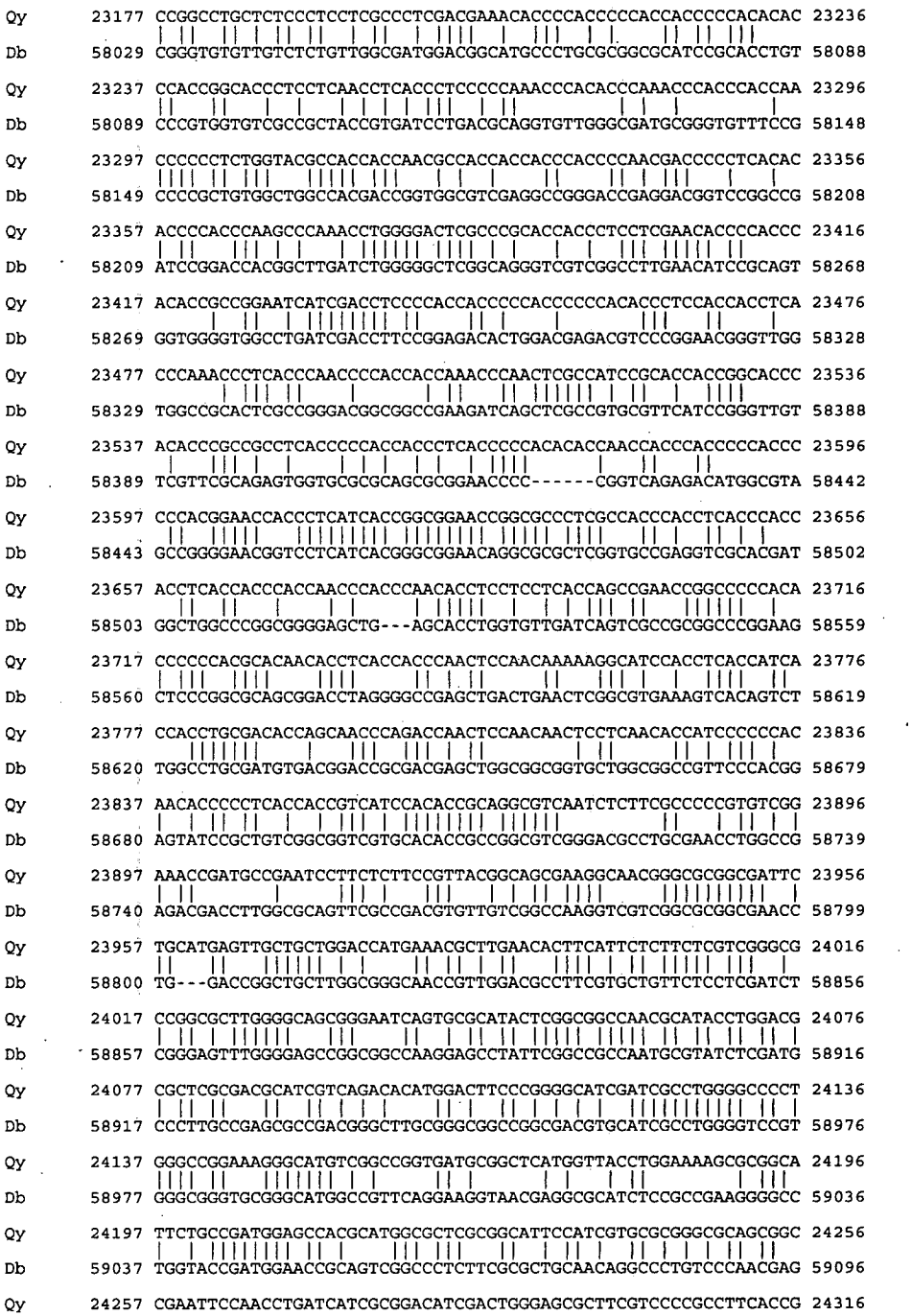

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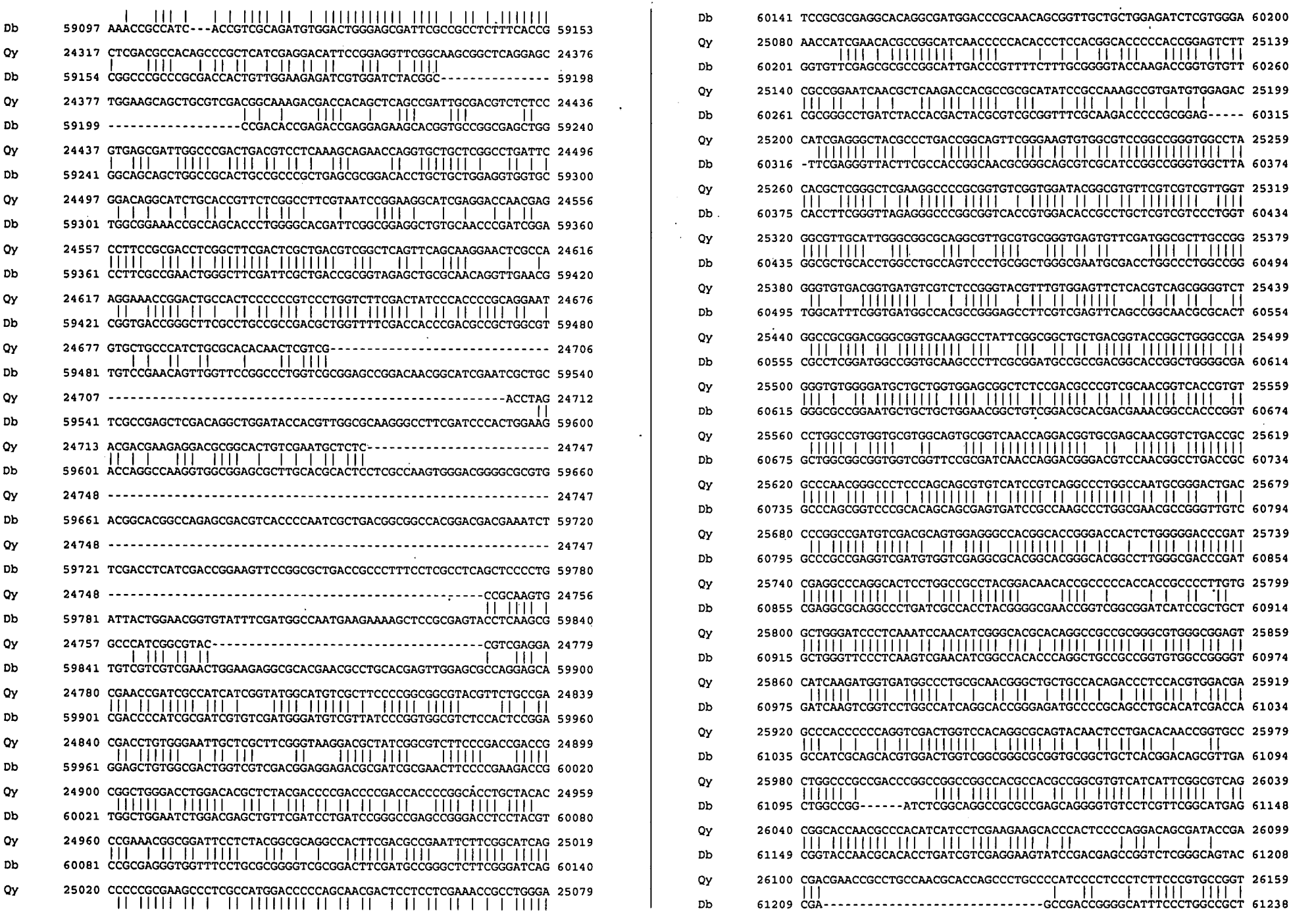

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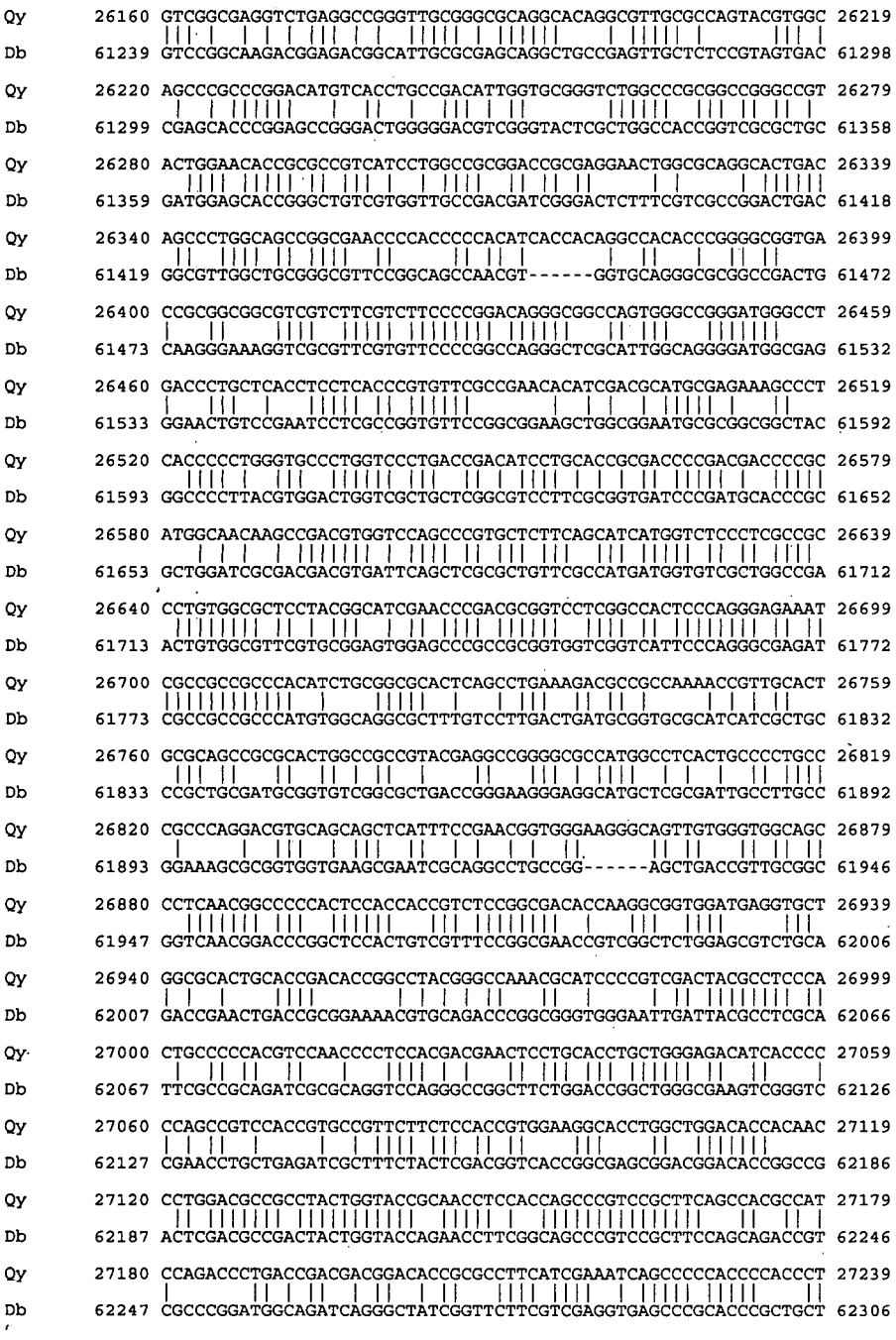

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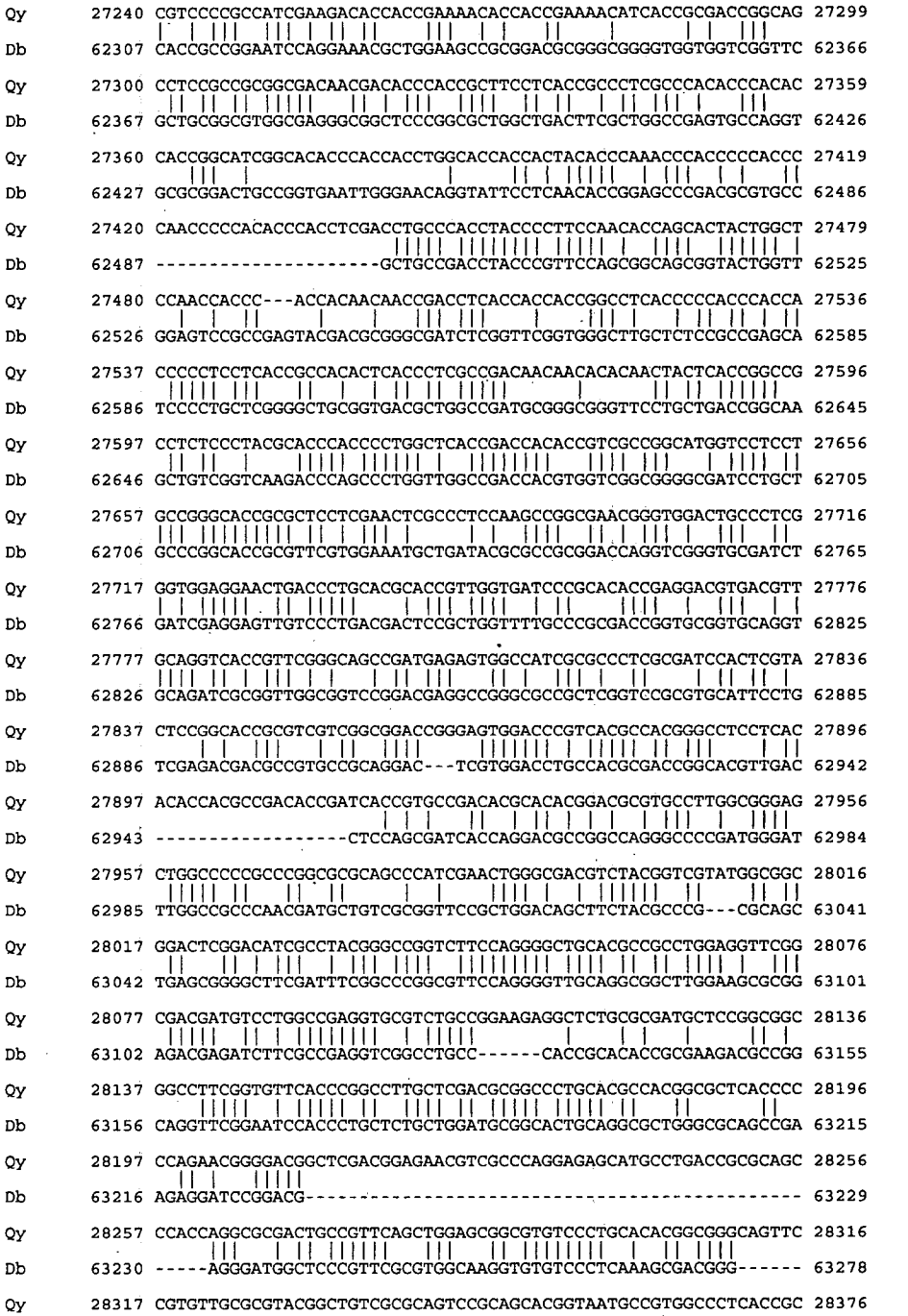

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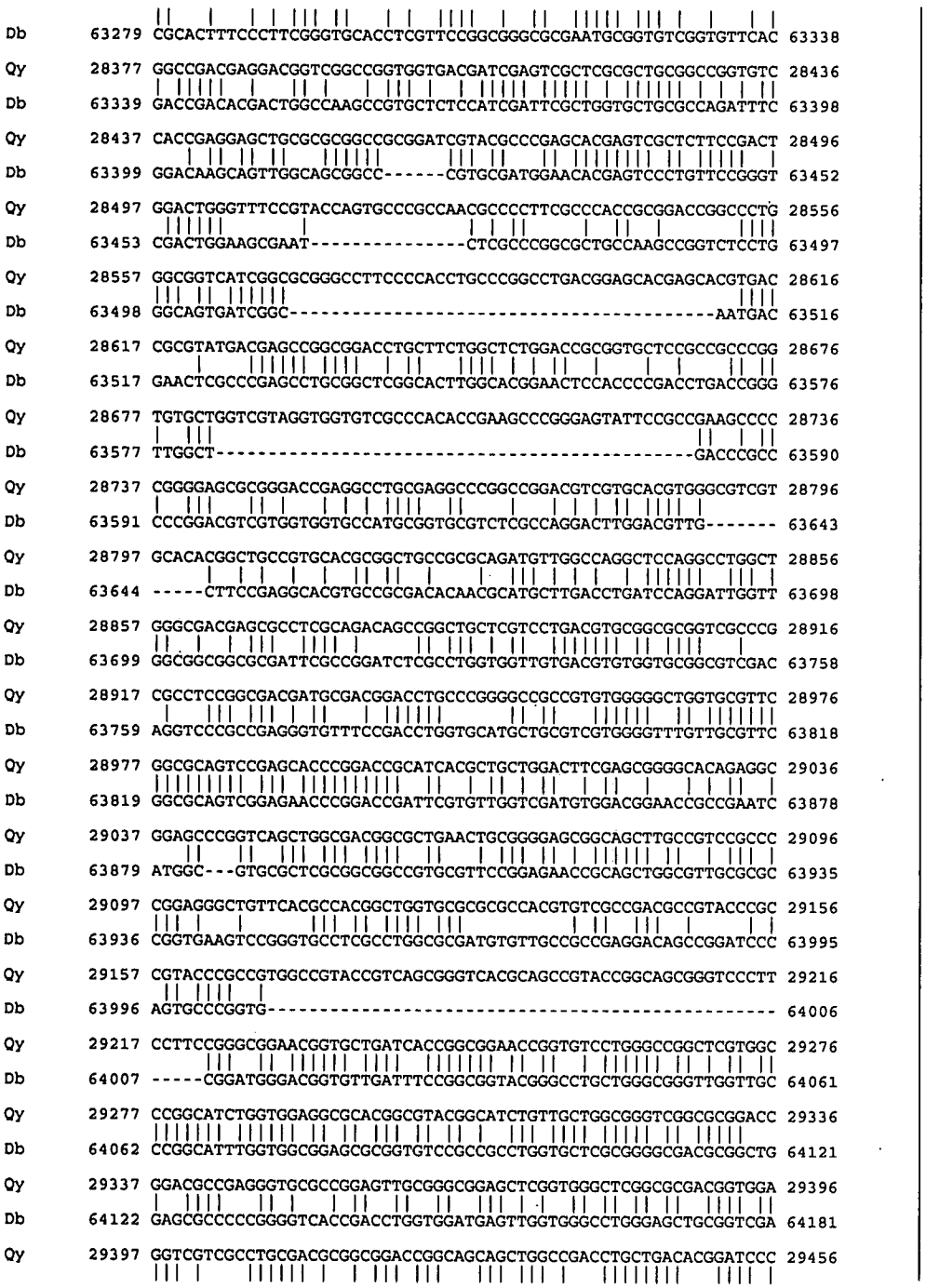







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RESULT 3
US-09-370-700-1
; Sequence 1, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J

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;  APPLICANT: Turner, Jan R
;  APPLICANT: Waldron, Clive
;  TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
;  FILE REFERENCE: 50489 DIV1
;  CURRENT APPLICATION NUMBER: US/09/370,700
;  CURRENT FILING DATE: 1999-08-09
;  EARLIER APPLICATION NUMBER: US 09/36987
;  EARLIER FILING DATE: 1998-03-09
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 80161
;   TYPE: DNA
;   ORGANISM: Saccharopolyspora spinosa
US-09-370-700-1

  Query Match             10.2%;  Score 3142;  DB 4;  Length 80161;
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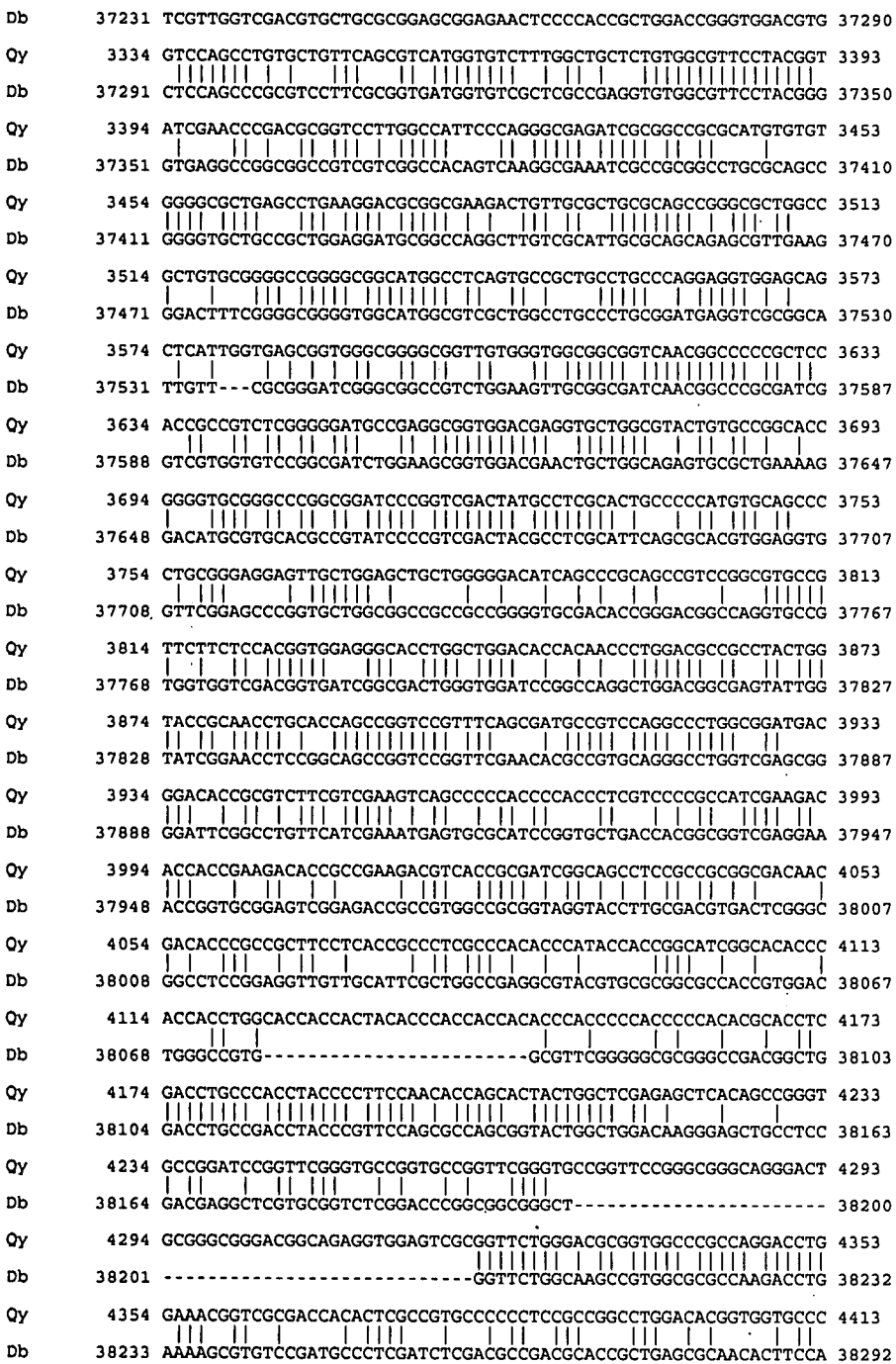
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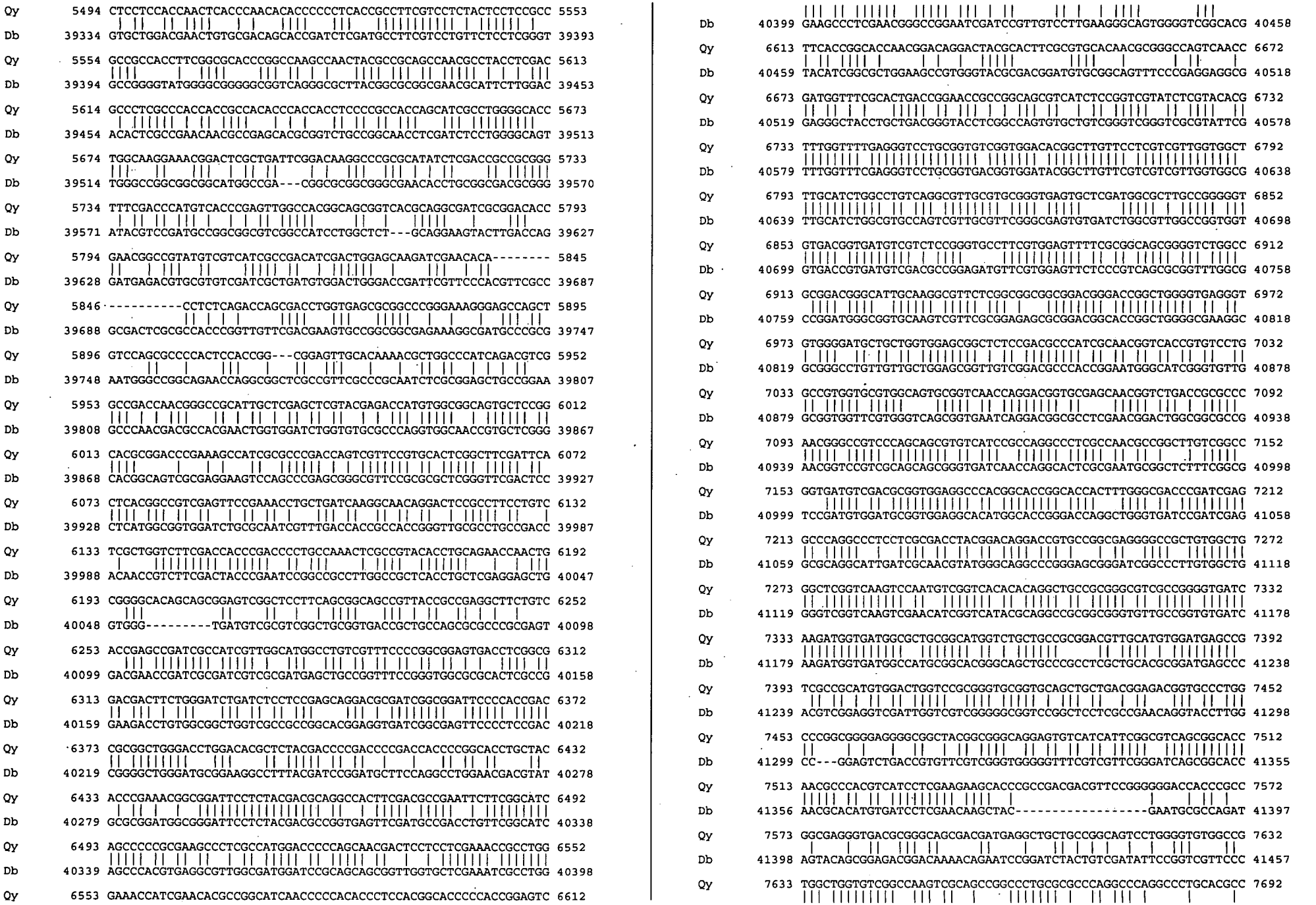
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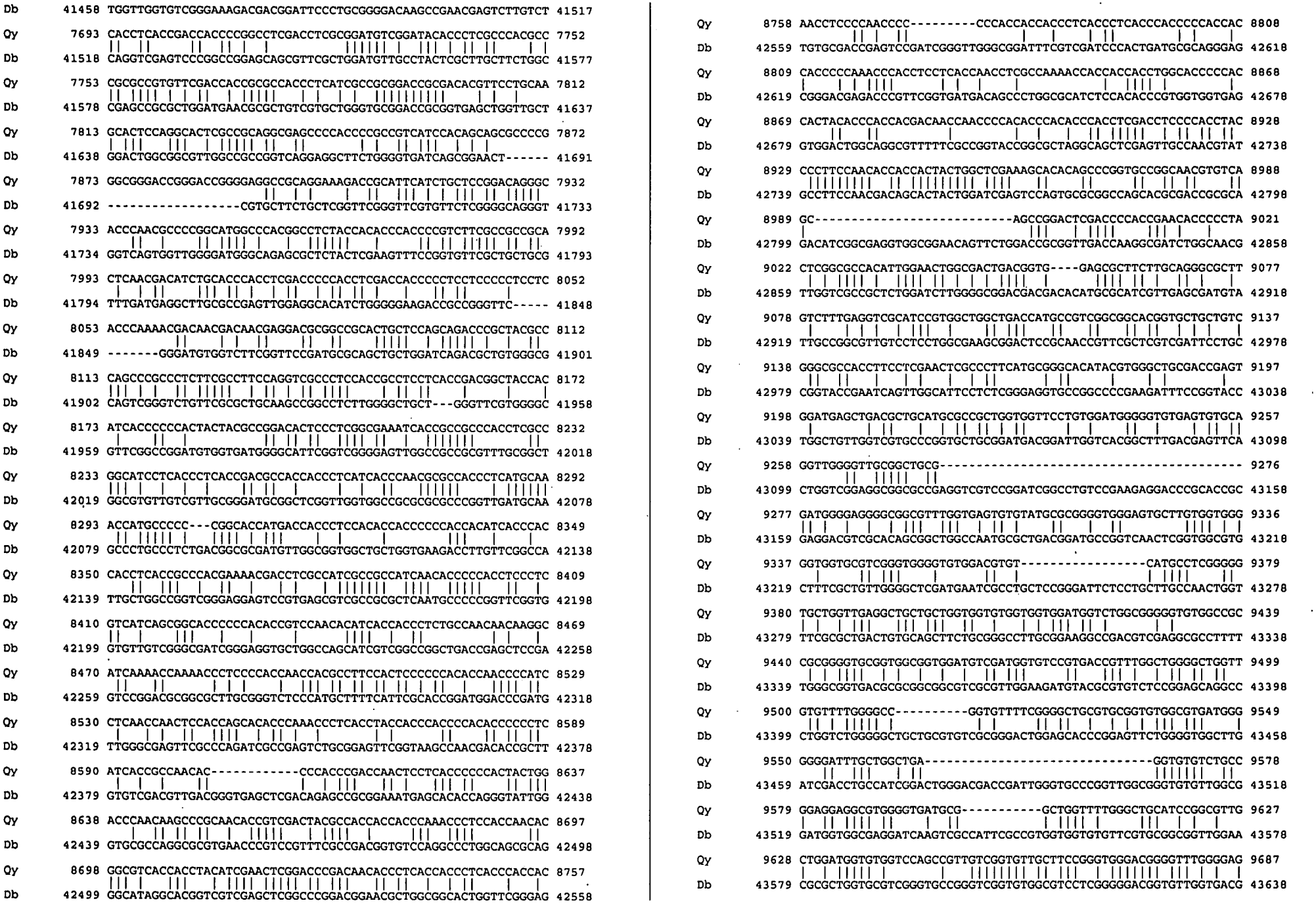
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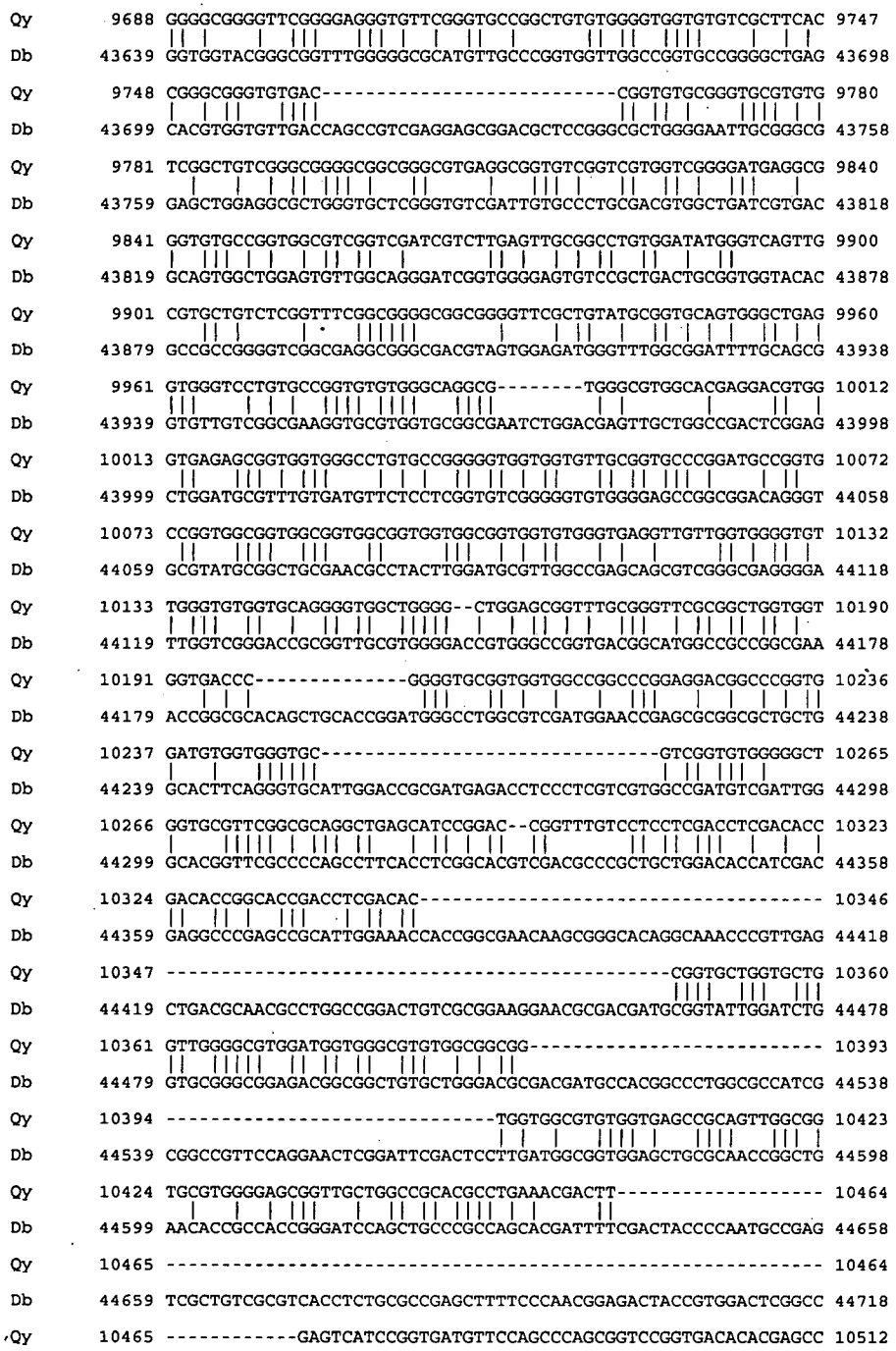
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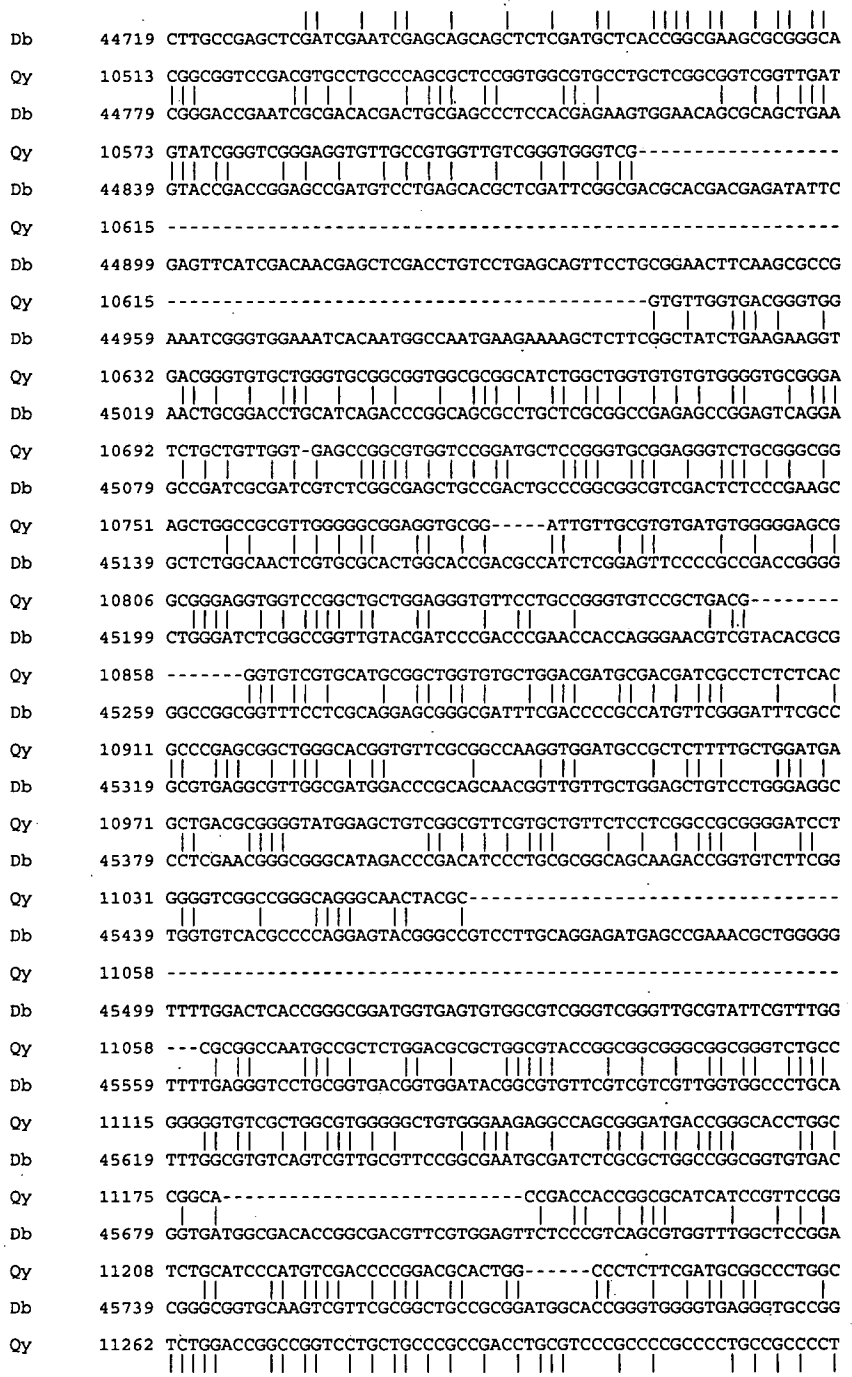
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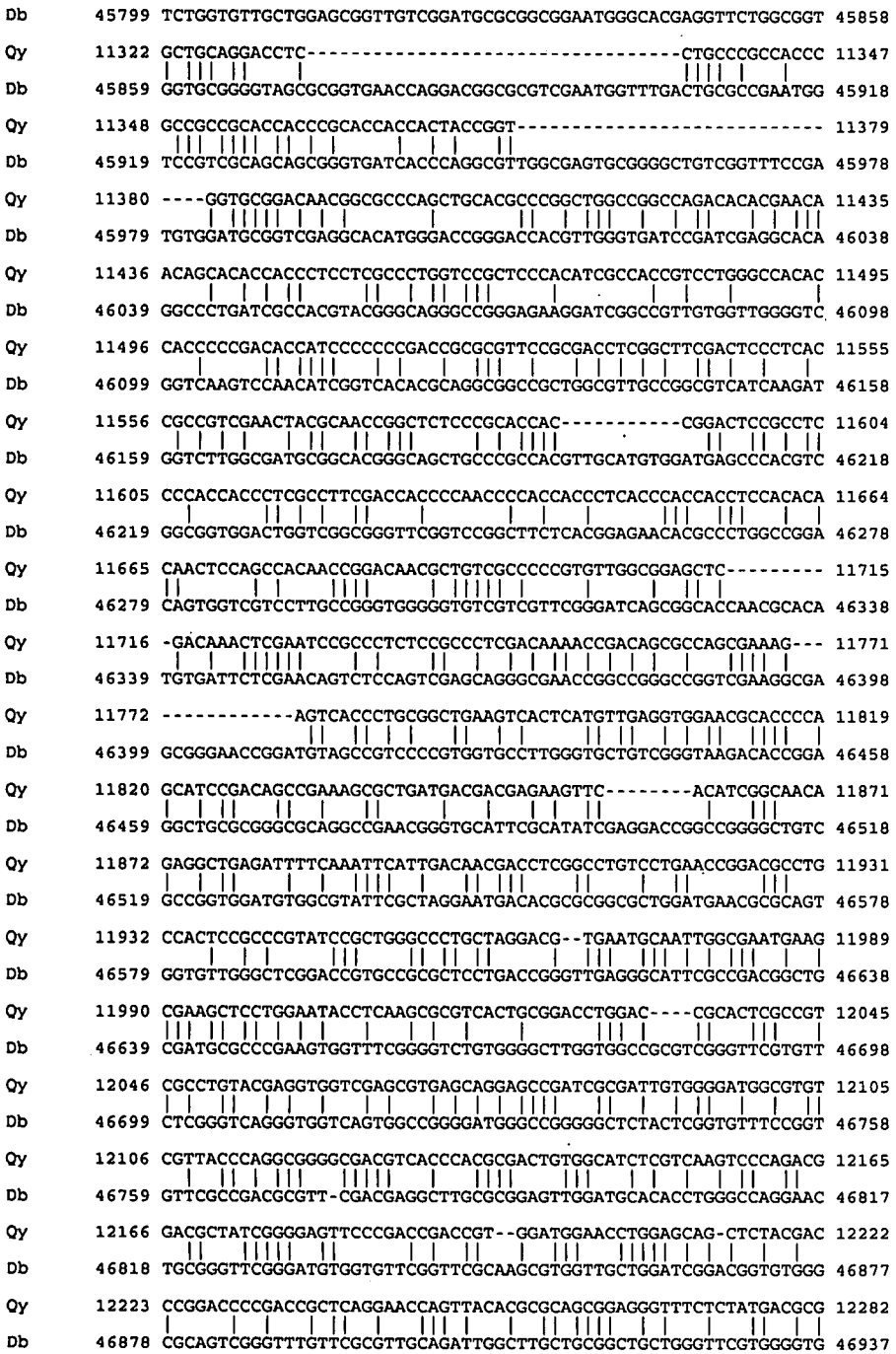

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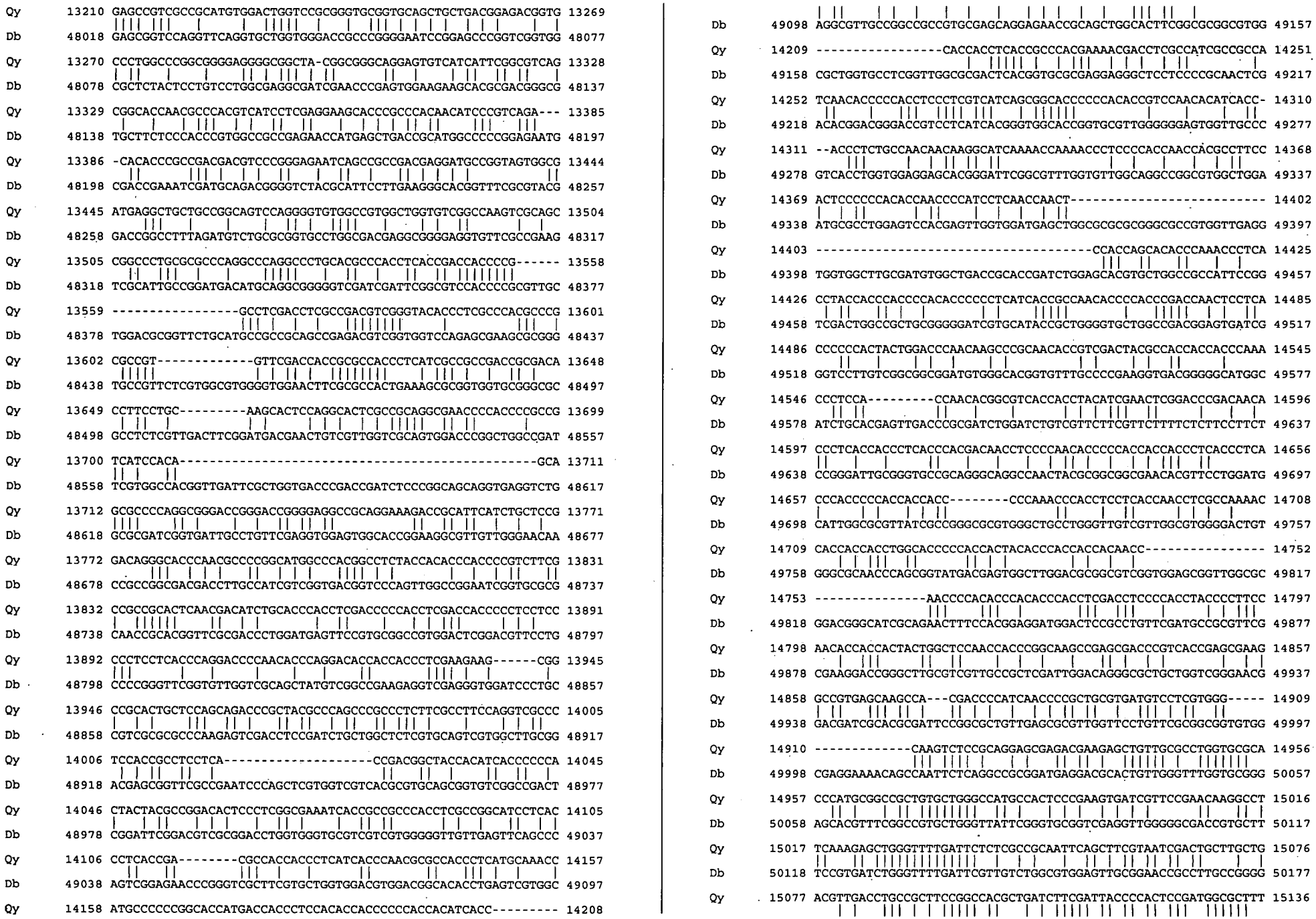


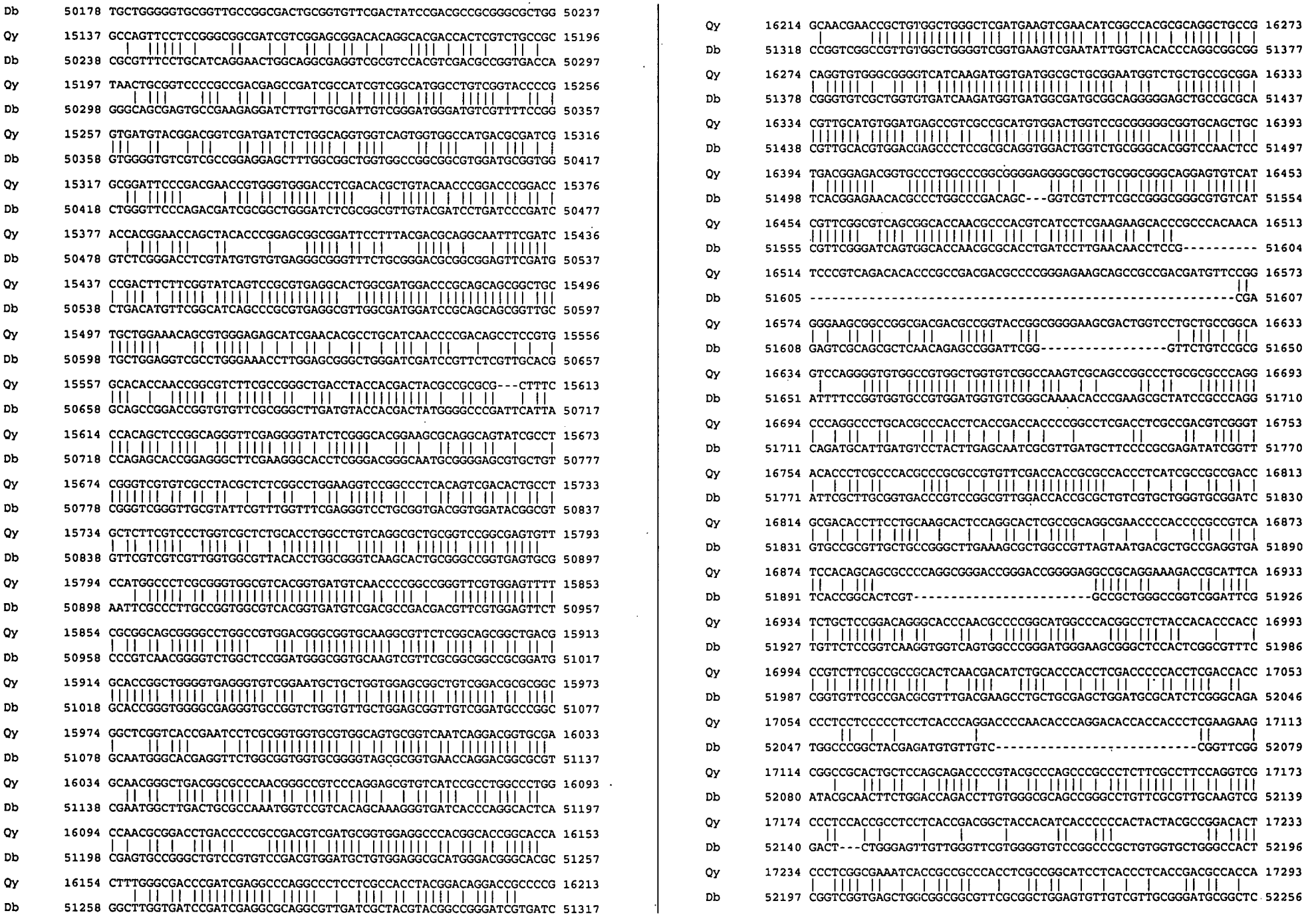


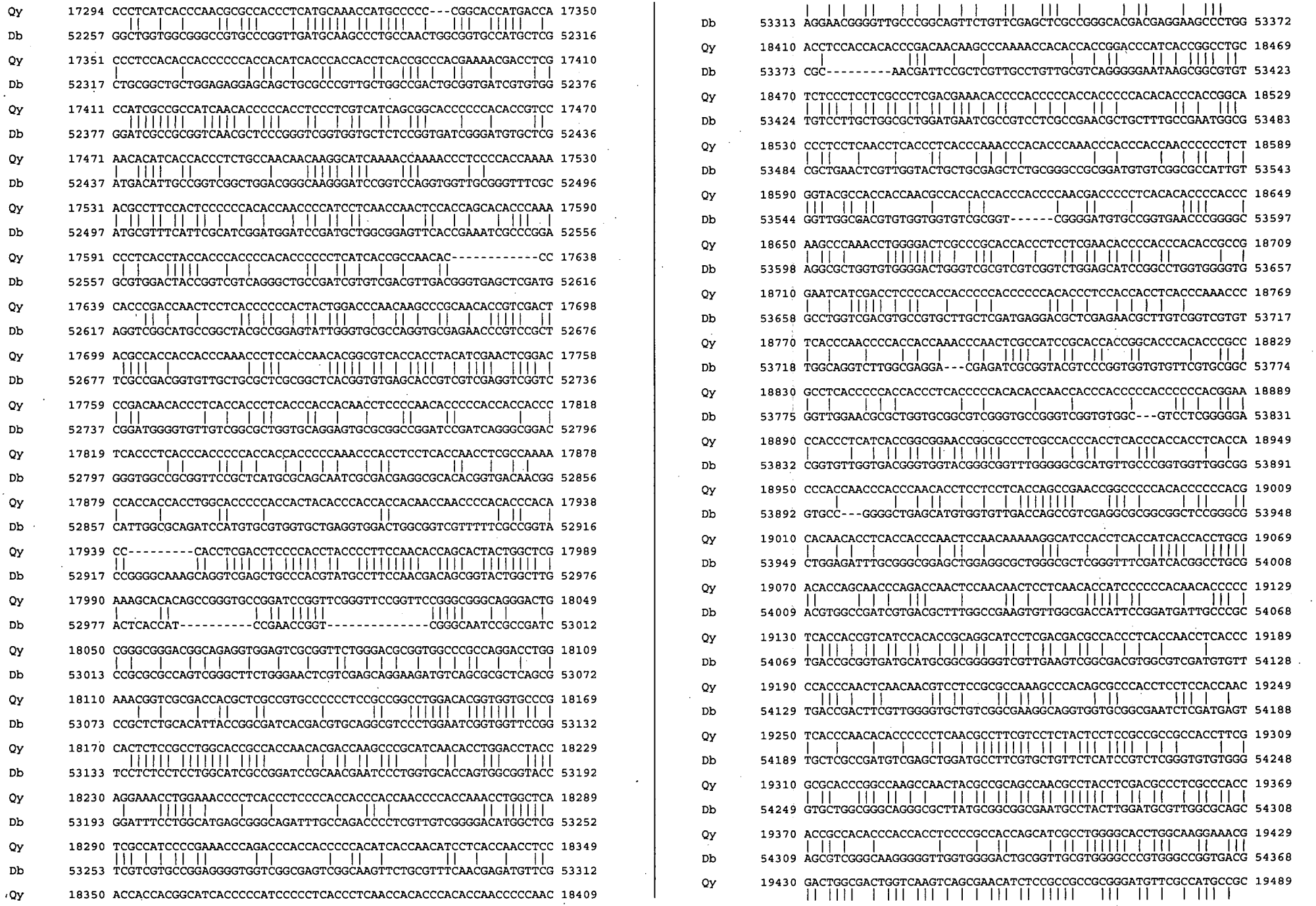


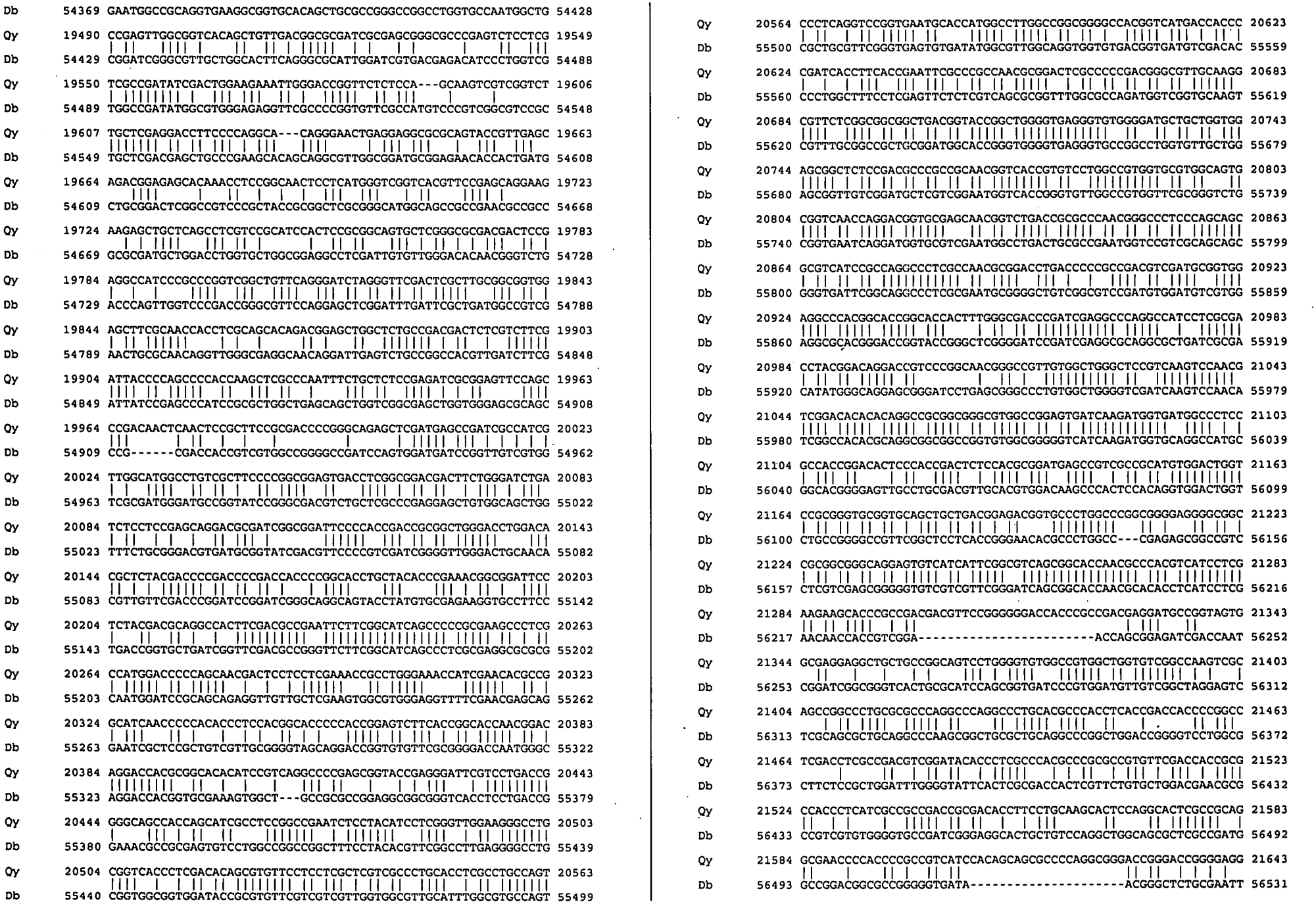


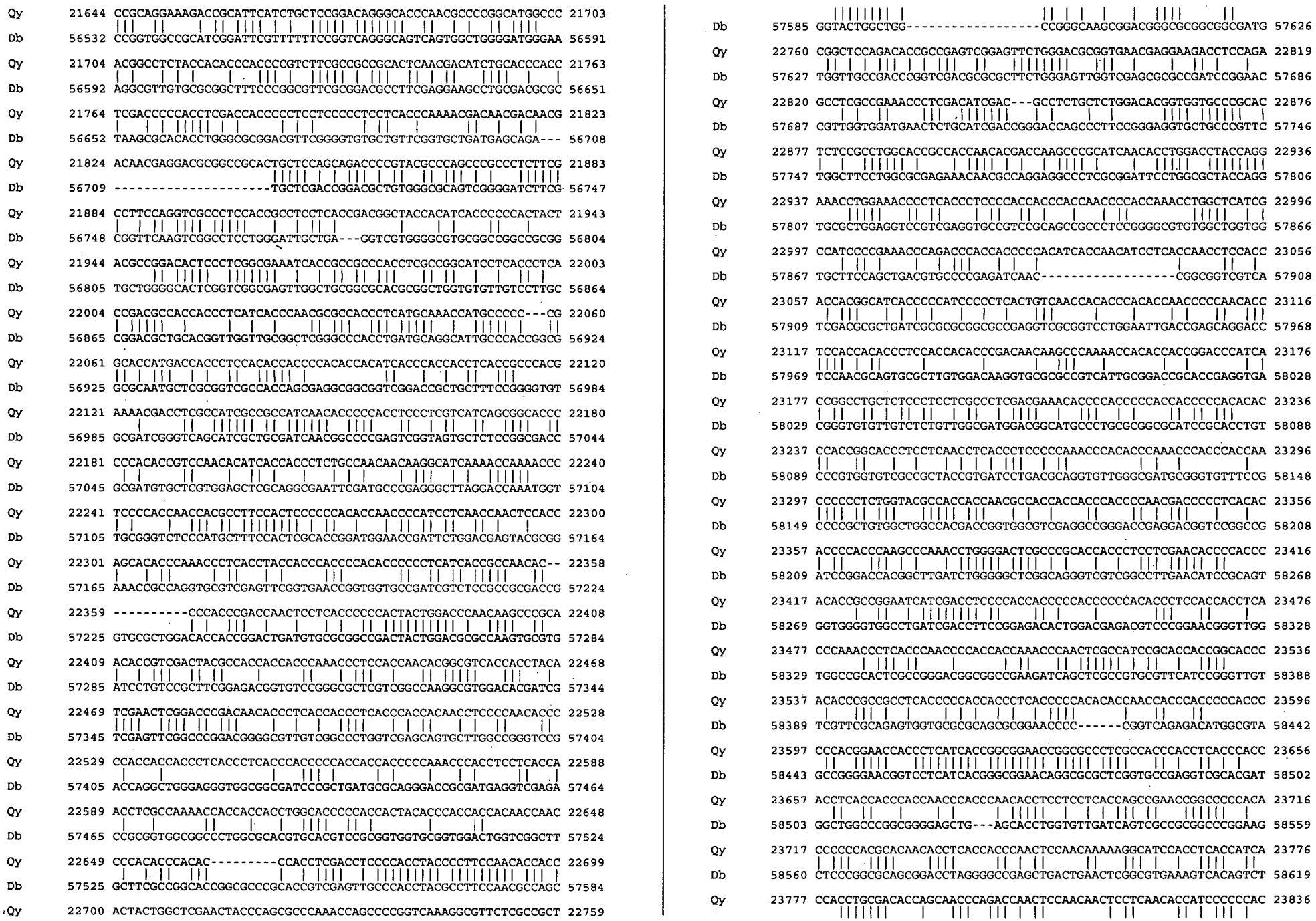

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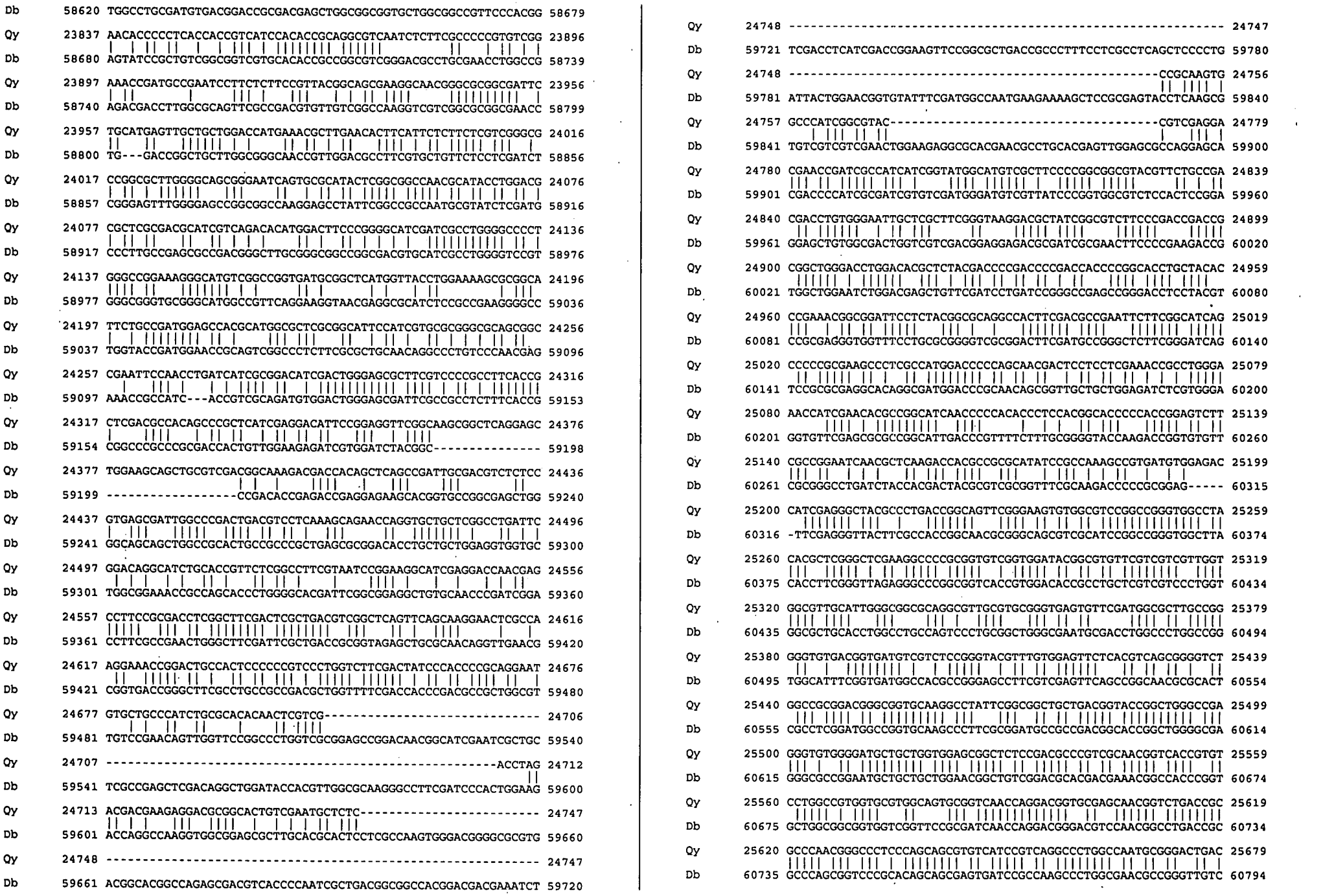


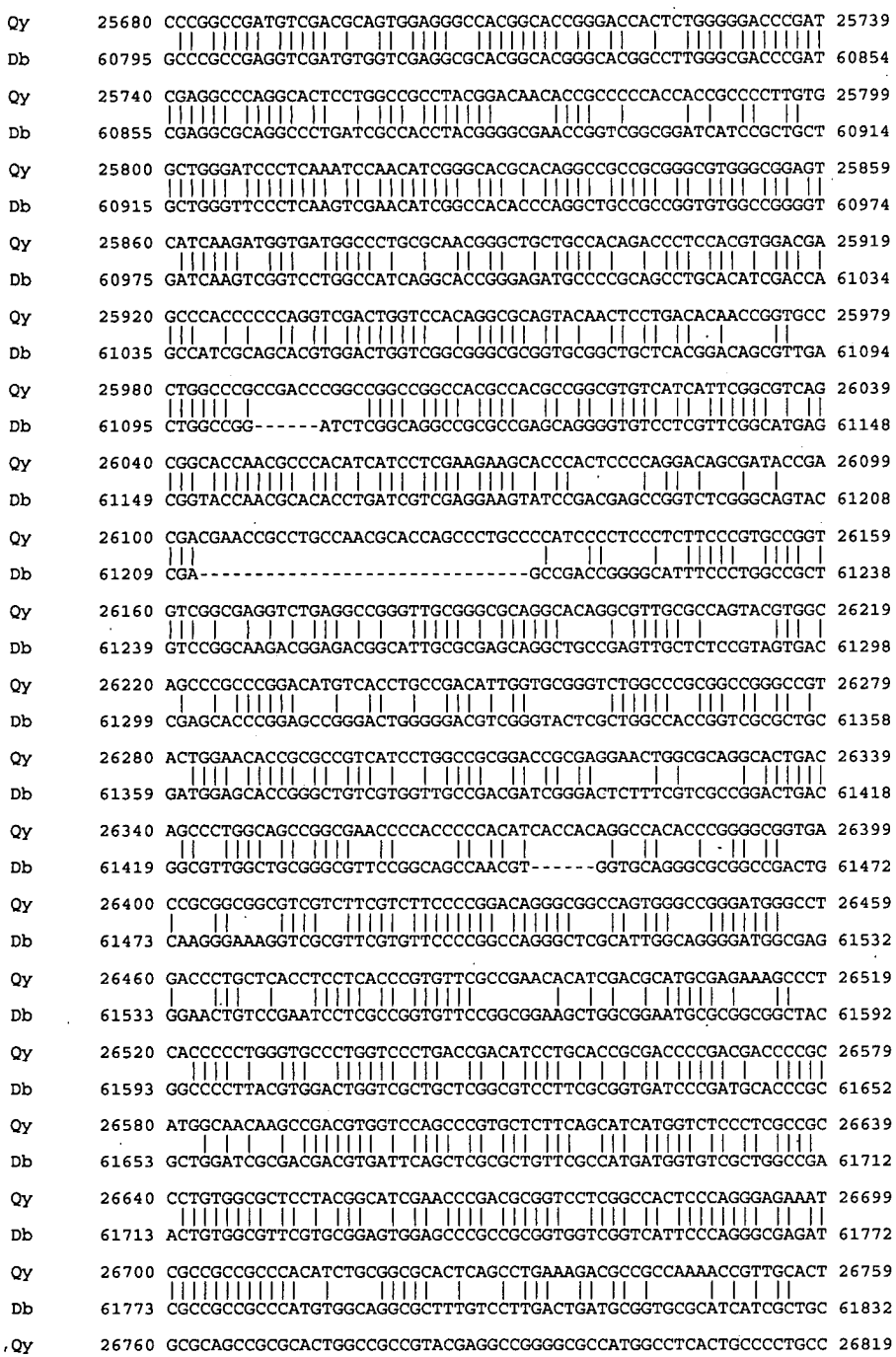


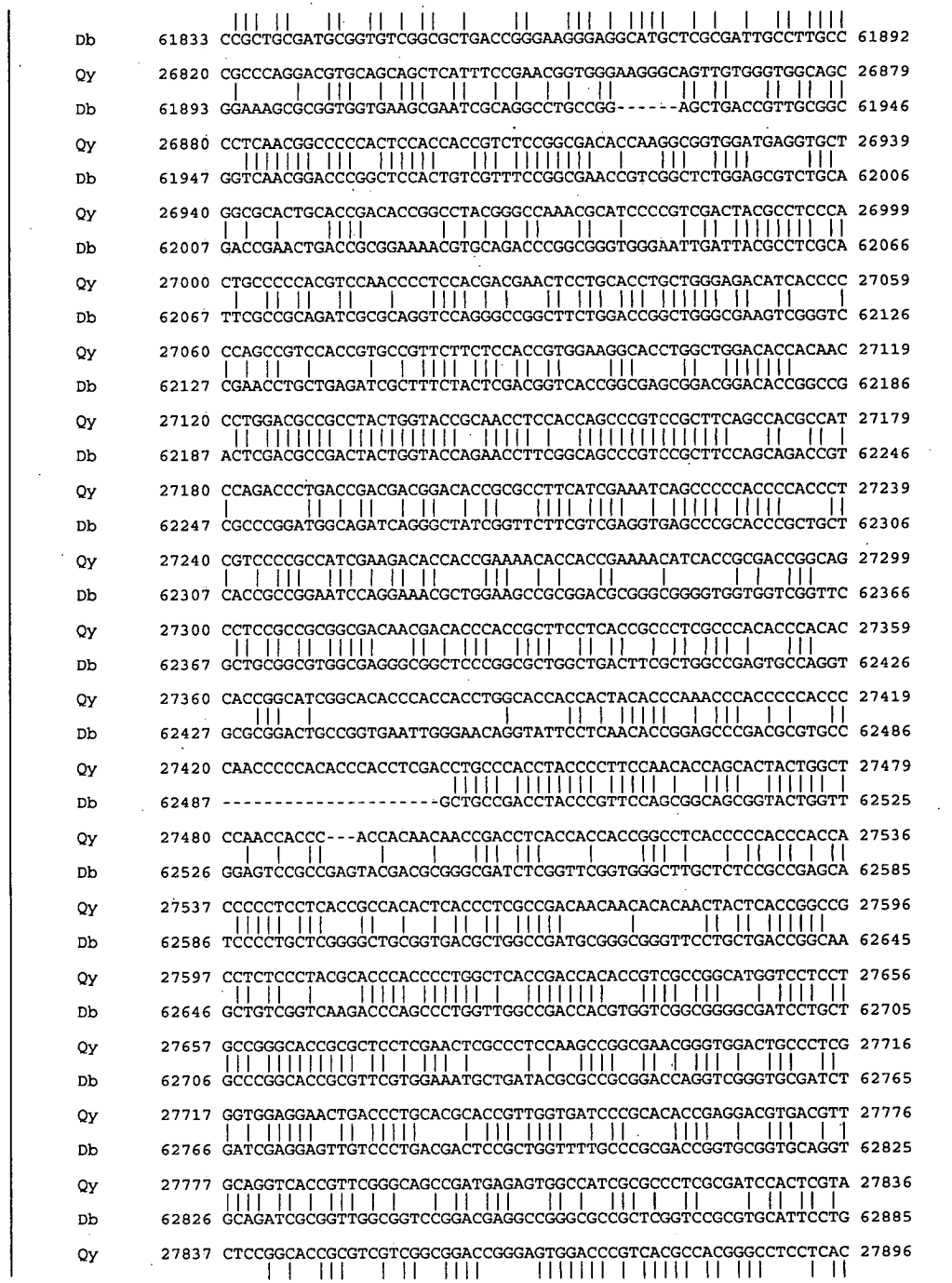


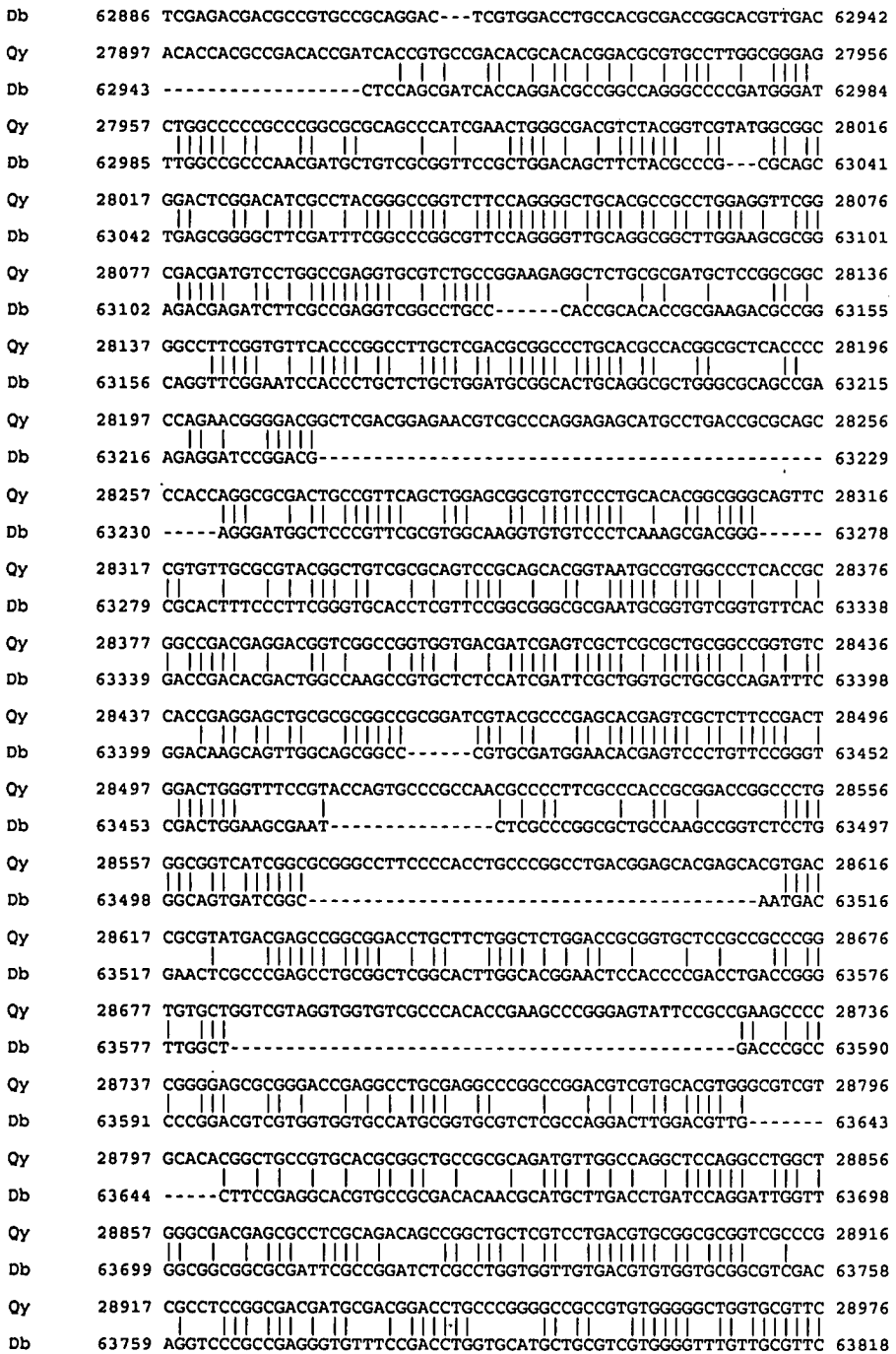











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RESULT 4
US-08-258-261B-6
; Sequence 6, Application US/08258261B
; Patent No. 5639949
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,261B
; FILING DATE: 08-JUN-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205
; FILING DATE: 01-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US-08-258-261B-6

Query Match 10.2%; Score 3140.6; DB 1; Length 28958;
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Matches 8239; Conservative 0; Mismatches 6284; Indels 698; Gaps 63;

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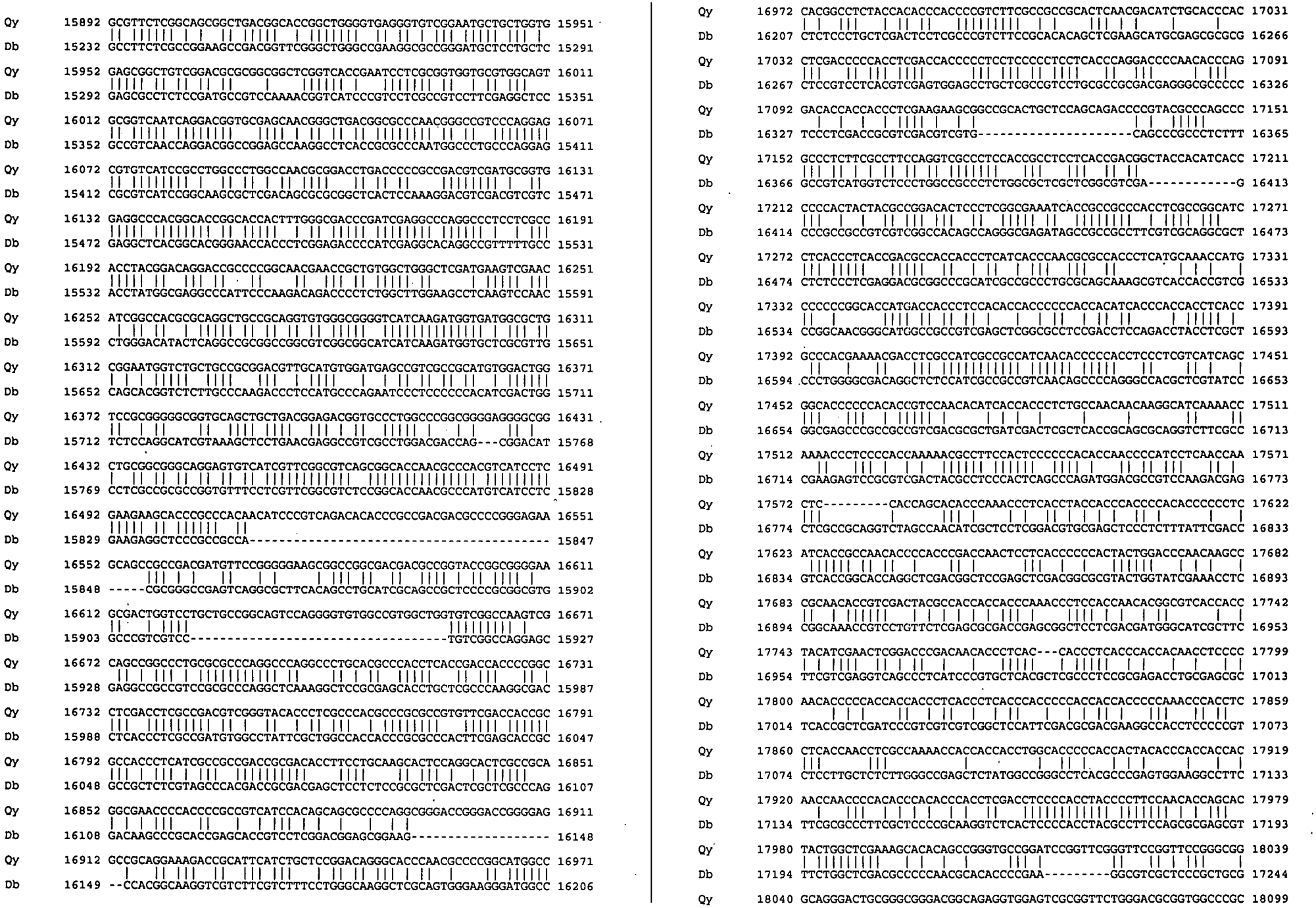
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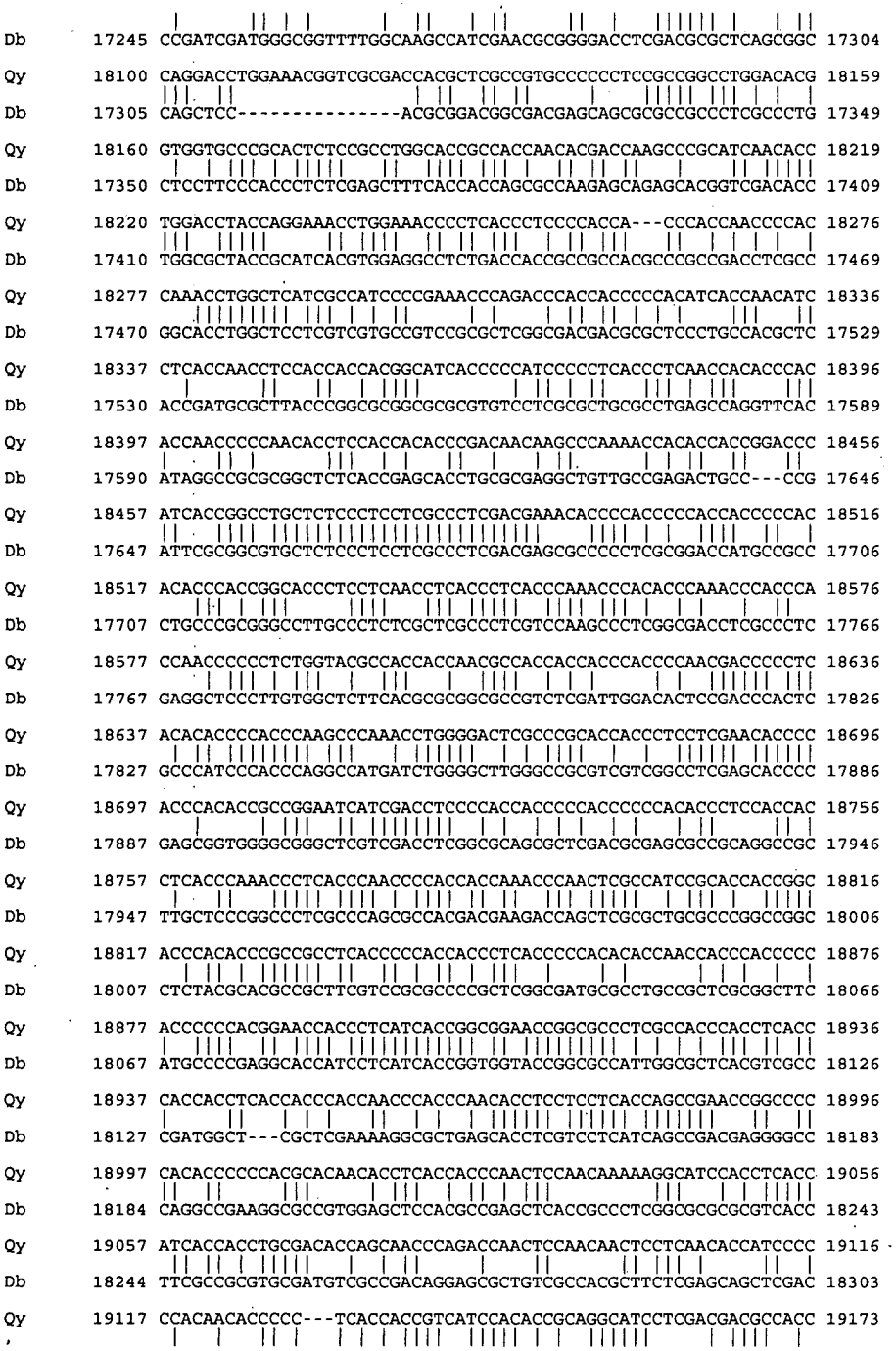
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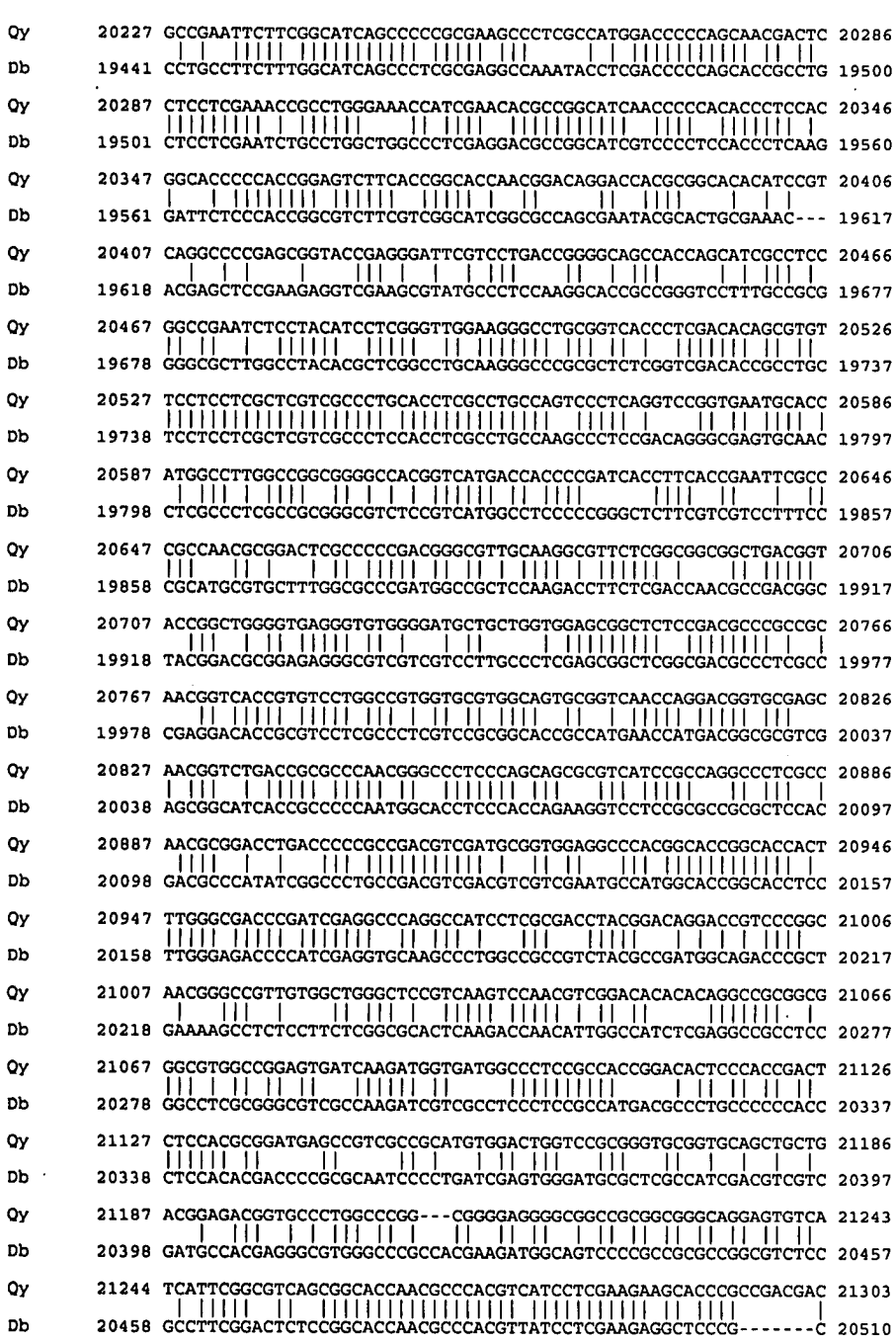
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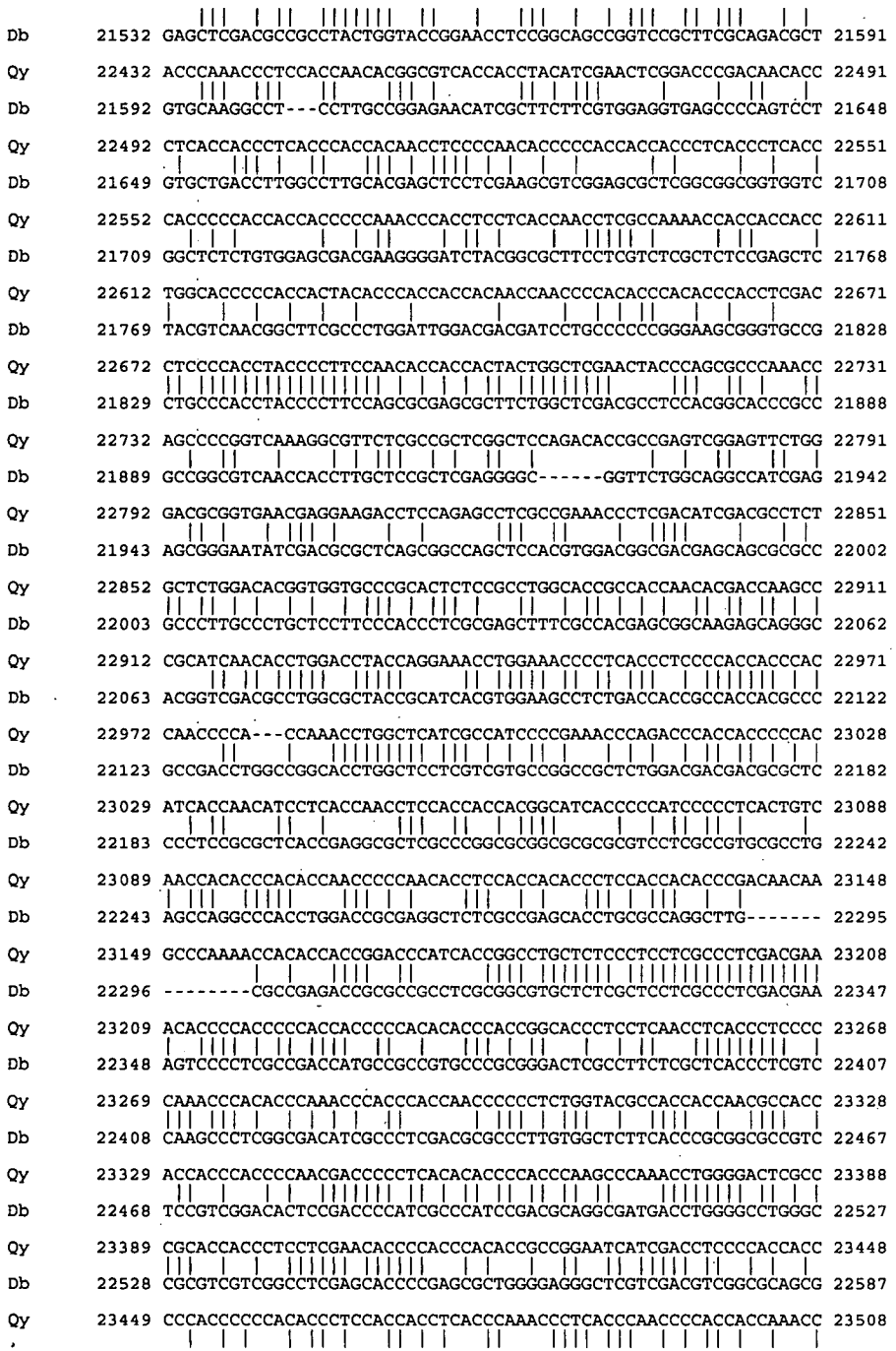
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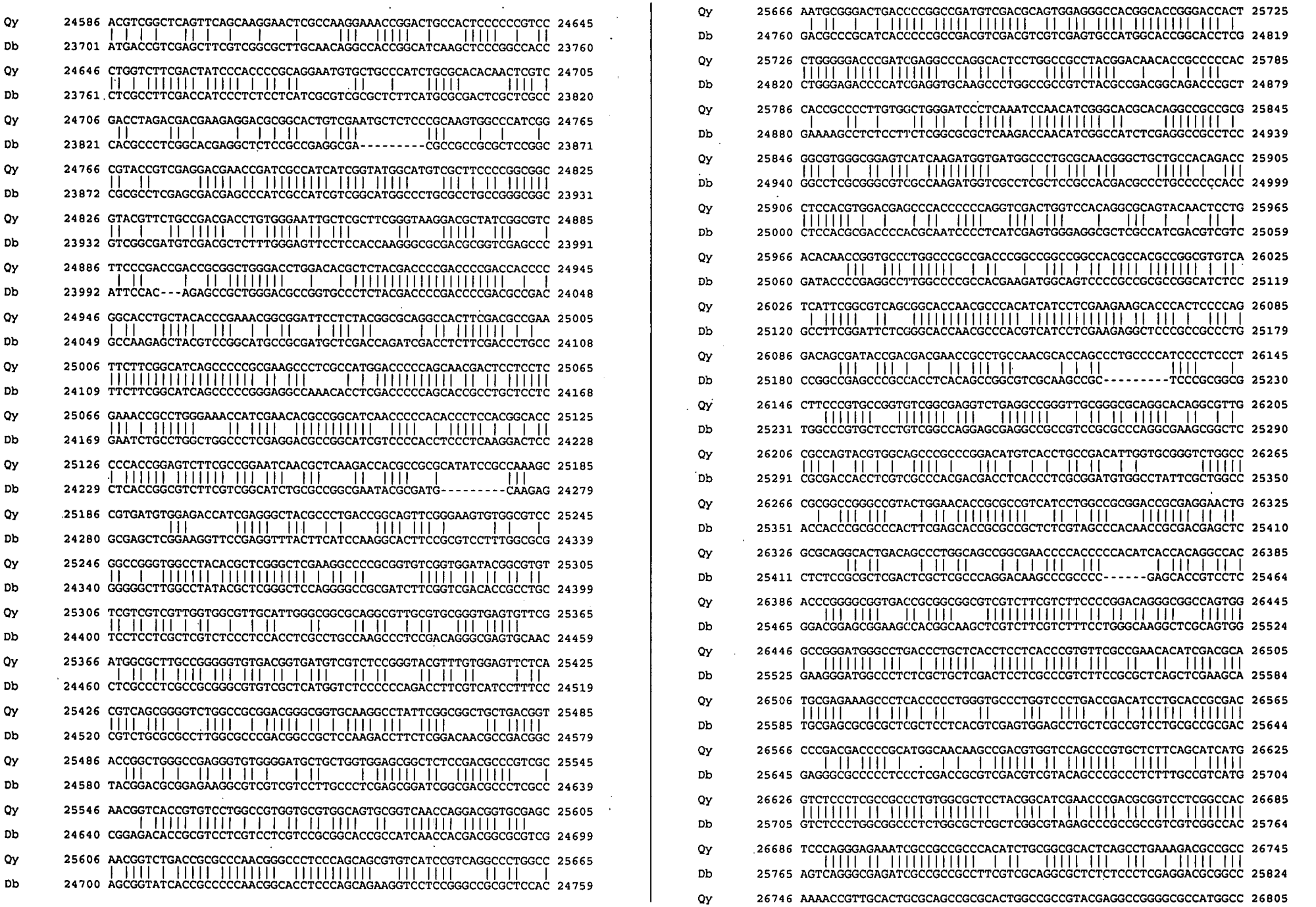
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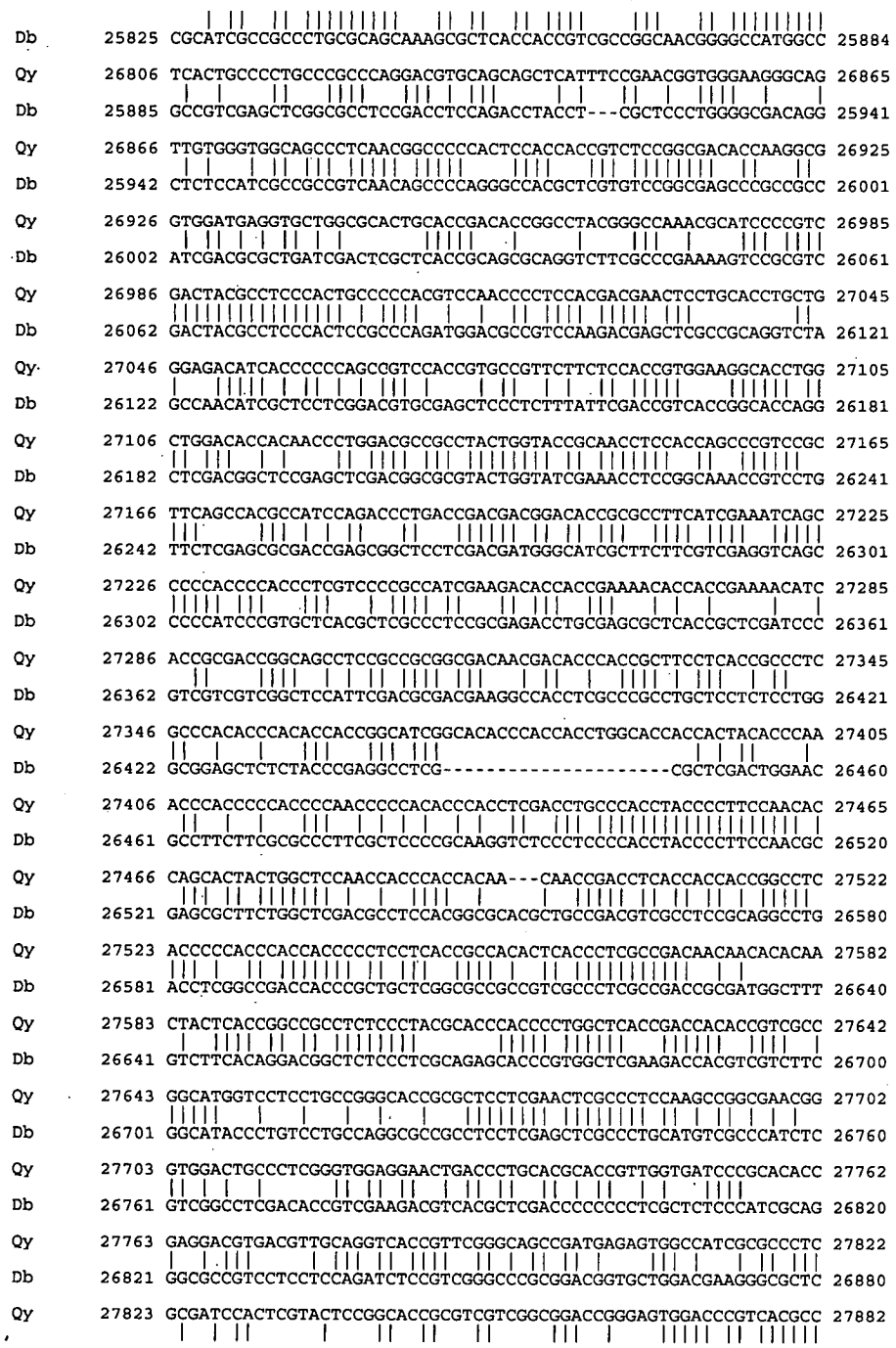


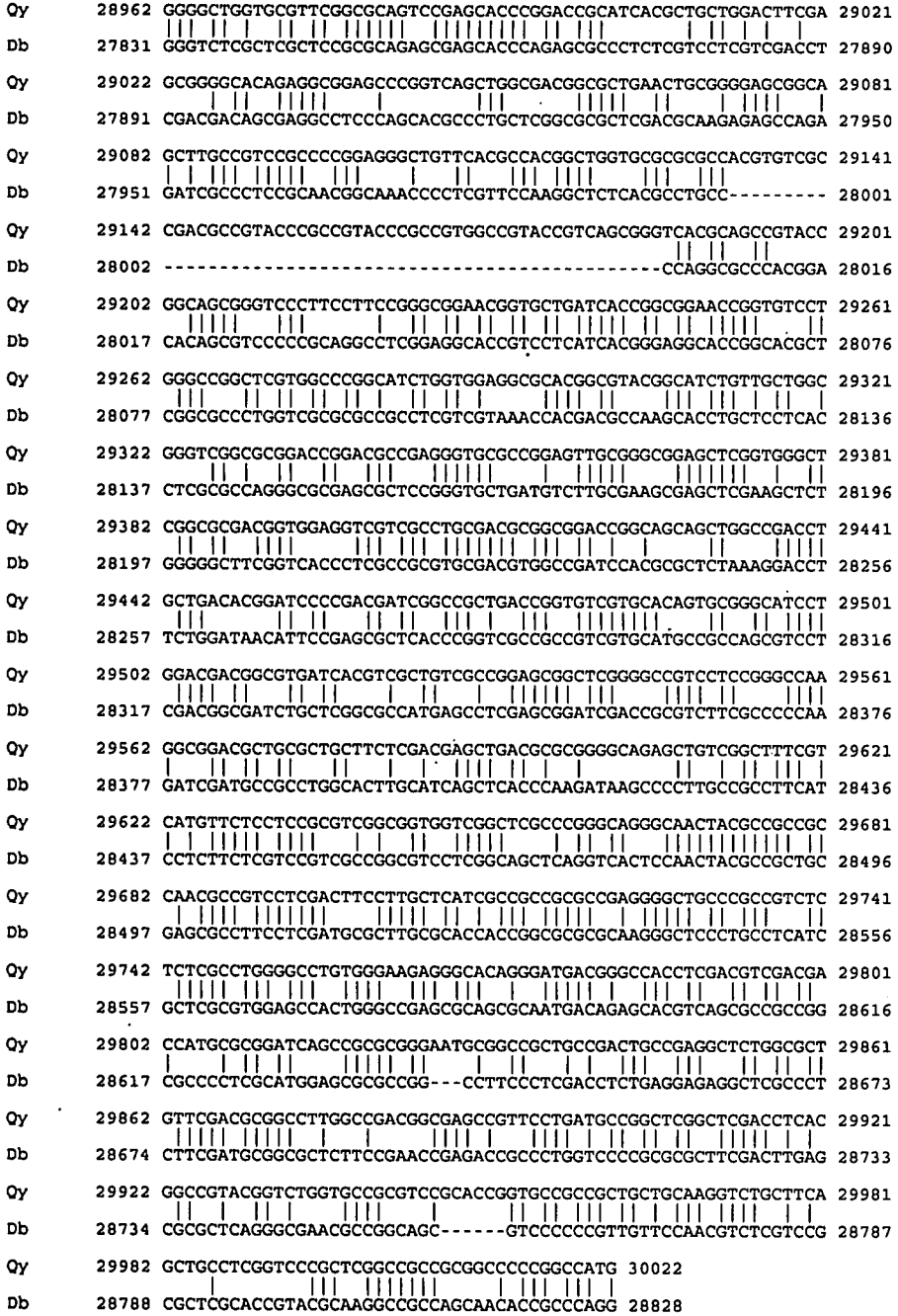

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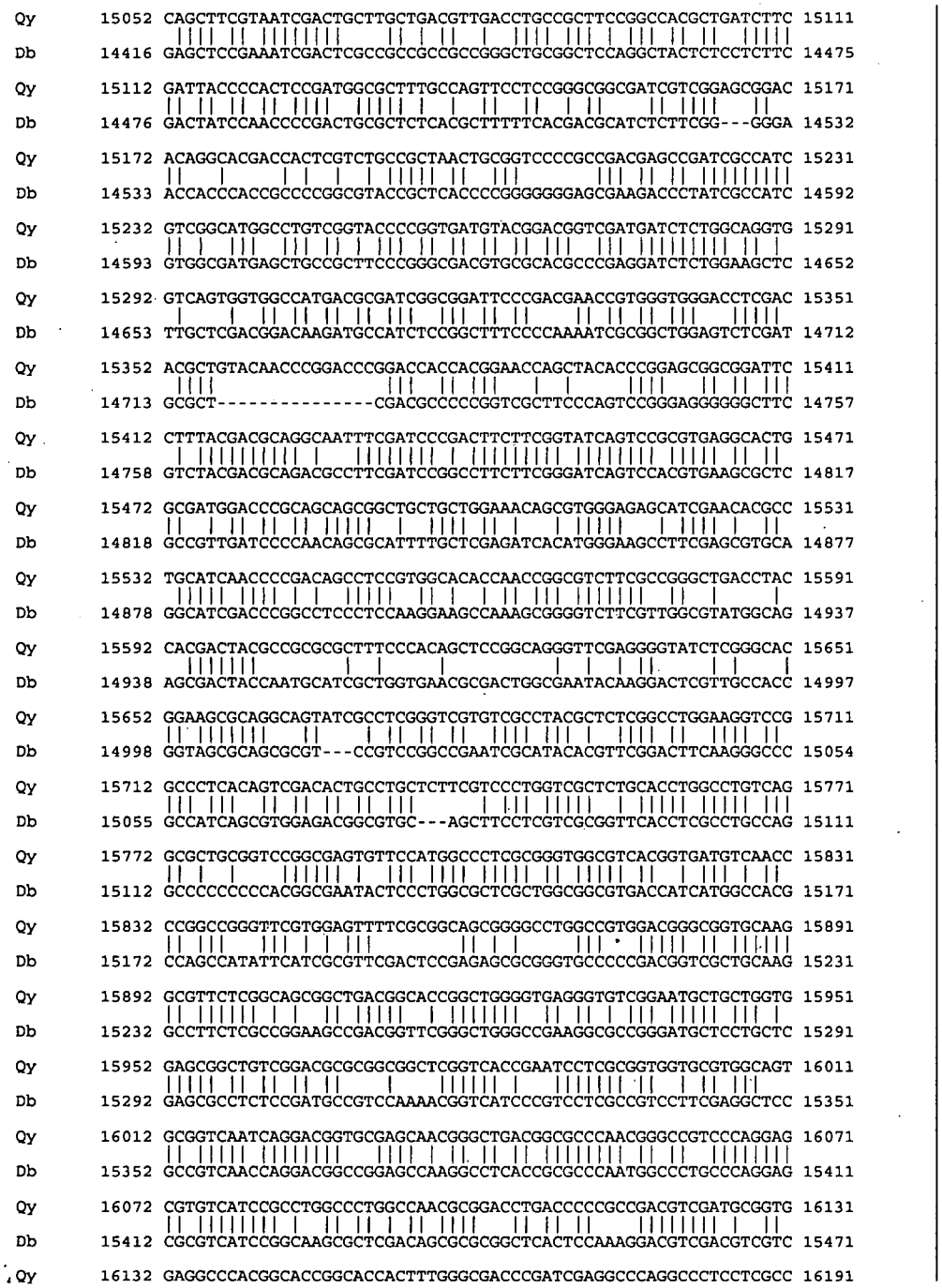

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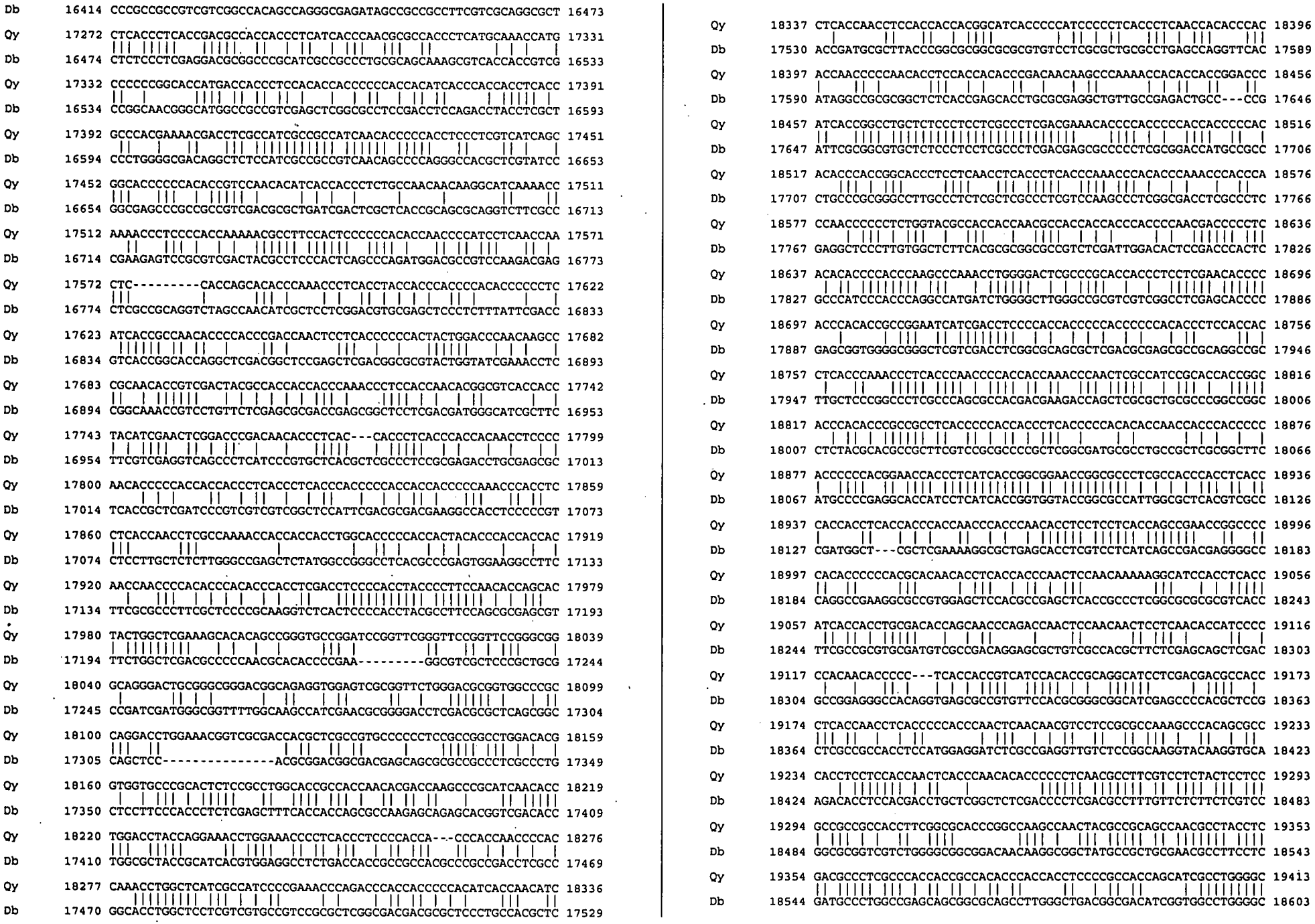


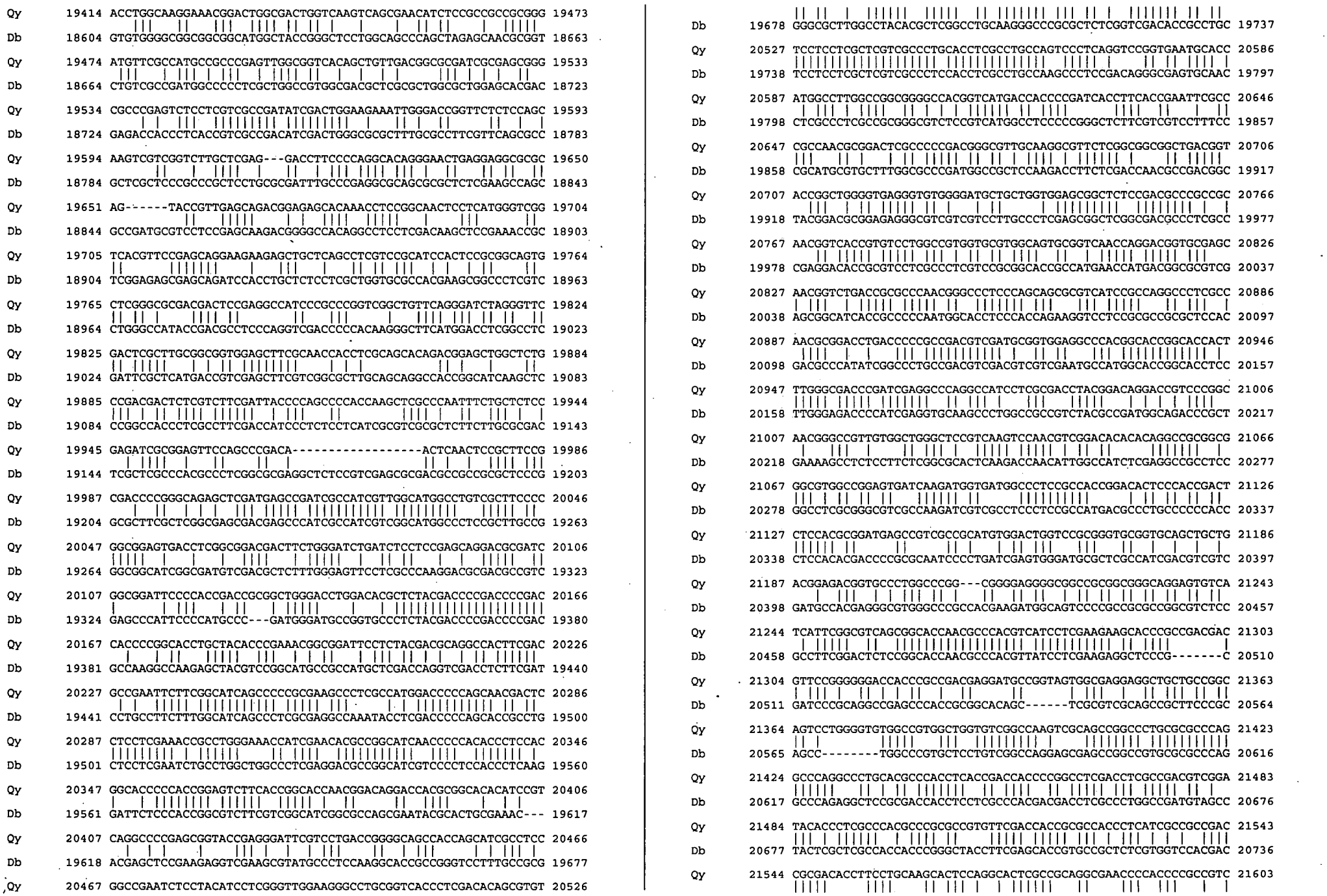
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; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
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; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,837
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/457,205
; FILING DATE: 01-JUN-1995
; APPLICATION NUMBER: 08/258,261
; FILING DATE: 08-Jun-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
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US-08-456-837-6

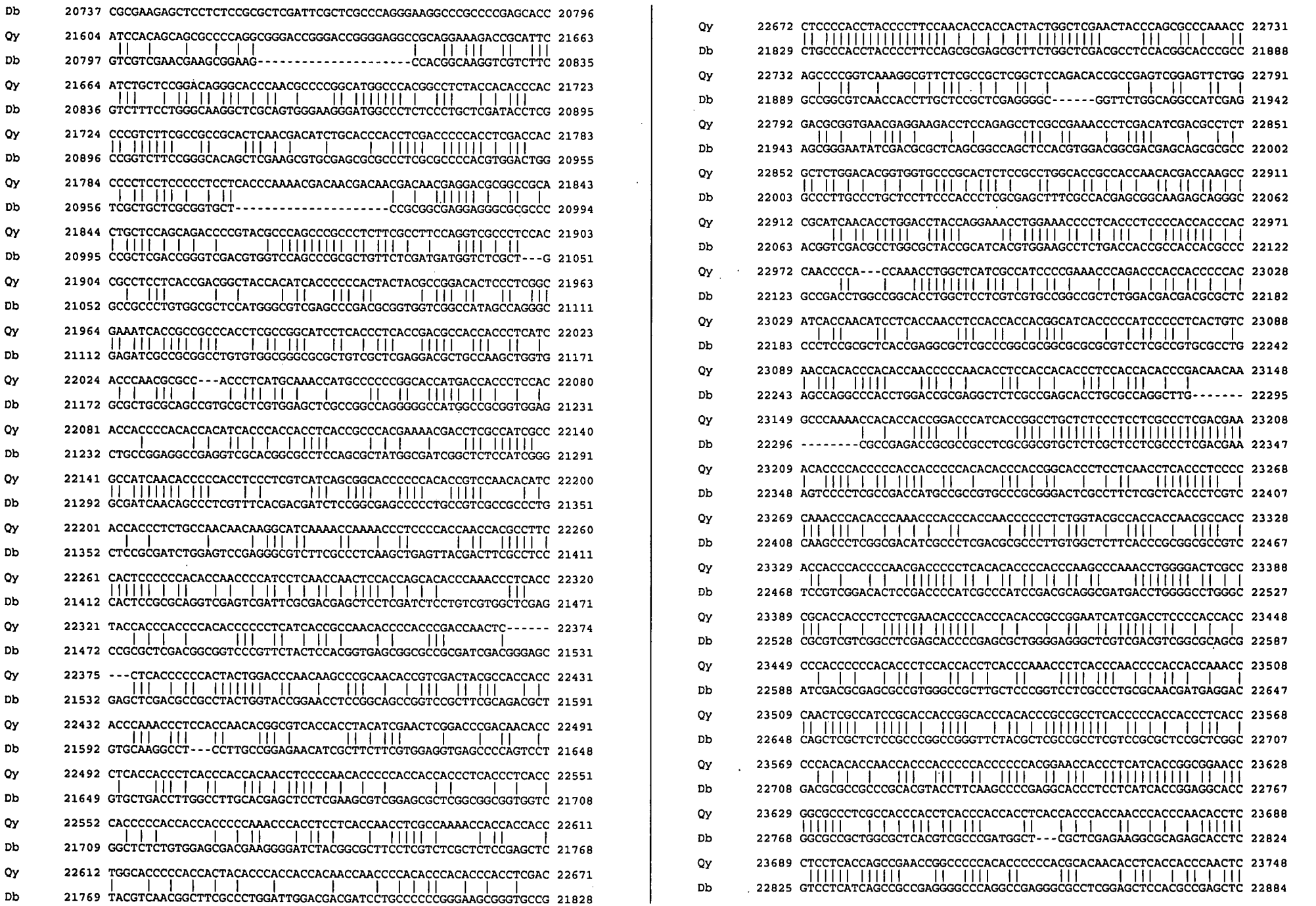
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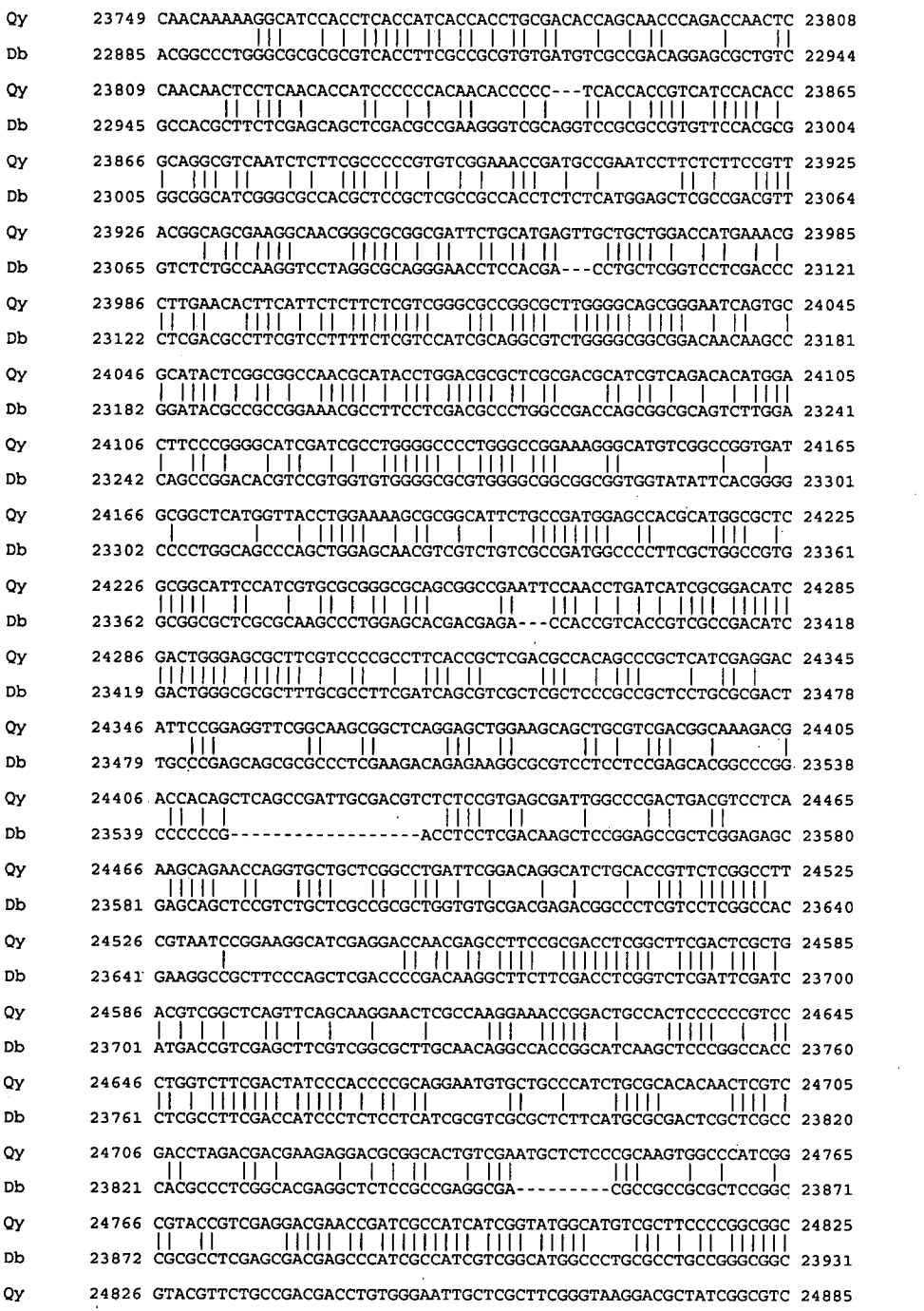


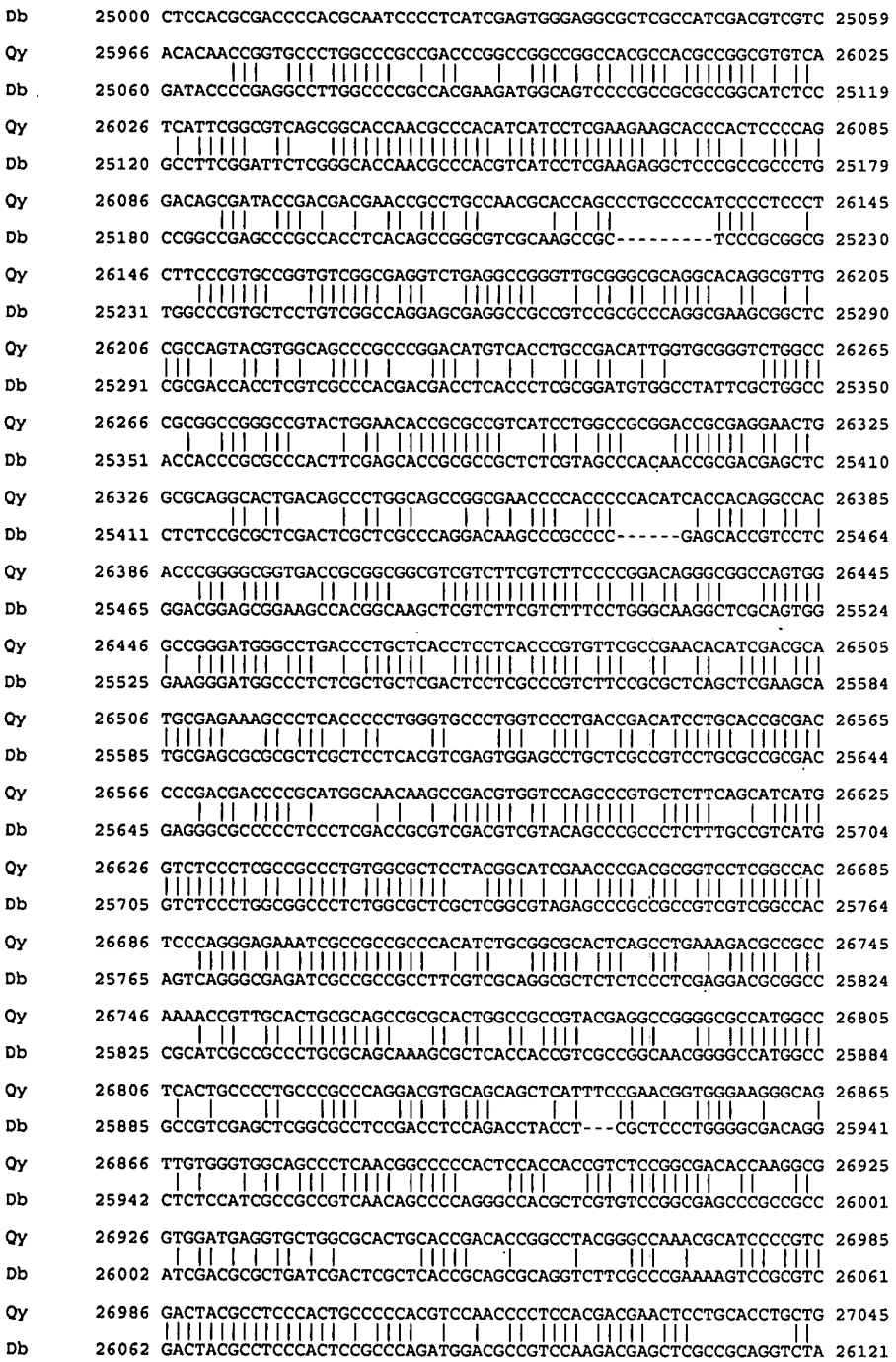


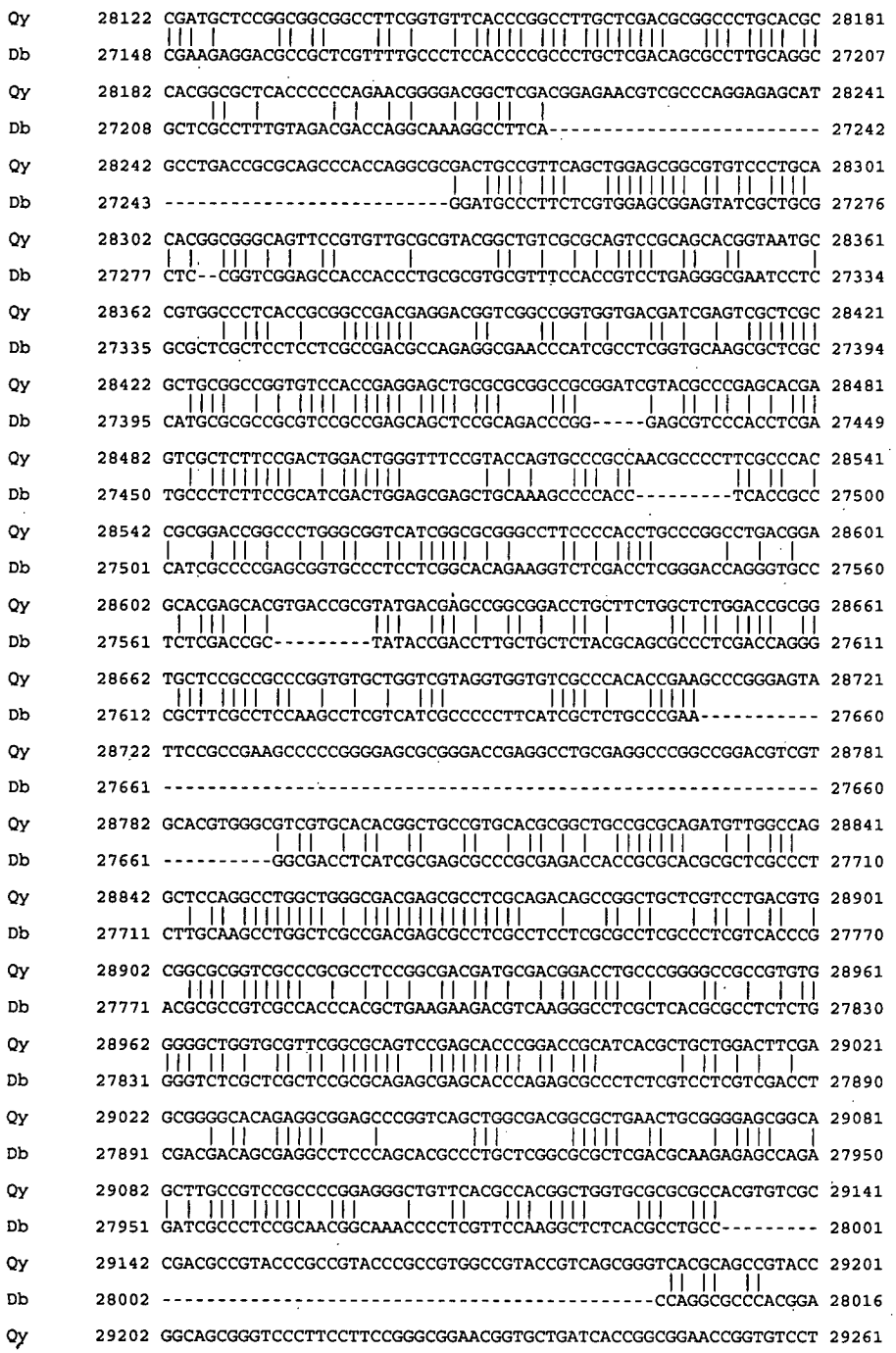







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Qy 27286 ACCGCGACCGGCAGCCTCCGCCGCGGCGACAACGACACCCACCGCTTCCTCACCGCCCTC 27345
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Qy 27523 ACCCCCACCCACCACCCCCTCCTCACCGCCACACTCACCCTCGCCGACAACAACACACAA 27582
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Qy 27763 GAGGACGTGACGTTGCAGGTCACCGTTCGGGCAGCCGATGAGAGTGGCCATCGCGCCCTC 27822
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RESULT 6
US-08-457-342-6
; Sequence 6, Application US/08457342
; Patent No. 5662898
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22

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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ciba-Geigy Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,342
;      FILING DATE:  01-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/457,205
;      FILING DATE:  01-JUN-1995
;      APPLICATION NUMBER:  08/258,261
;      FILING DATE:  08-Jun-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elmer, James Scott
;      REGISTRATION NUMBER:  36,129
;      REFERENCE/DOCKET NUMBER:  CGC 1506/CIP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8614
;      TELEFAX:  919-541-8689
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28958 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-457-342-6

  Query Match             10.2%;  Score 3140.6;  DB 1;  Length 28958;
  Best Local Similarity   54.1%;  Pred. No. 0;
  Matches 8239;  Conservative    0;  Mismatches 6284;  Indels  698;  Gaps   63;

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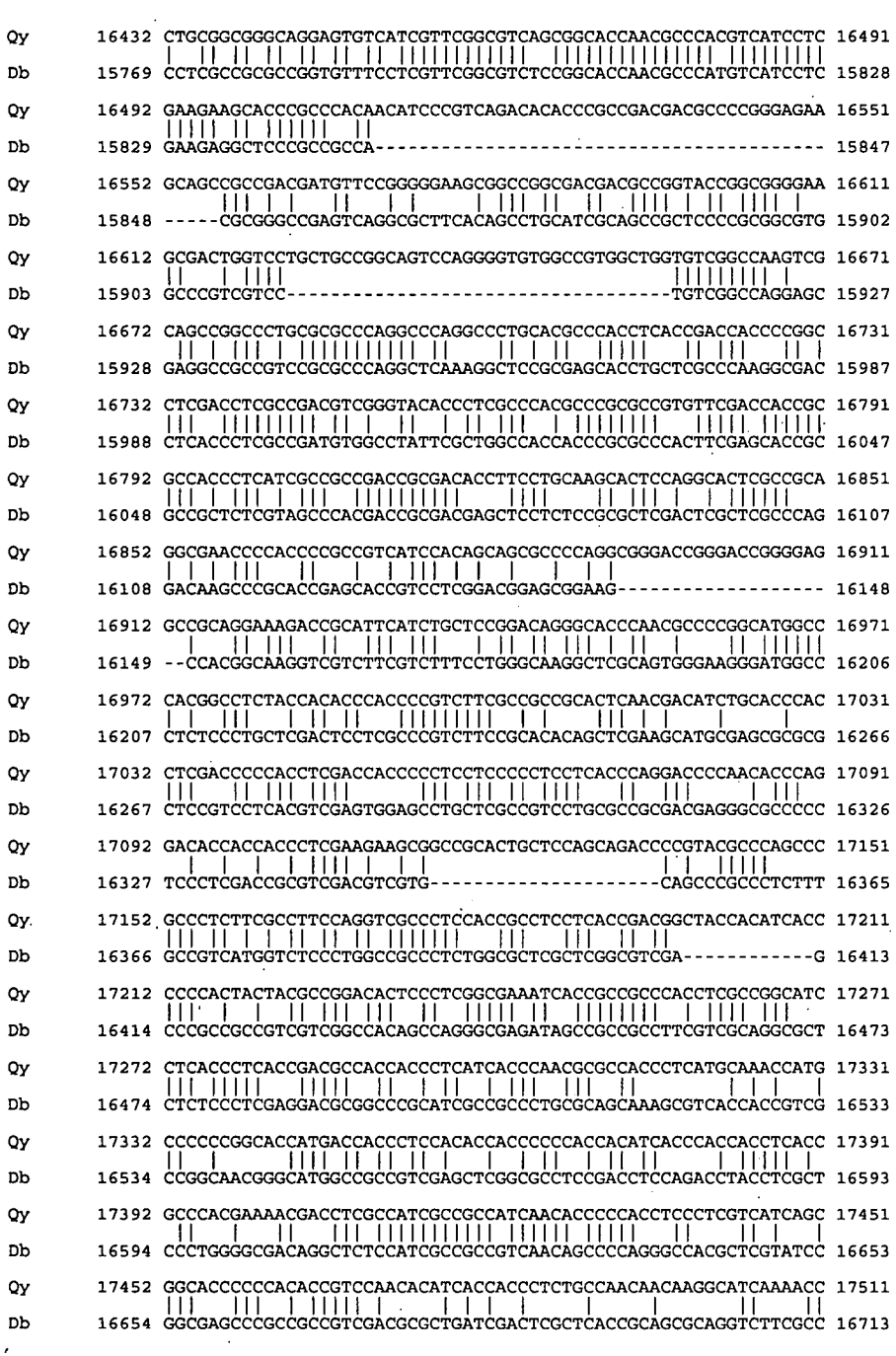
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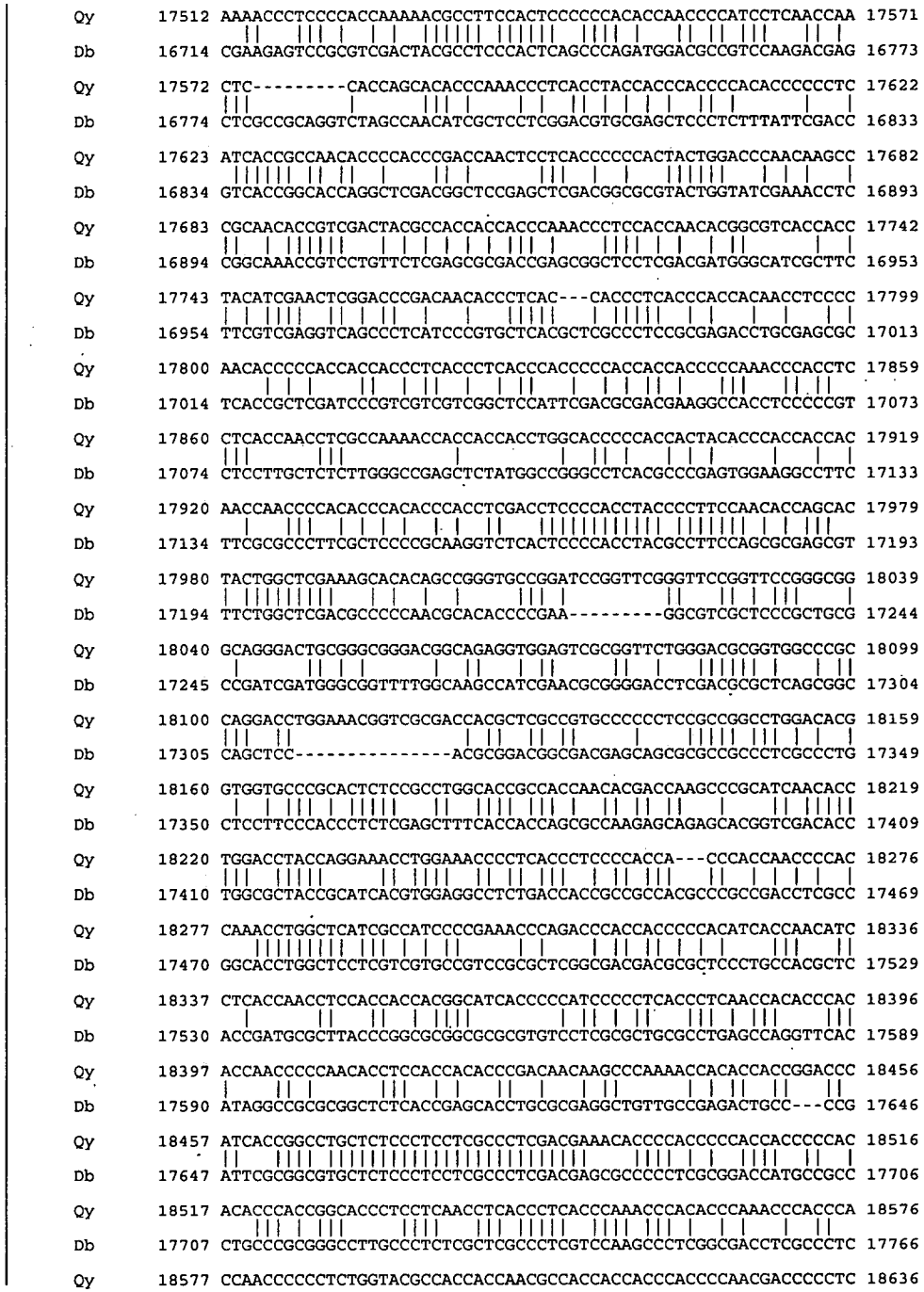
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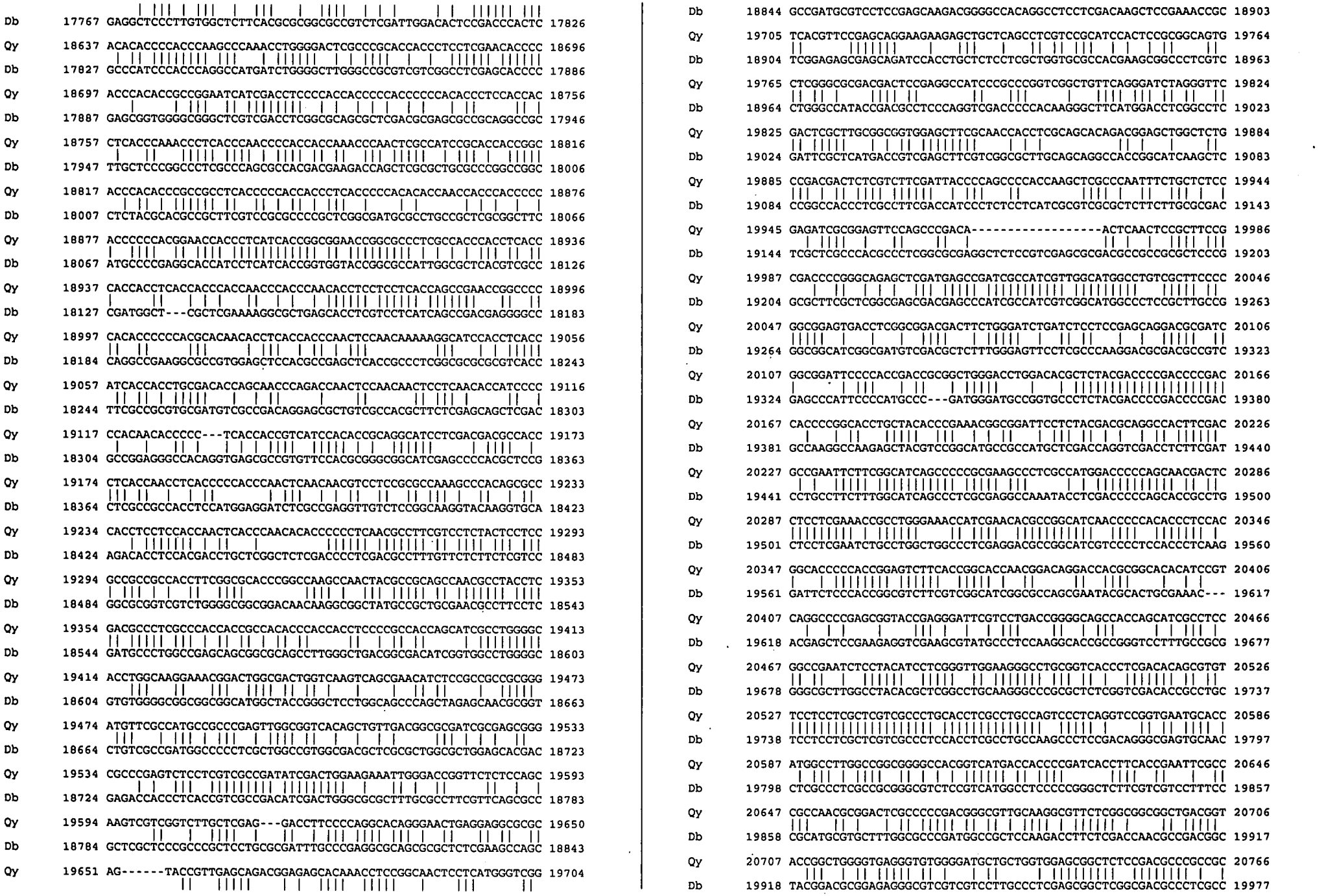
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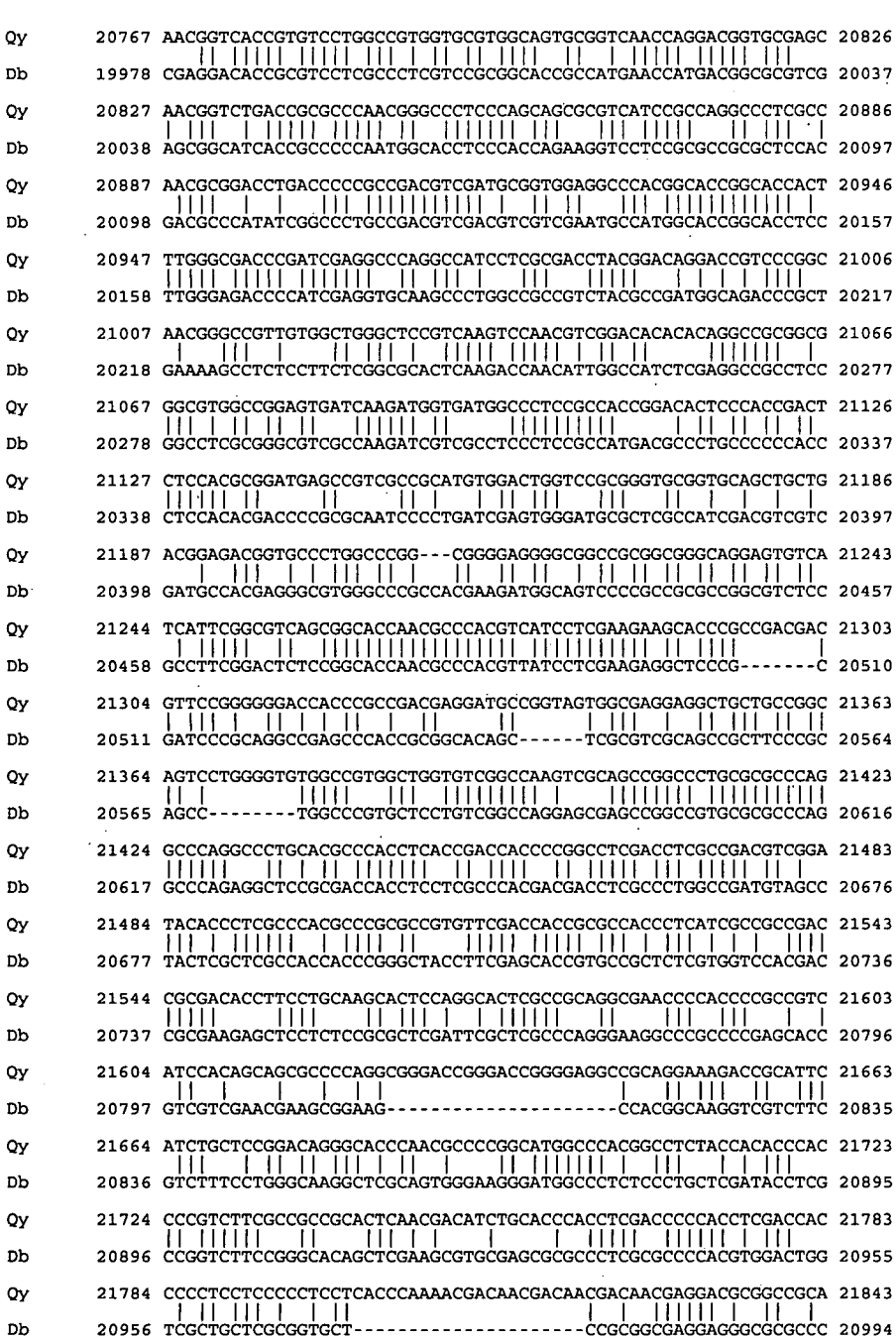
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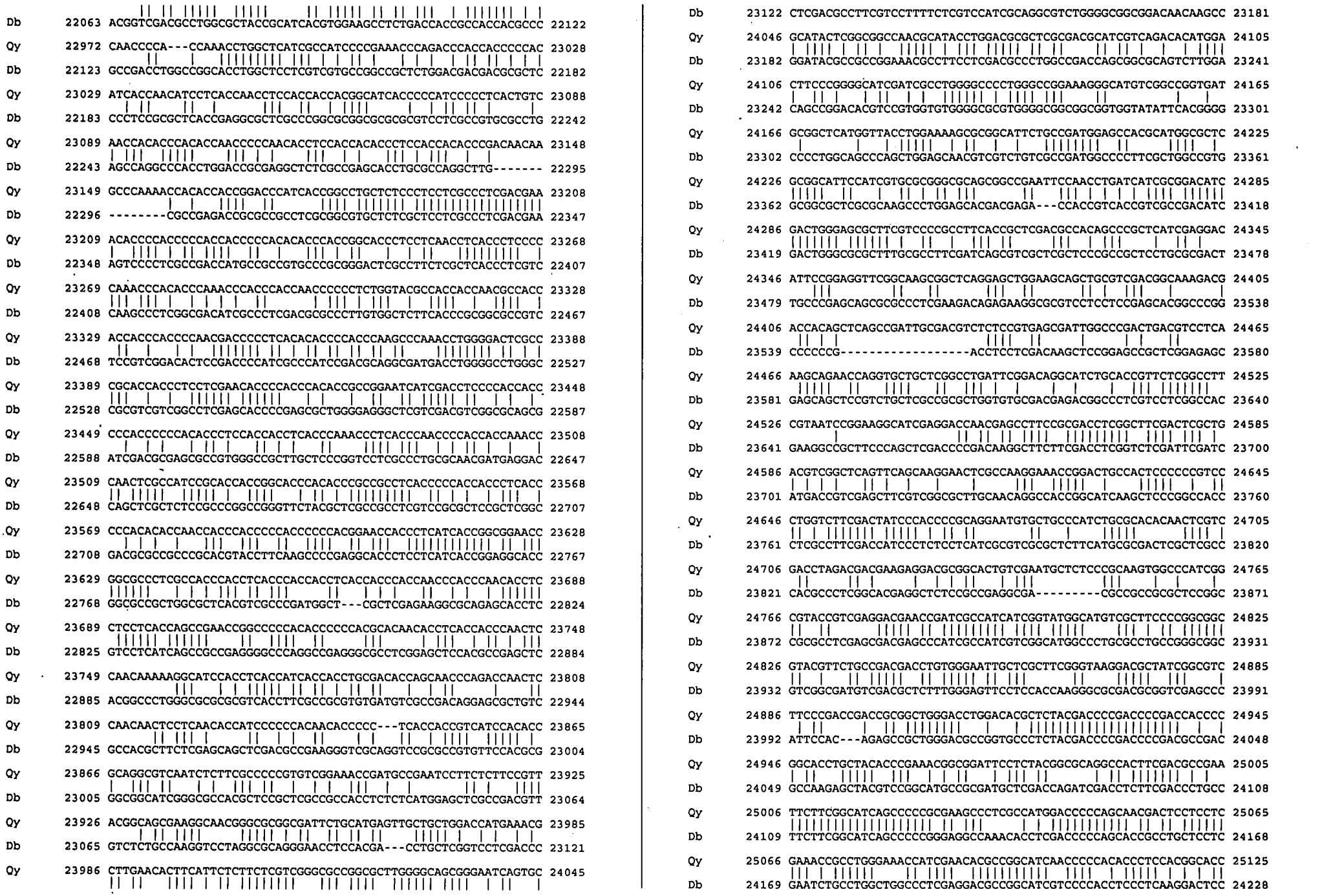
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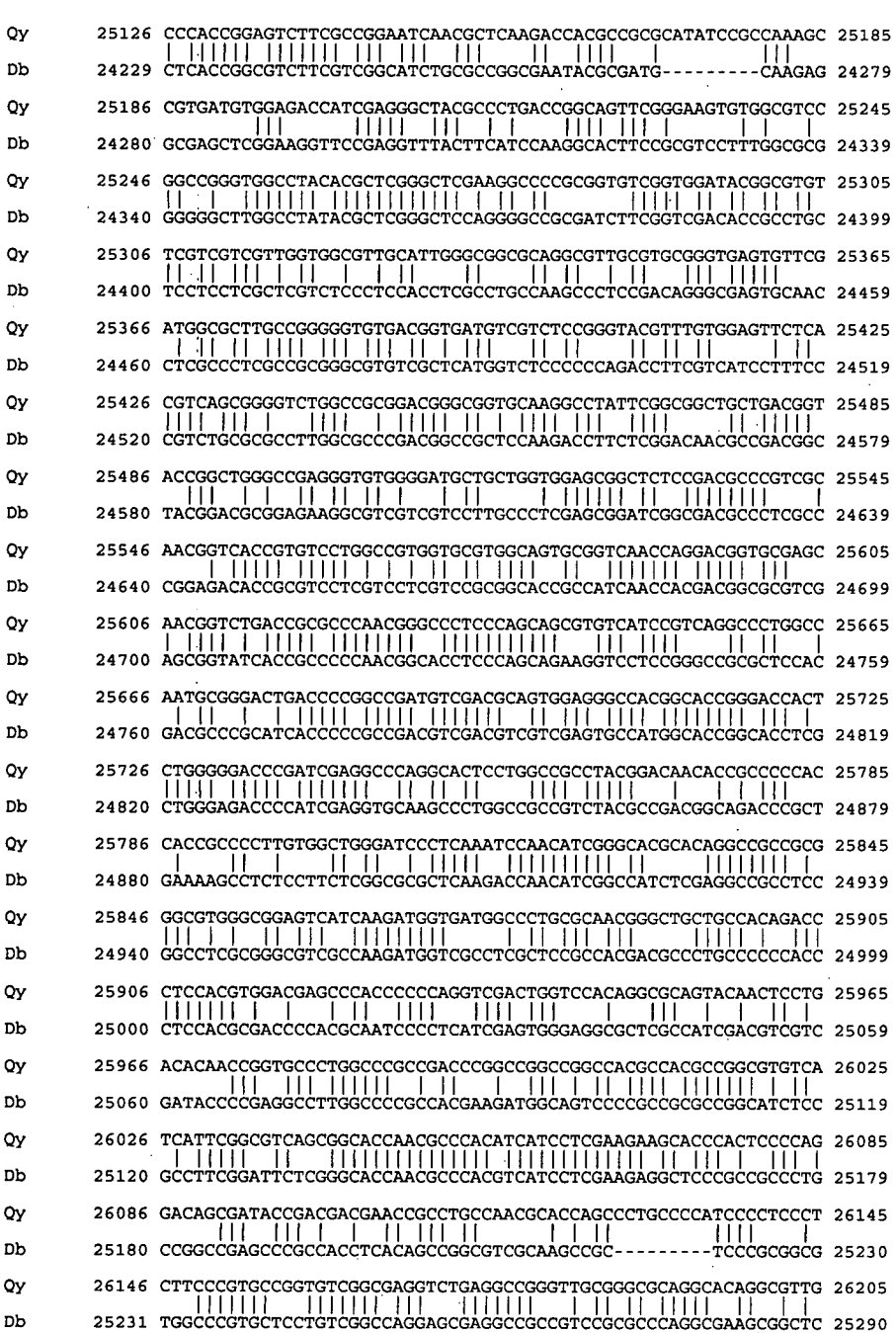


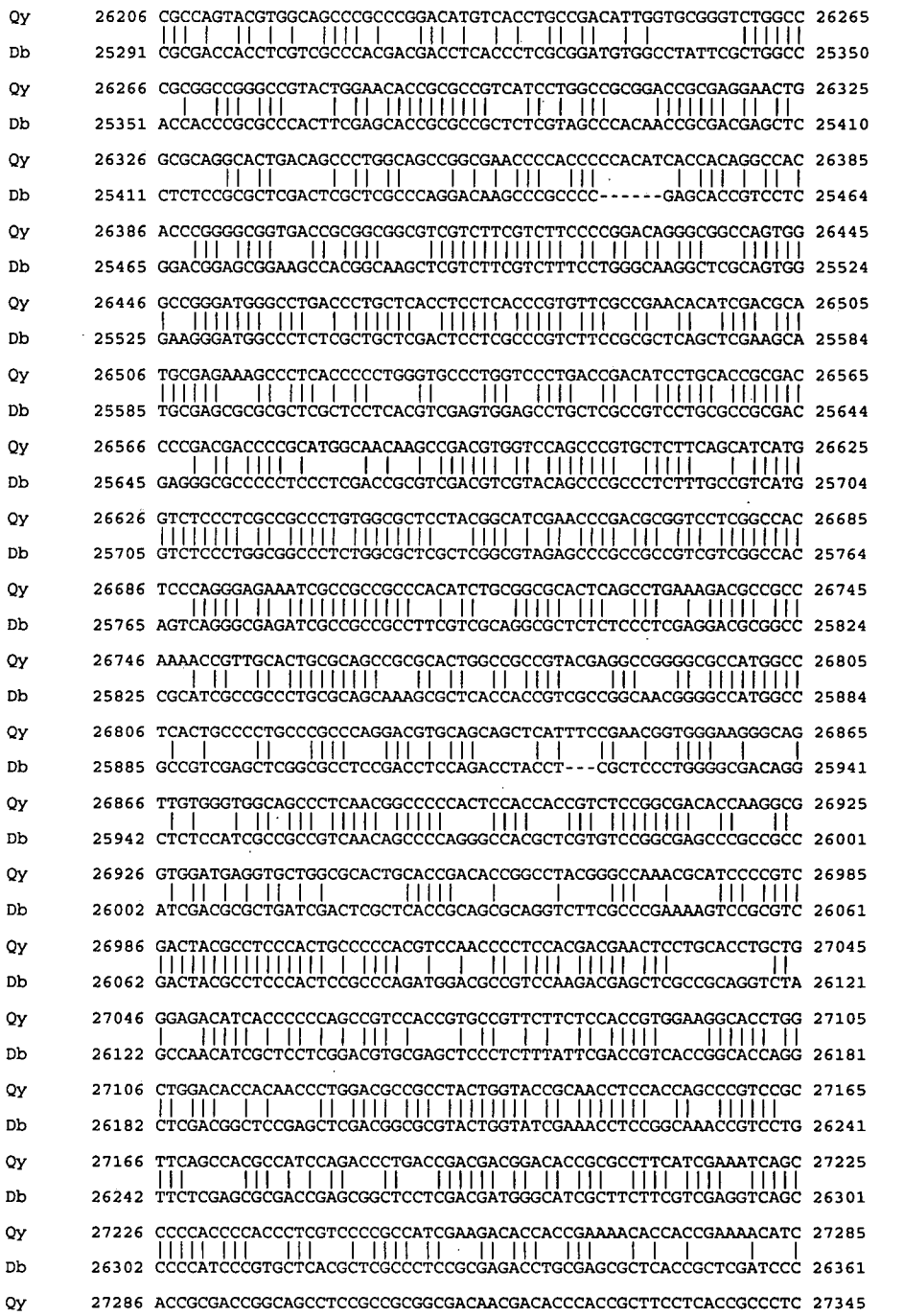


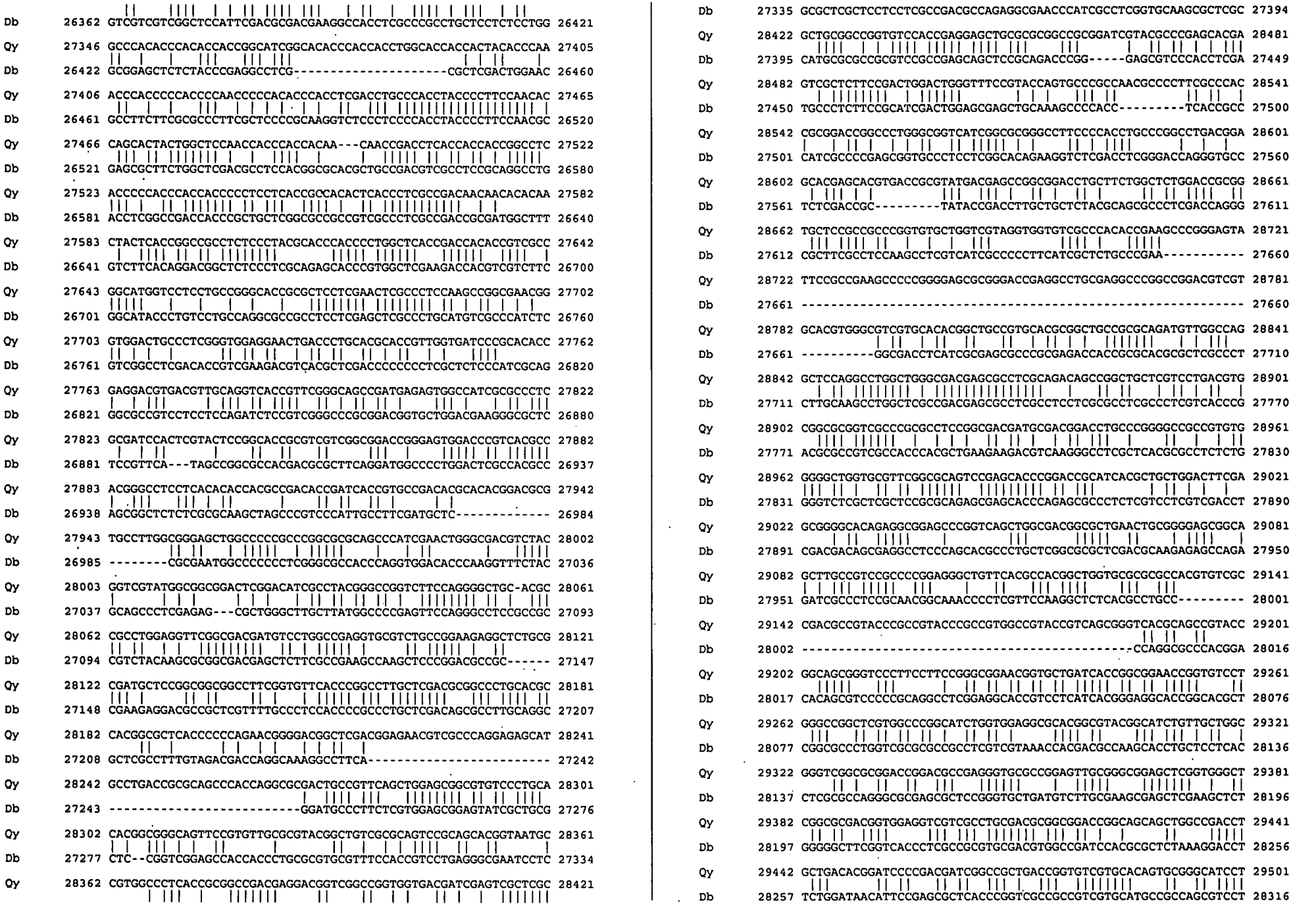

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Db 19918 TACGGACGCGGAGAGGGCGTCGTCGTCCTTGCCCTCGAGCGGCTCGGCGACGCCCTCGCC 19977


Qy 20767 AACGGTCACCGTGTCCTGGCCGTGGTGCGTGGCAGTGCGGTCAACCAGGACGGTGCGAGC 20826
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Qy 20827 AACGGTCTGACCGCGCCCAACGGGCCCTCCCAGCAGCGCGTCATCCGCCAGGCCCTCGCC 20886
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Db 20098 GACGCCCATATCGGCCCTGCCGACGTCGACGTCGTCGAATGCCATGGCACCGGCACCTCC 20157
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Qy 21484 TACACCCTCGCCCACGCCCGCGCCGTGTTCGACCACCGCGCCACCCTCATCGCCGCCGAC 21543
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Db      28617 CGCCCCTCGCATGGAGCGCGCCGG---CCTTCCCTCGACCTCTGAGGAGAGGCTCGCCCT 28673

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RESULT 7
US-08-457-646A-6
; Sequence 6, Application US/08457646A
; Patent No. 5679560
;  GENERAL INFORMATION:
;    APPLICANT:  Schupp, Thomas
;    APPLICANT:  Ligon, James M.
;    APPLICANT:  Beck, James Joseph
;    APPLICANT:  Hill, Dwight Steven
;    APPLICANT:  Ryals, John Andrew
;    APPLICANT:  Gaffney, Thomas Deane
;    APPLICANT:  Lam, Stephen Ting
;    APPLICANT:  Hammer, Phillip E.
;    APPLICANT:  Uknes, Scott Joseph
;    TITLE OF INVENTION:  Genes for the synthesis of
;    TITLE OF INVENTION:  antipathogenic substances
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ciba-Geigy Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,646A
;      FILING DATE:  01-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/457,205
;      FILING DATE:  01-JUN-1995
;      APPLICATION NUMBER:  08/258,261
;      FILING DATE:  08-Jun-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elmer, James Scott
;      REGISTRATION NUMBER:  36,129
;      REFERENCE/DOCKET NUMBER:  CGC 1506/CIP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8614
;      TELEFAX:  919-541-8689
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28958 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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Qy      15052 CAGCTTCGTAATCGACTGCTTGCTGACGTTGACCTGCCGCTTCCGGCCACGCTGATCTTC 15111
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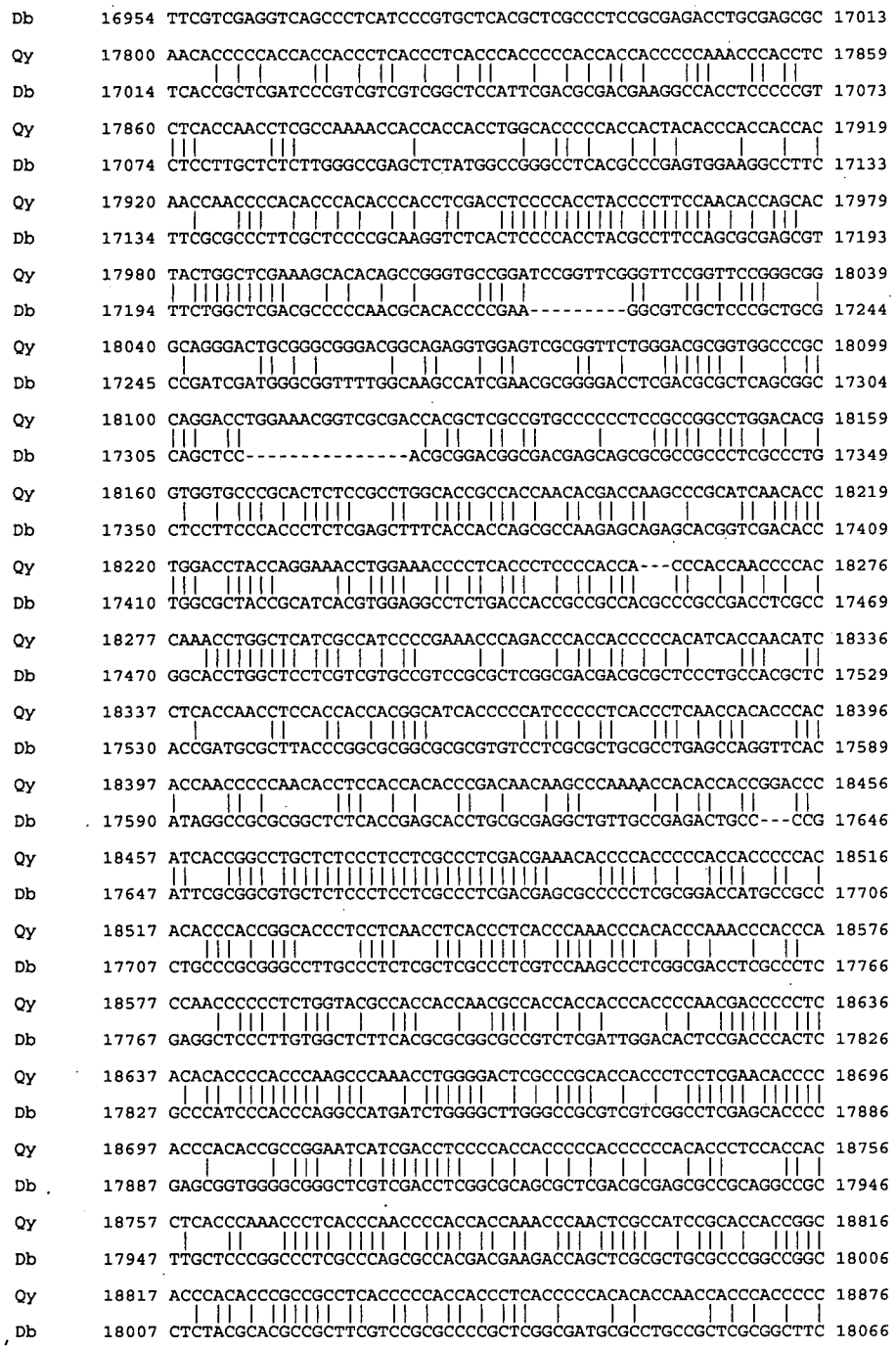
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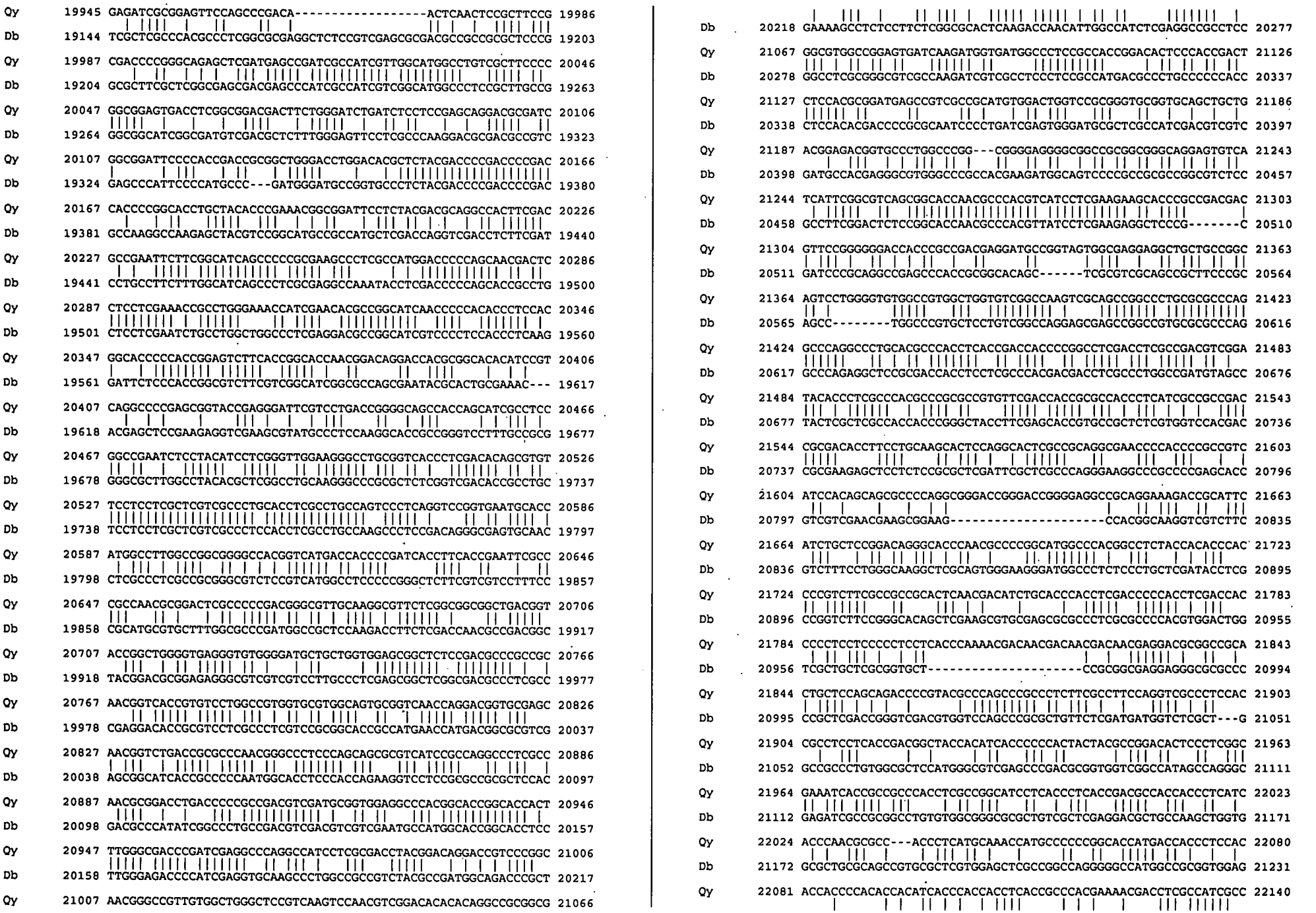
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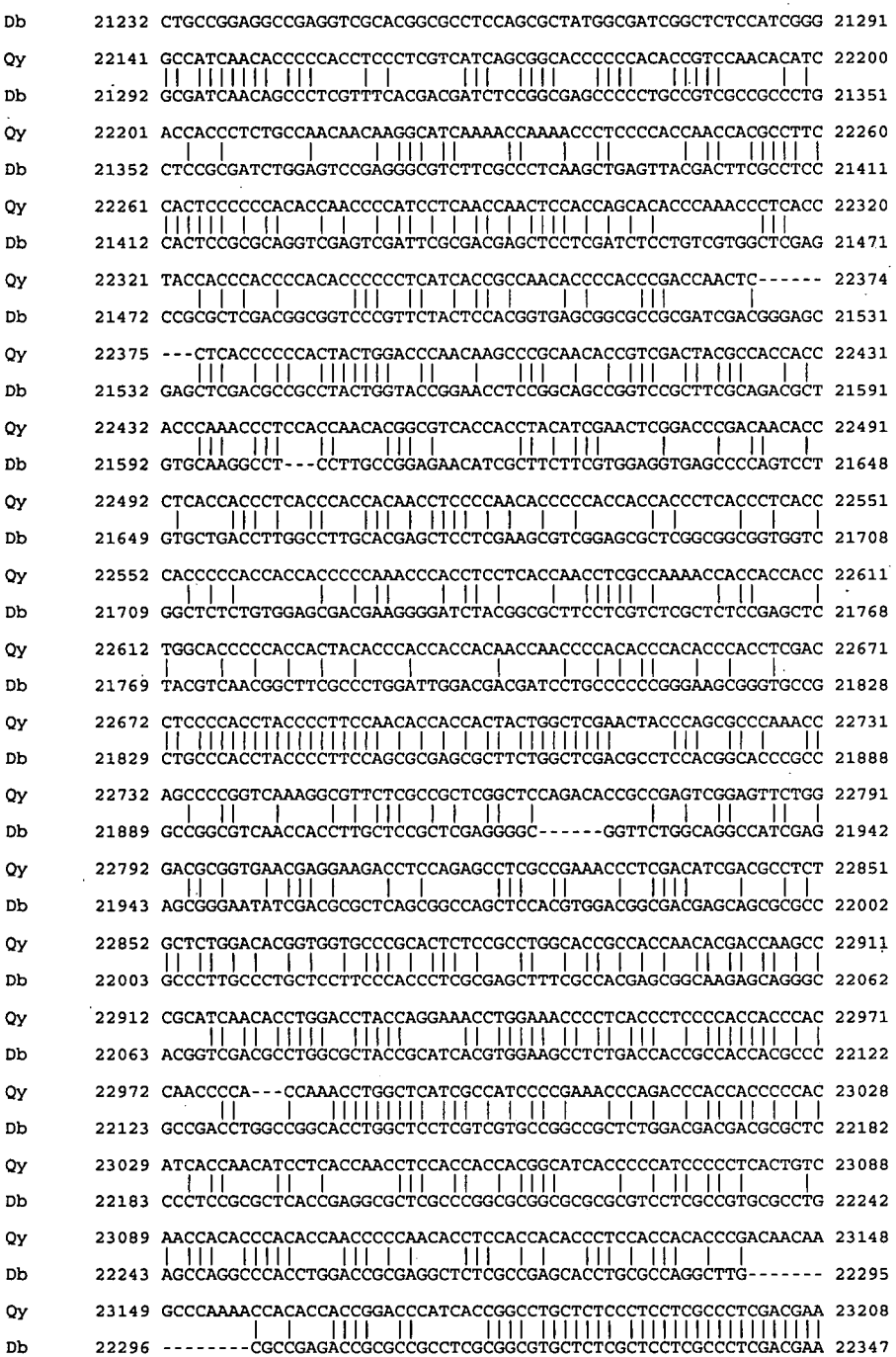
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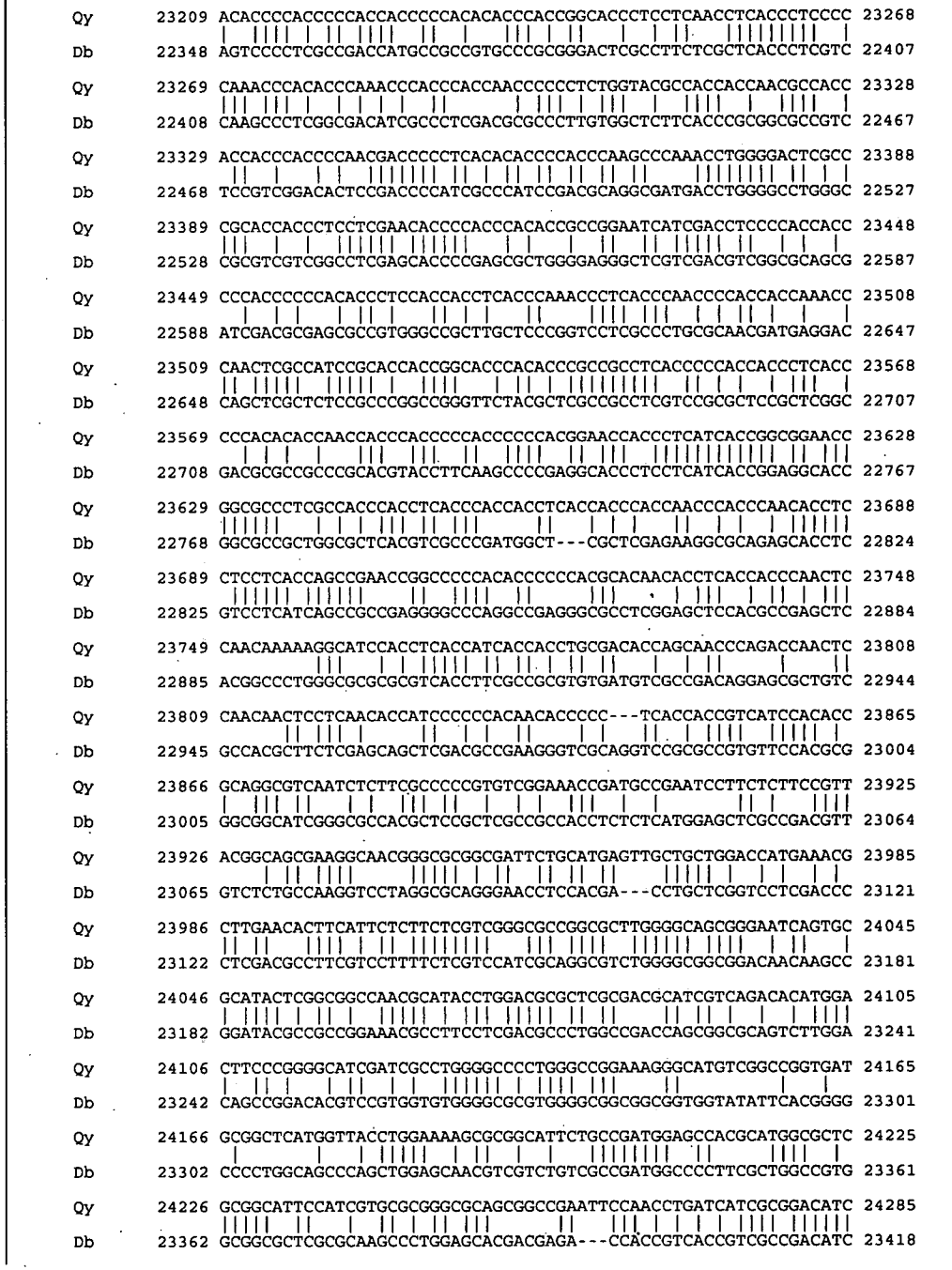
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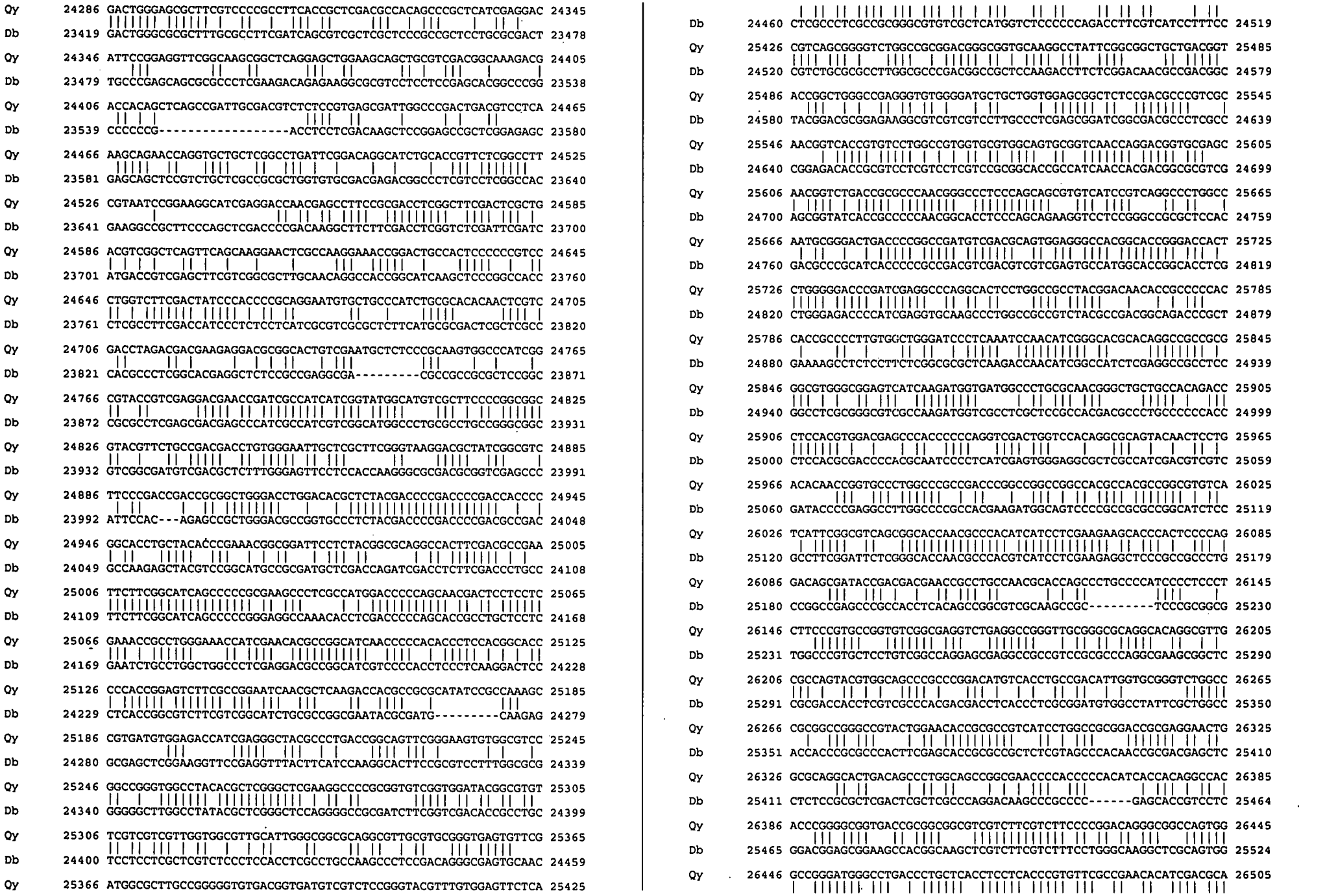


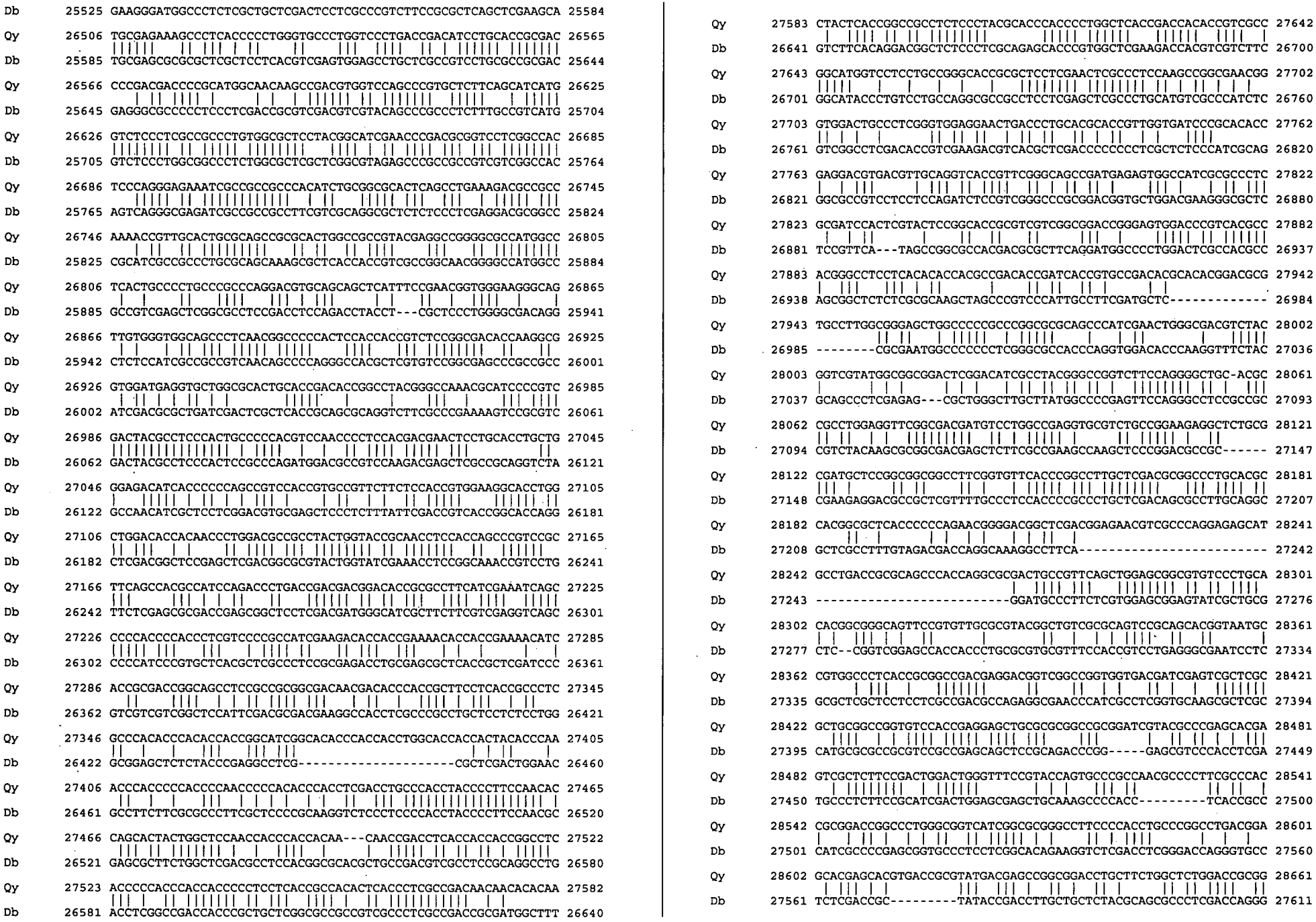

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Qy 17860 CTCACCAACCTCGCCAAAACCACCACCACCTGGCACCCCCACCACTACACCCACCACCAC 17919
Db 17074 CTCCTTGCTCTCTTGGGCCGAGCTCTATGGCCGGGCCTCACGCCCGAGTGGAAGGCCTTC 17133
Qy 17920 AACCAACCCCACACCCACACCCACCTCGACCTCCCCACCTACCCCTTCCAACACCAGCAC 17979
Db 17134 TTCGCGCCCTTCGCTCCCCGCAAGGTCTCACTCCCCACCTACGCCTTCCAGCGCGAGCGT 17193
Qy 17980 TACTGGCTCGAAAGCACACAGCCGGGTGCCGGATCCGGTTCGGGTTCCGGTTCCGGGCGG 18039
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Qy 18040 GCAGGGACTGCGGGCGGGACGGCAGAGGTGGAGTCGCGGTTCTGGGACGCGGTGGCCCGC 18099
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Qy 18397 ACCAACCCCCAACACCTCCACCACACCCGACAACAAGCCCAAAACCACACCACCGGACCC 18456
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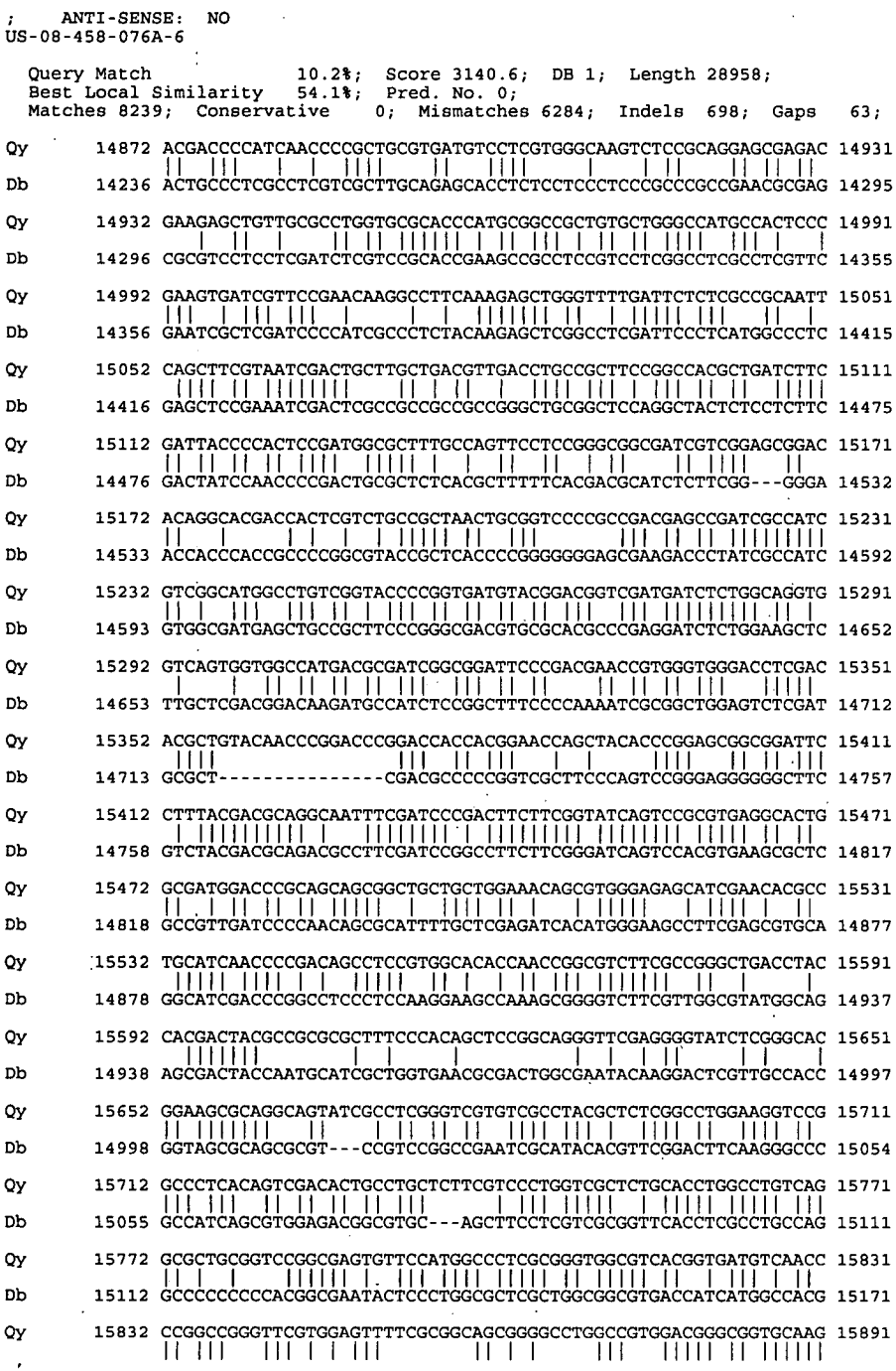
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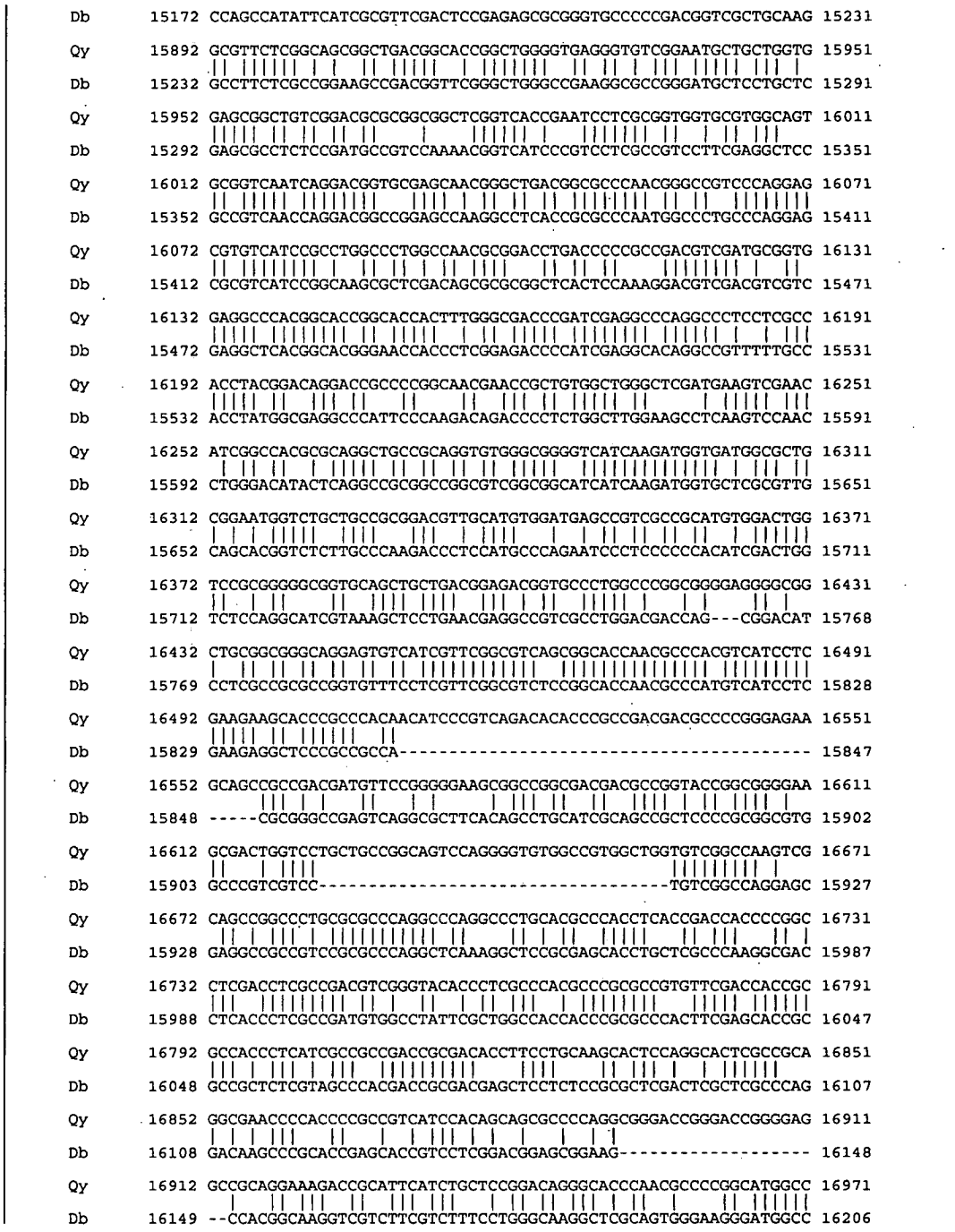
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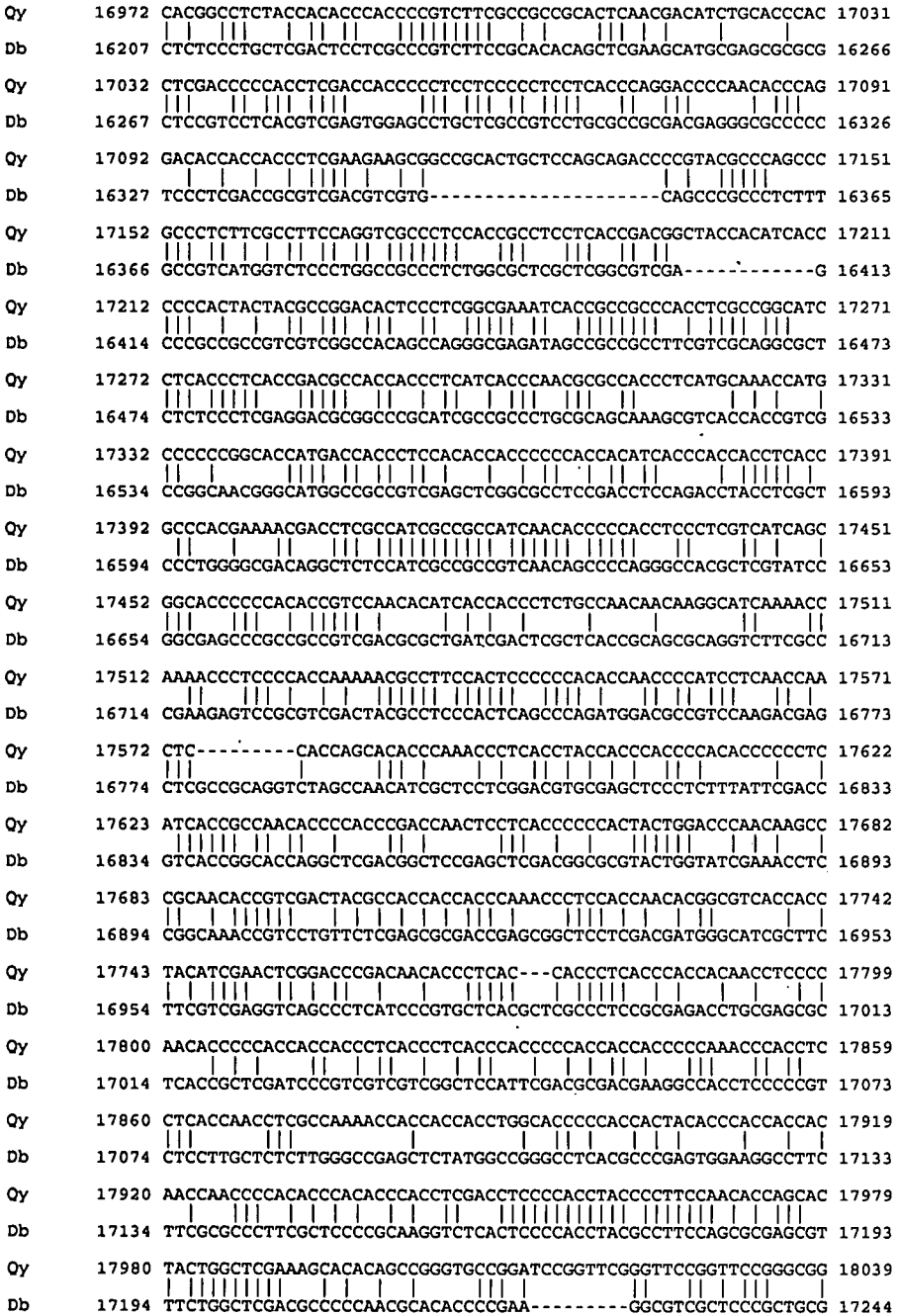
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RESULT 8
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; Sequence 6, Application US/08458076A
; Patent No. 5698425
;  GENERAL INFORMATION:
;    APPLICANT:  Schupp, Thomas
;    APPLICANT:  Ligon, James M.
;    APPLICANT:  Beck, James Joseph
;    APPLICANT:  Hill, Dwight Steven
;    APPLICANT:  Ryals, John Andrew
;    APPLICANT:  Gaffney, Thomas Deane
;    APPLICANT:  Lam, Stephen Ting
;    APPLICANT:  Hammer, Phillip E.
;    APPLICANT:  Uknes, Scott Joseph
;    TITLE OF INVENTION:  Genes for the synthesis of
;    TITLE OF INVENTION:  antipathogenic substances
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ciba-Geigy Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;      FILING DATE:  01-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/457,205
;      FILING DATE:  01-JUN-1995
;      APPLICATION NUMBER:  08/258,261
;      FILING DATE:  08-Jun-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elmer, James Scott
;      REGISTRATION NUMBER:  36,129
;      REFERENCE/DOCKET NUMBER:  CGC 1506/CIP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8614
;      TELEFAX:  919-541-8689
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28958 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
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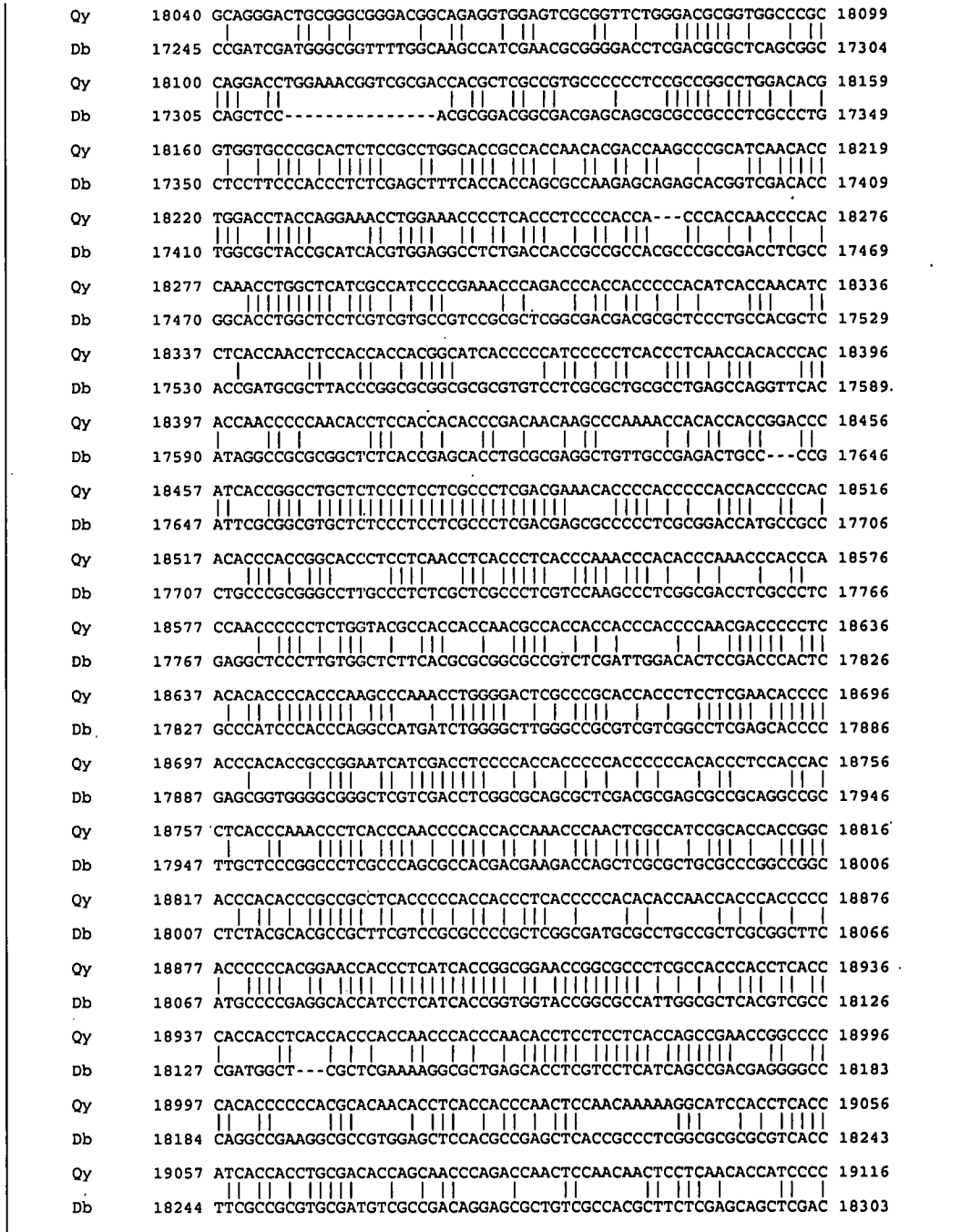
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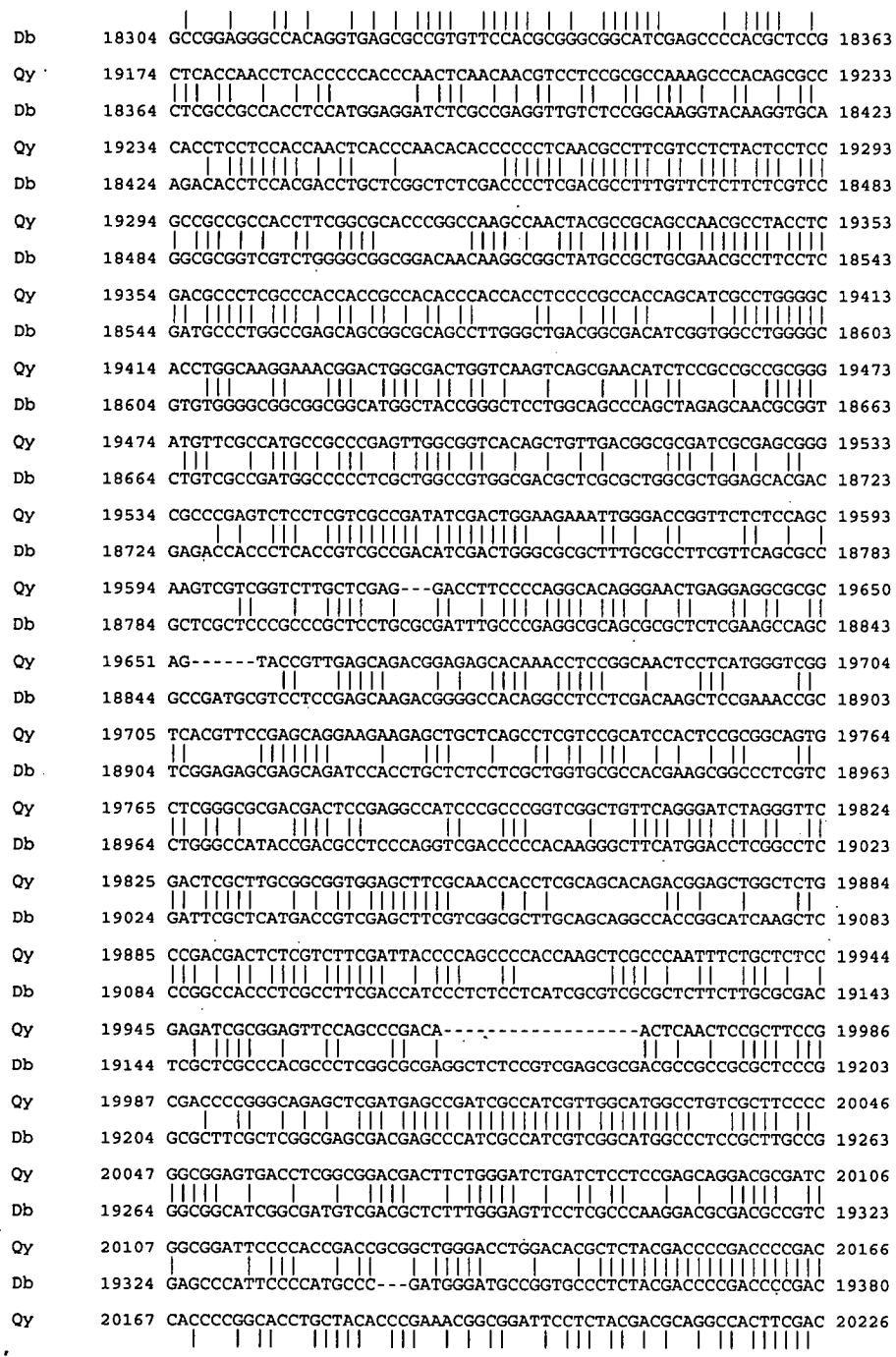
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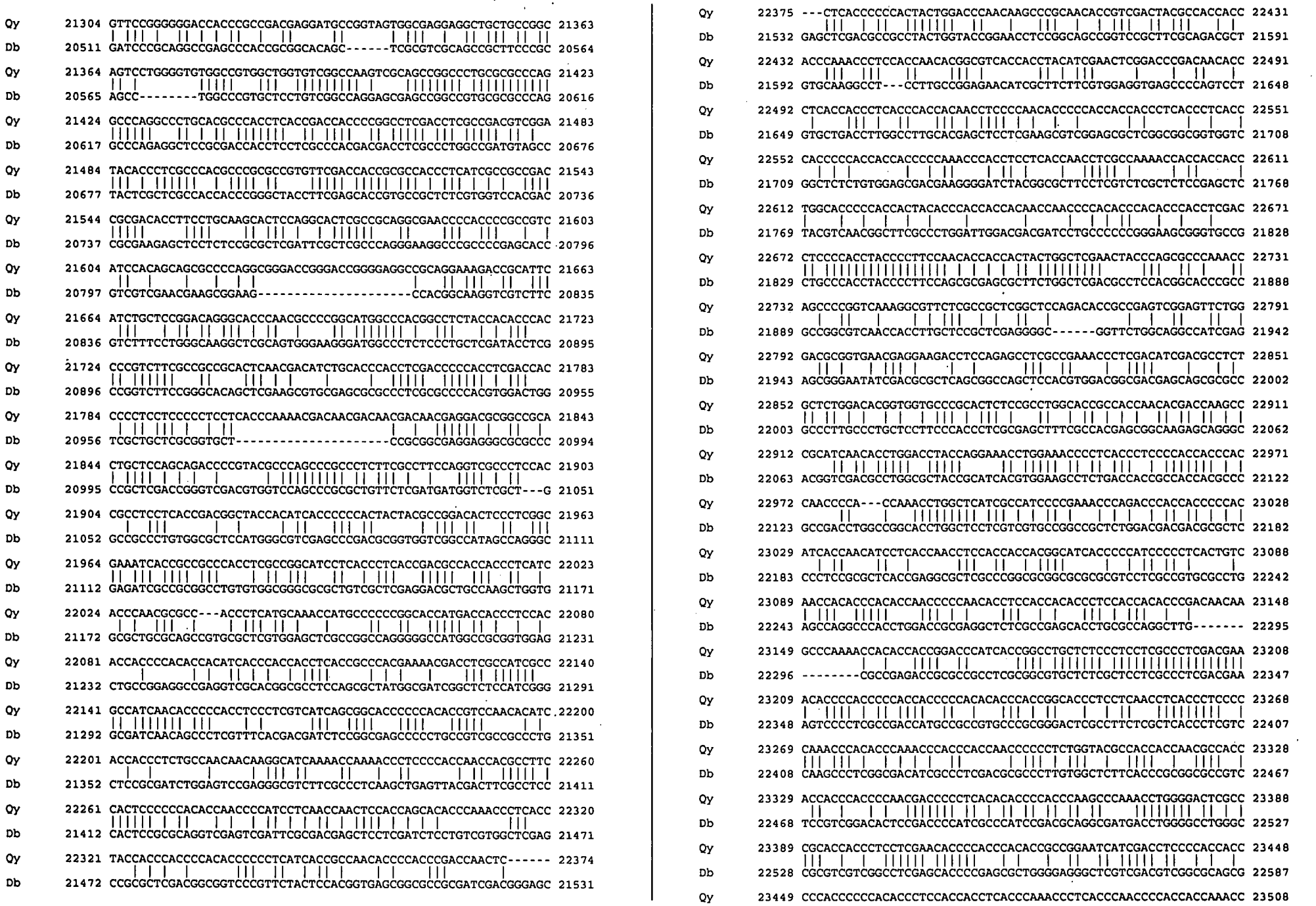


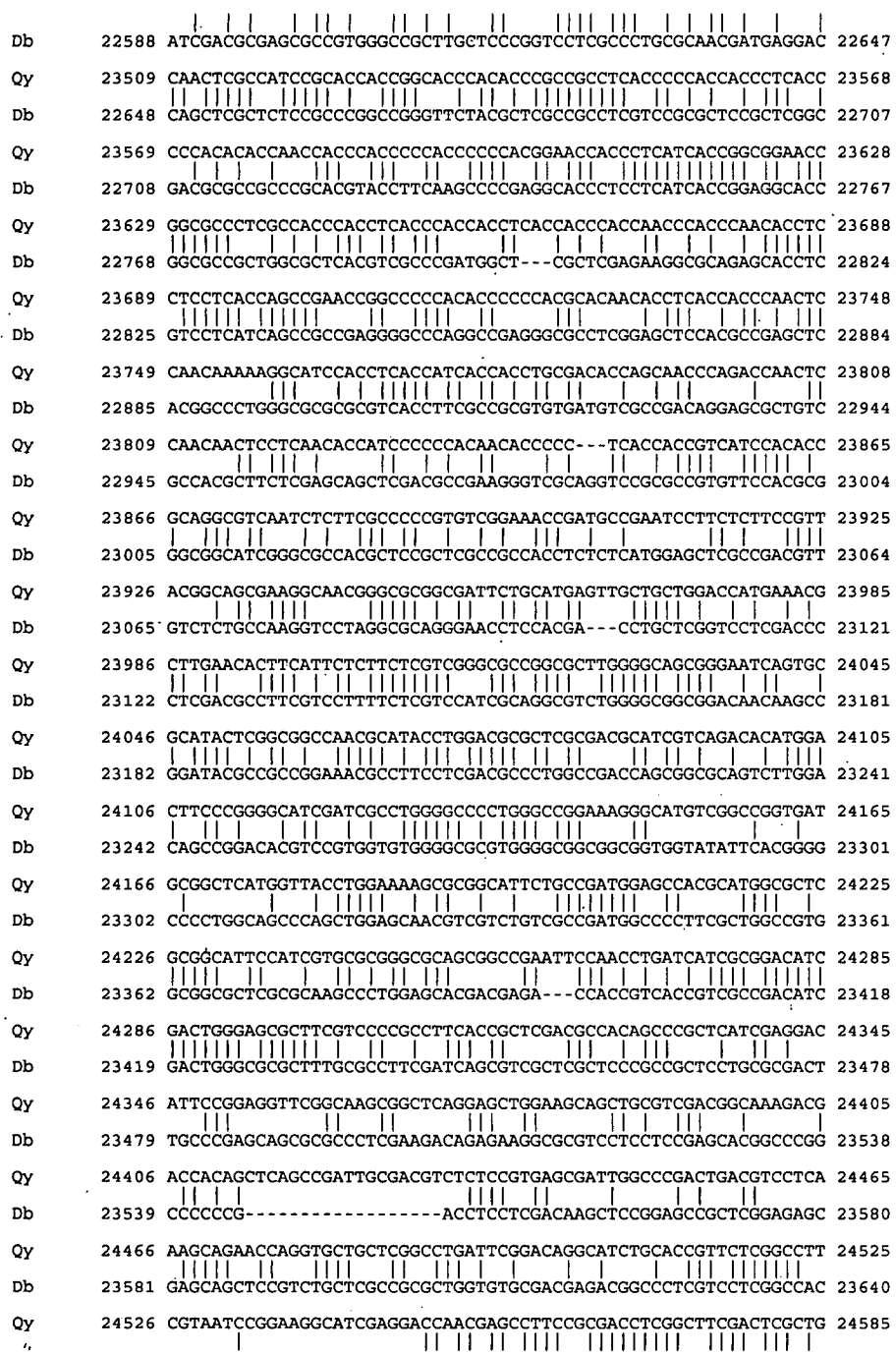


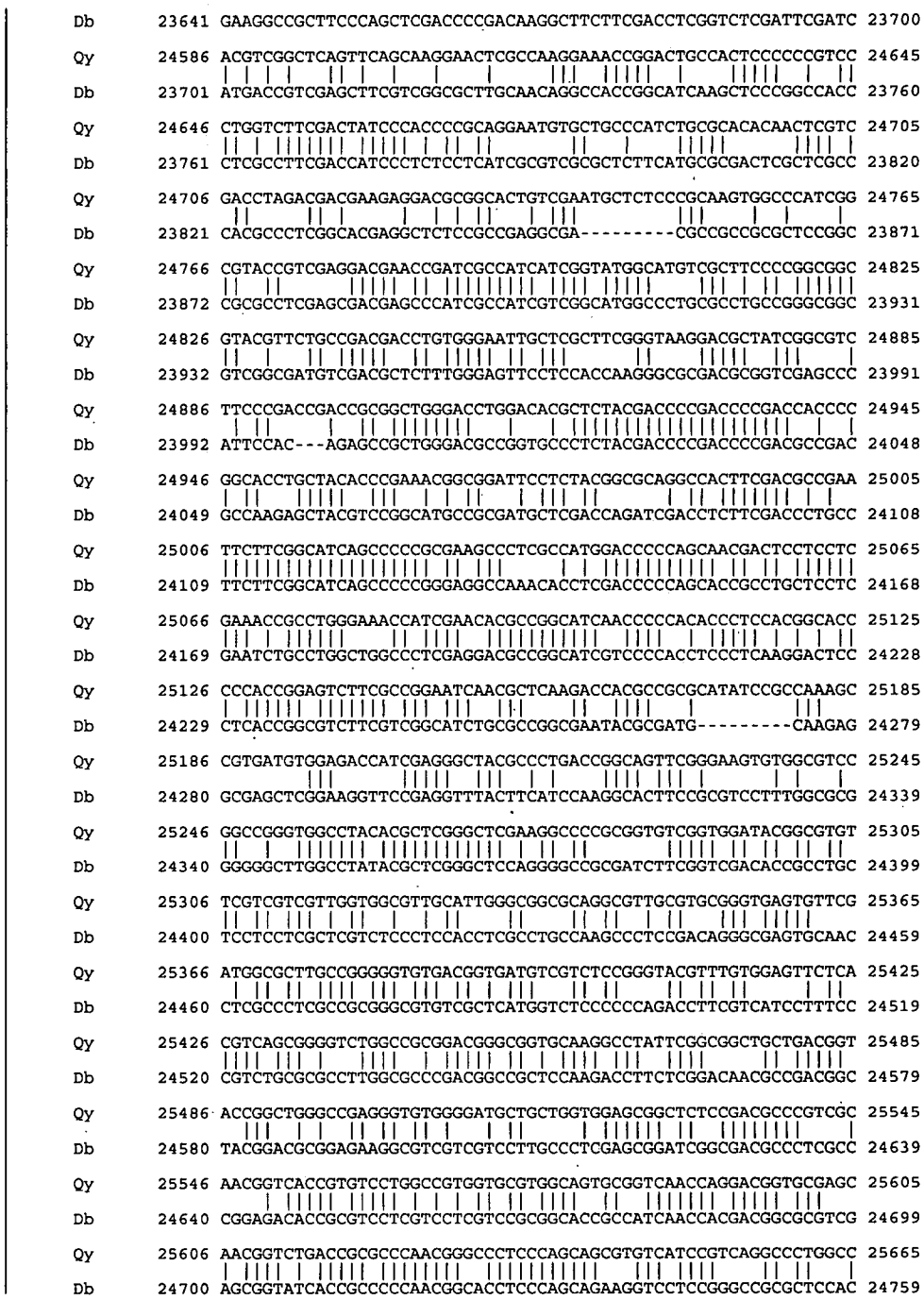


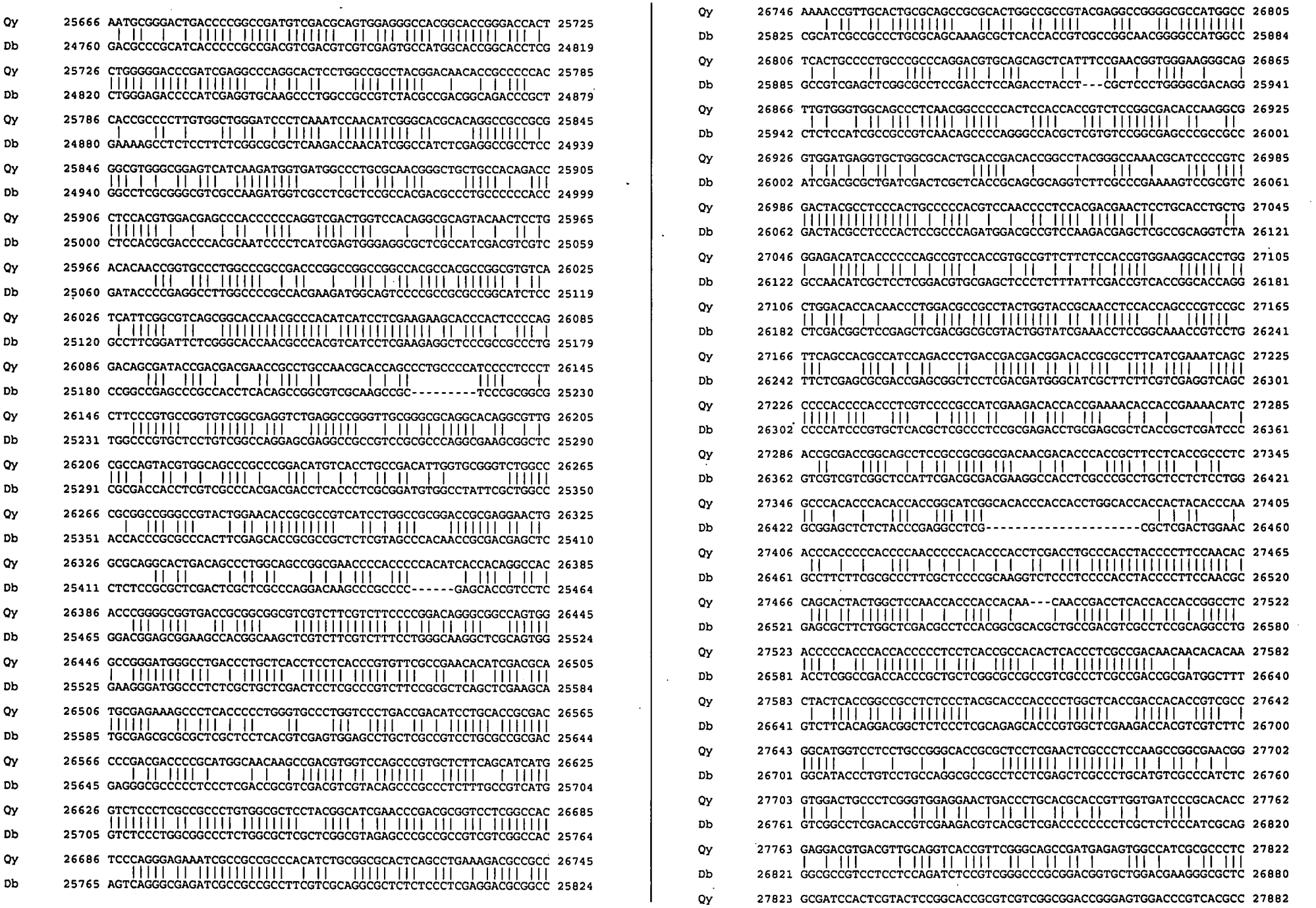


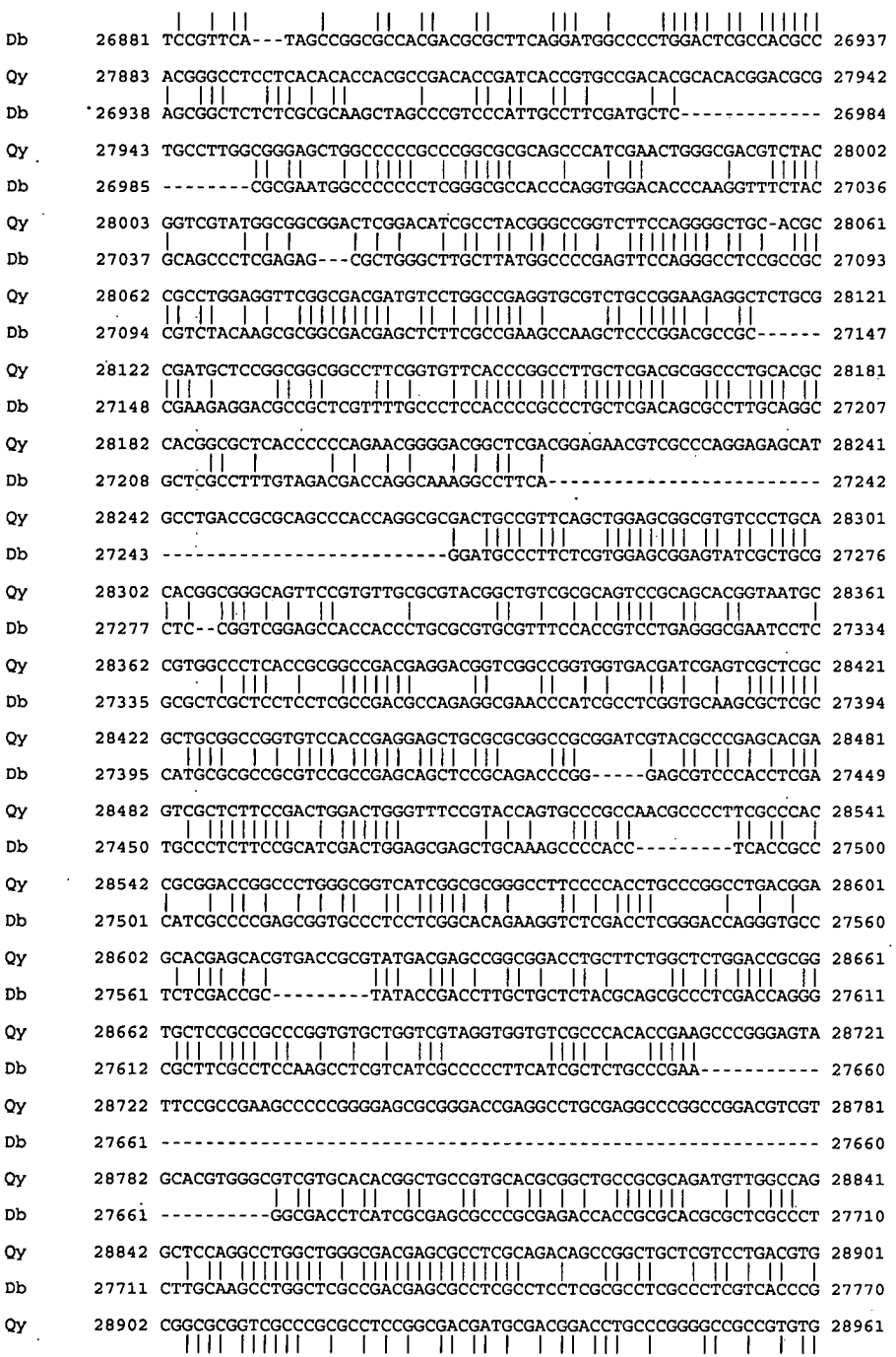

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; Sequence 4, Application US/08764233A
; Patent No. 5716849
; GENERAL INFORMATION:
;   APPLICANT:  Ligon, James M.
;   APPLICANT:  Schupp, Thomas
;   APPLICANT:  Beck, James J.
;   APPLICANT:  Hill, Dwight S.
;   APPLICANT:  Neff, Snezanna
;   APPLICANT:  Ryals, John A.
;   TITLE OF INVENTION:  Genes For The Biosynthesis Of Soraphen
;   NUMBER OF SEQUENCES:  10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Ciba-Geigy Corporation
;     STREET:  520 White Plains Road, P.O. Box 2005
;     CITY:  Tarrytown
;     STATE:  NY
;     COUNTRY:  USA
;     ZIP:  10591
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/764,233A
;     FILING DATE:
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/729,214
;     FILING DATE:  09-OCT-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/258,261
;     FILING DATE:  08-JUN-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Meigs, J. Timothy
;     REGISTRATION NUMBER:  38,241
;     REFERENCE/DOCKET NUMBER:  1506/CIP6
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (919) 541-8587
;     TELEFAX:  (919) 541-8689
; INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  28958 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
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US-08-764-233A-4

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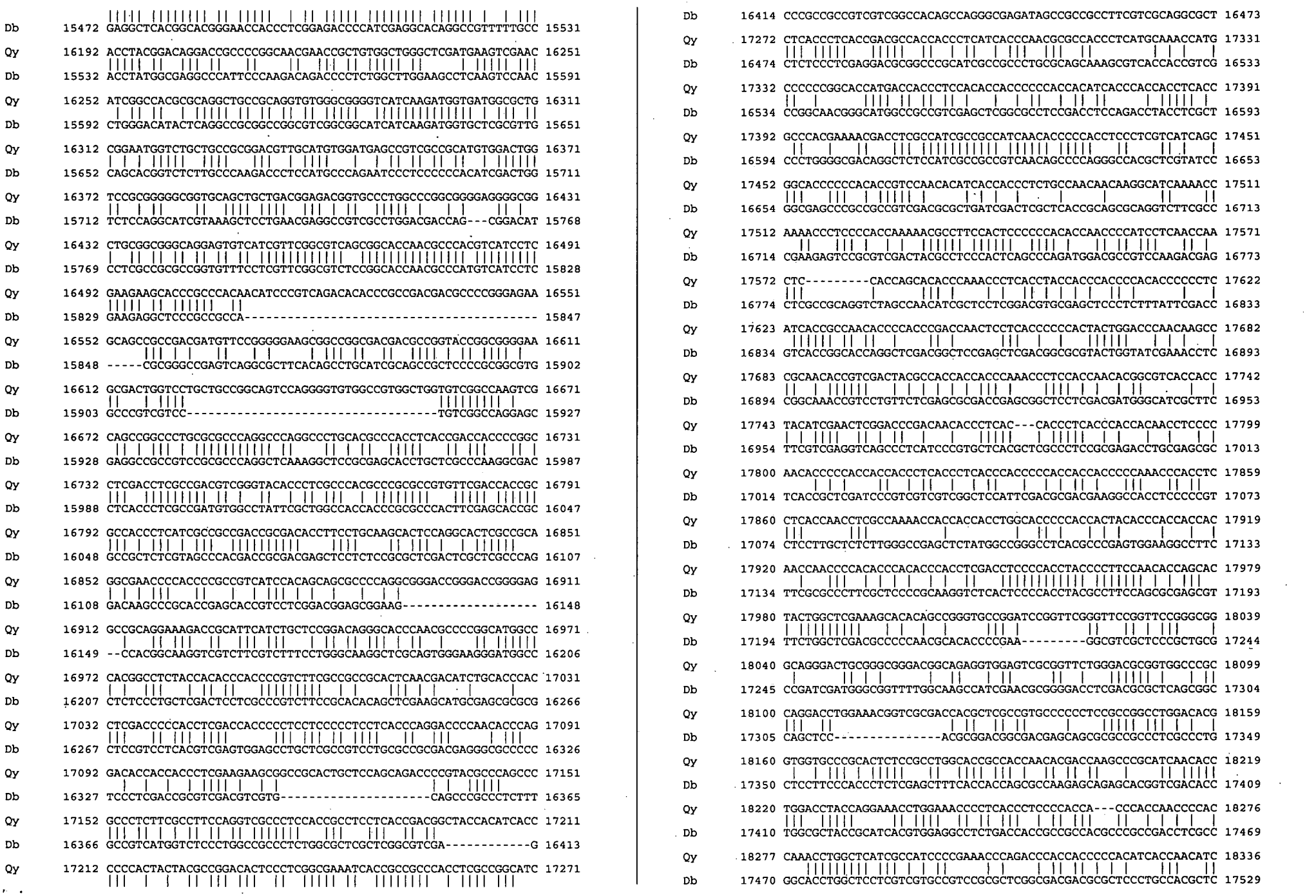
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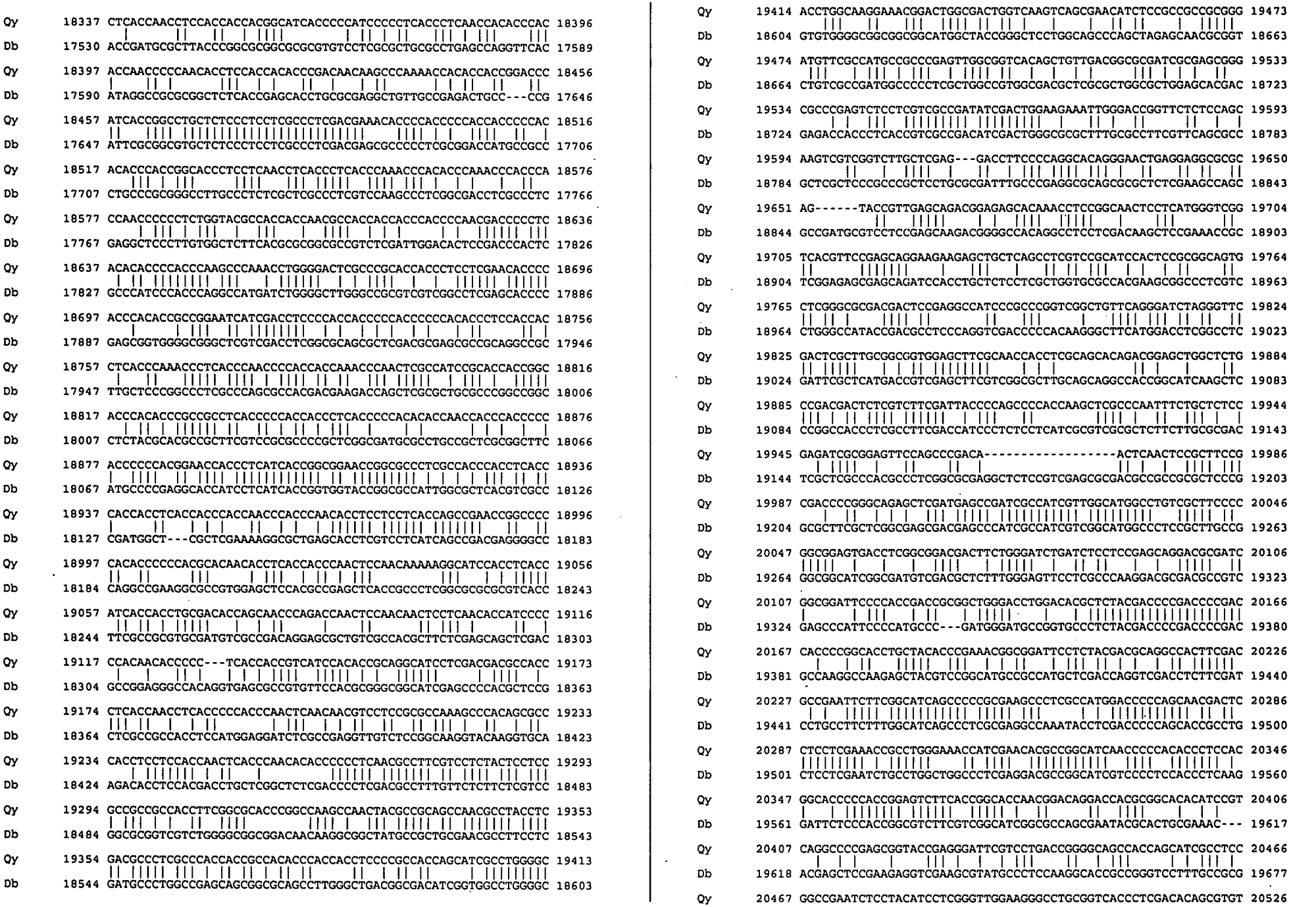
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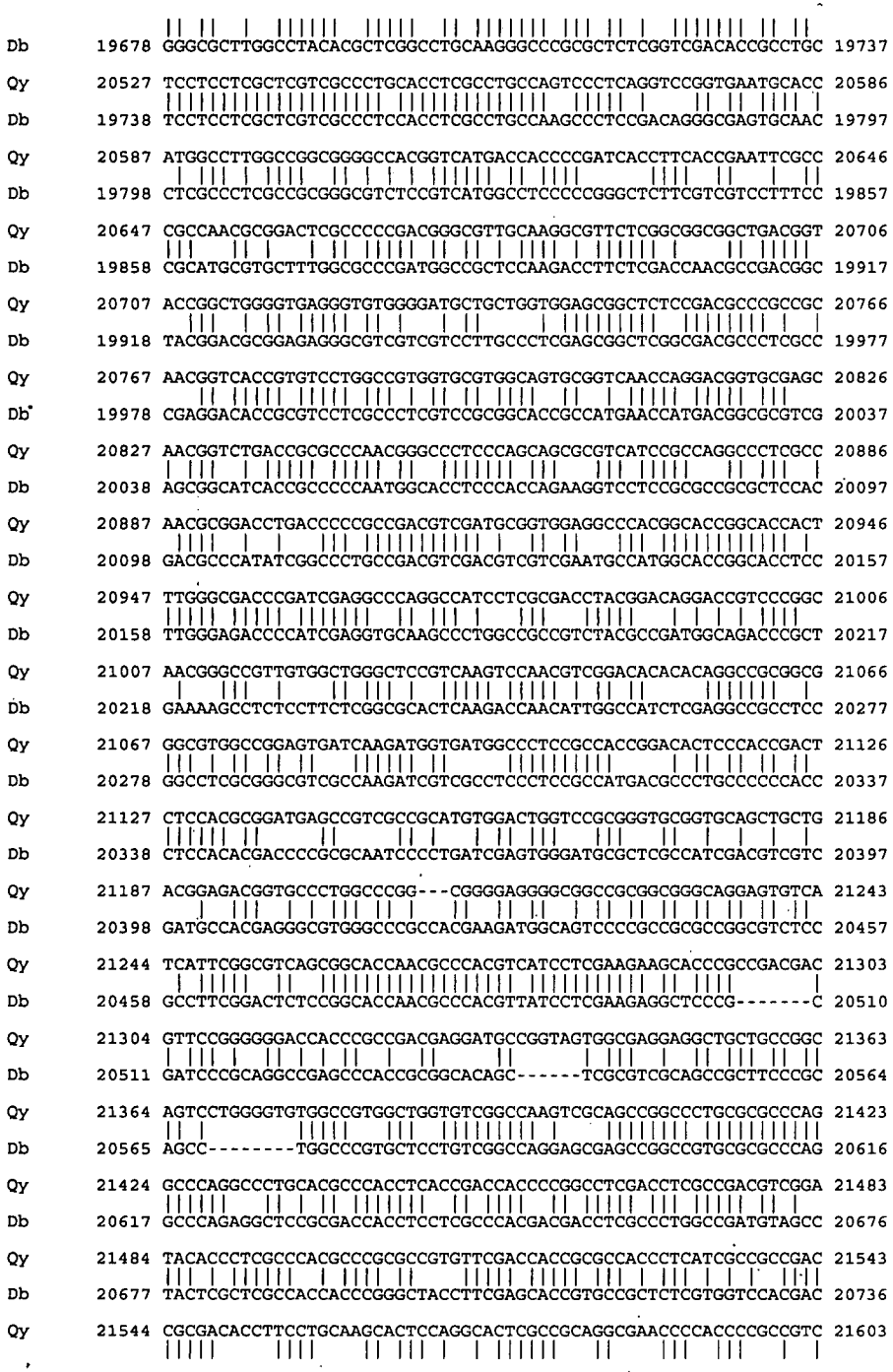
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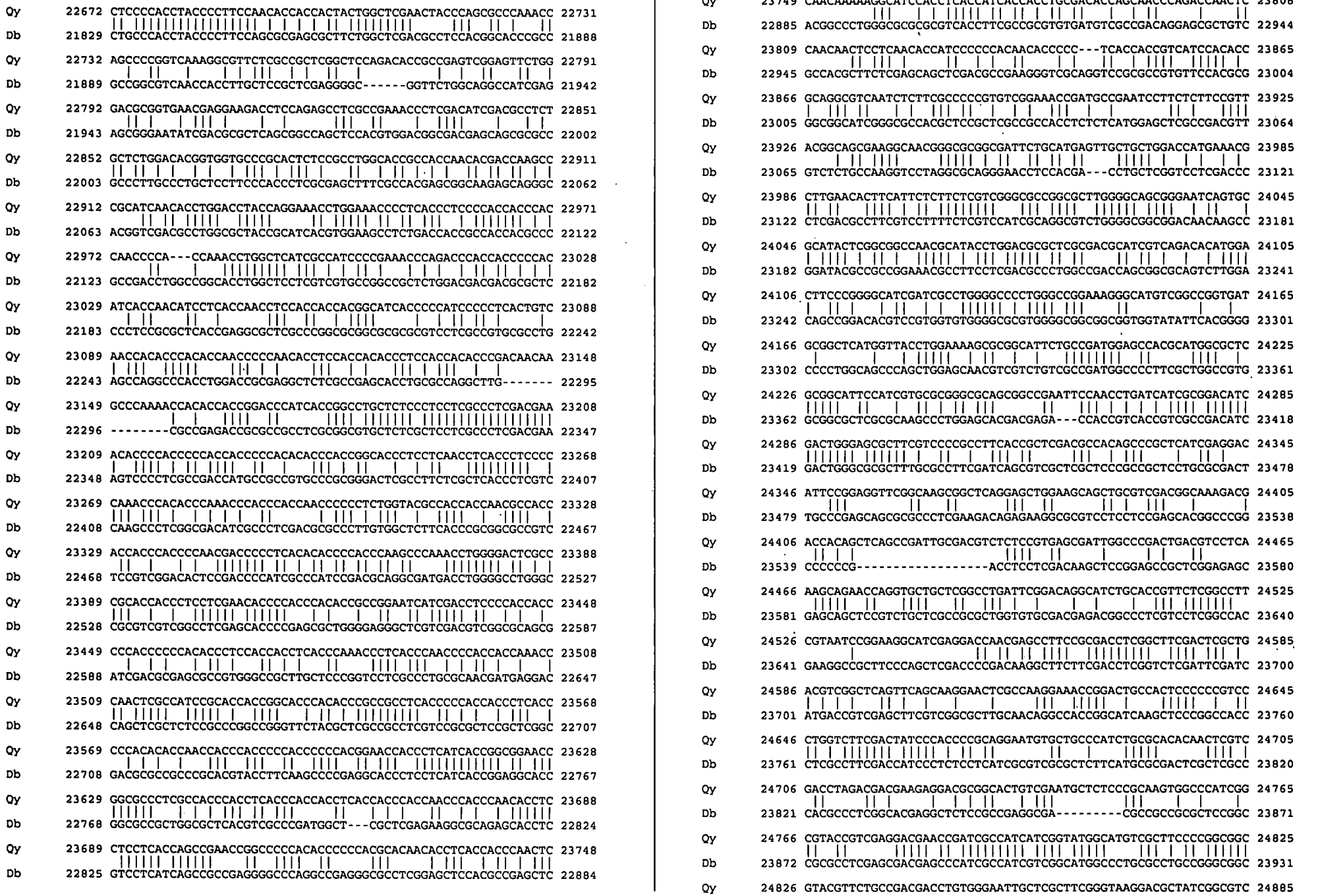
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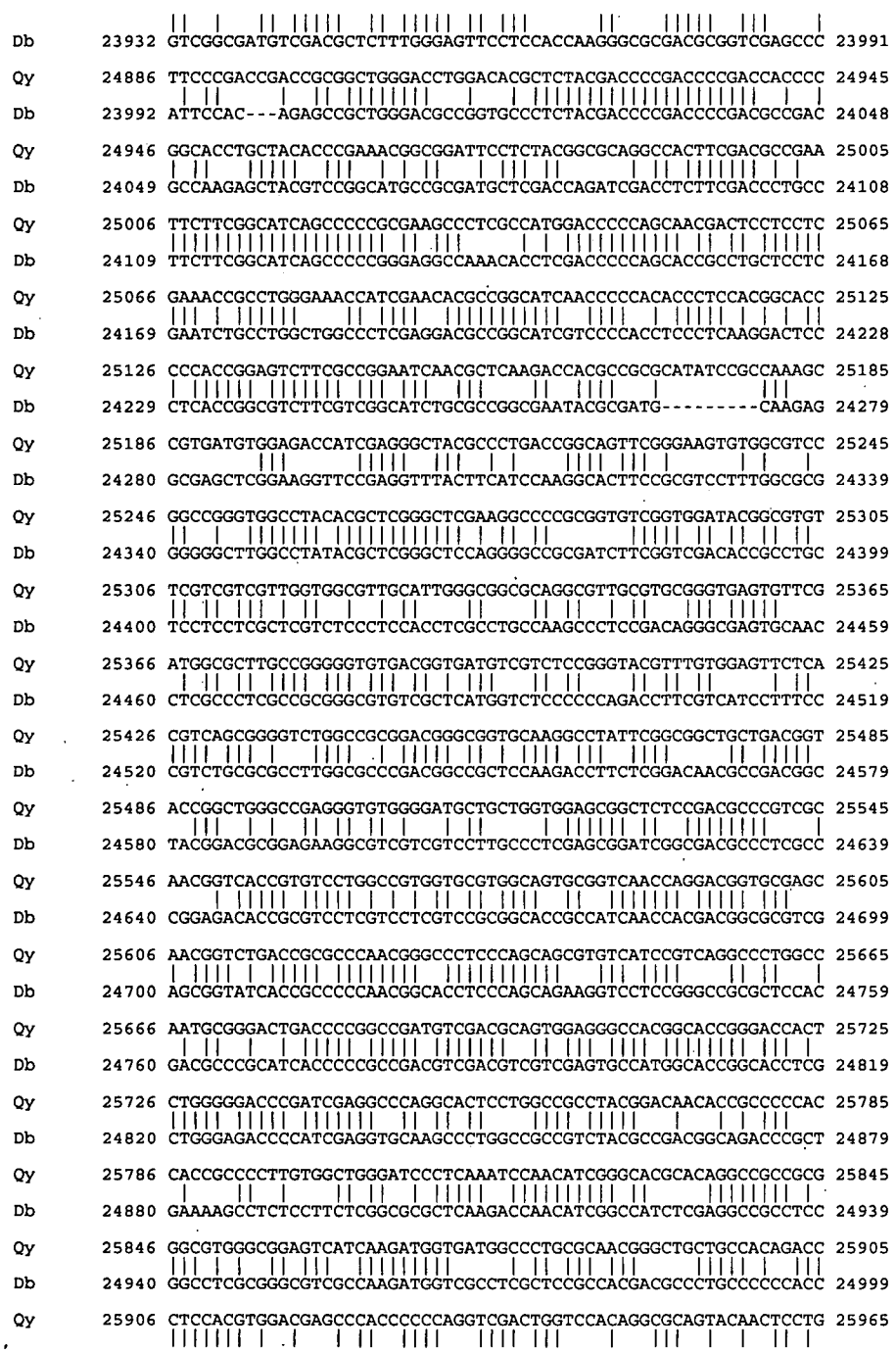
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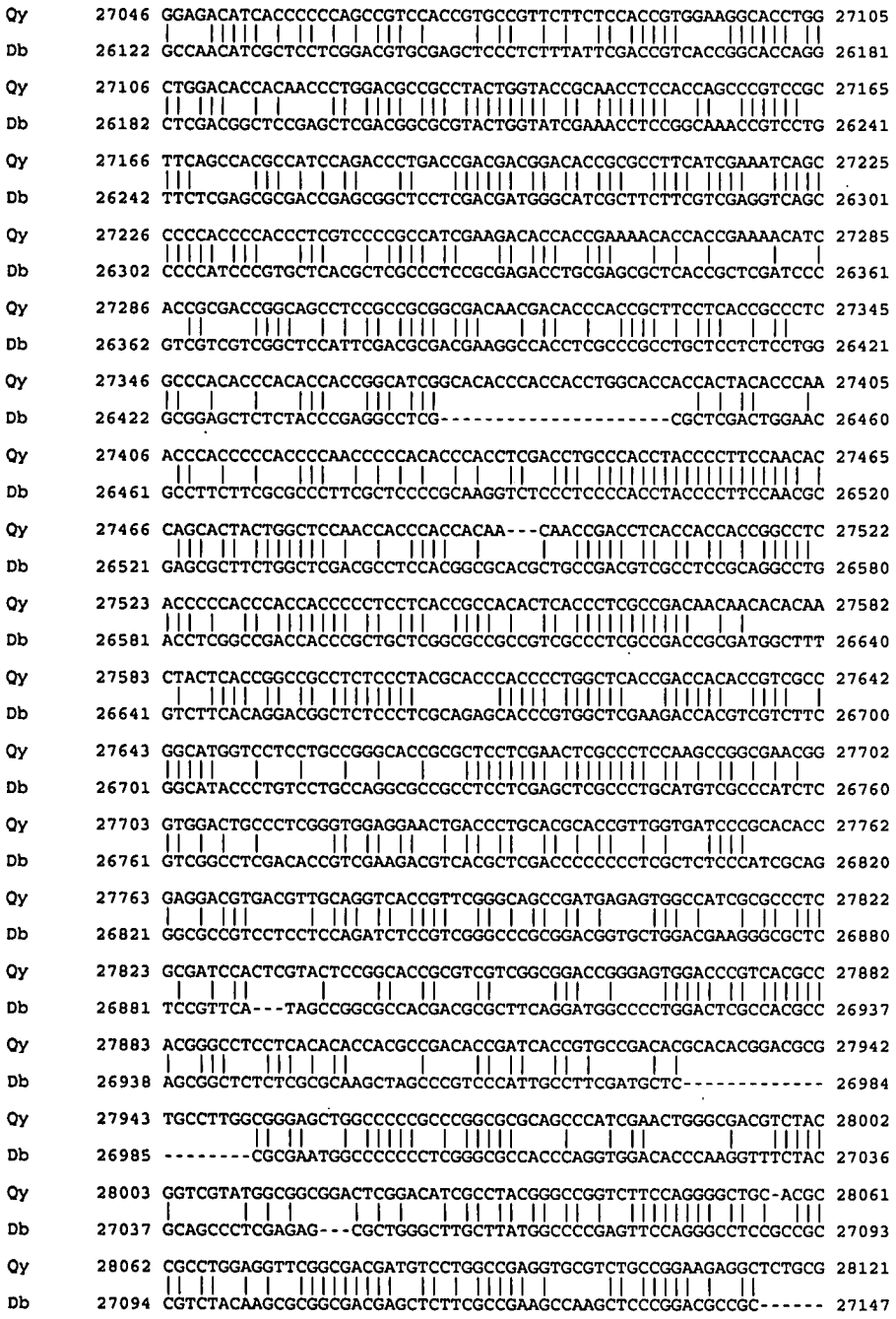


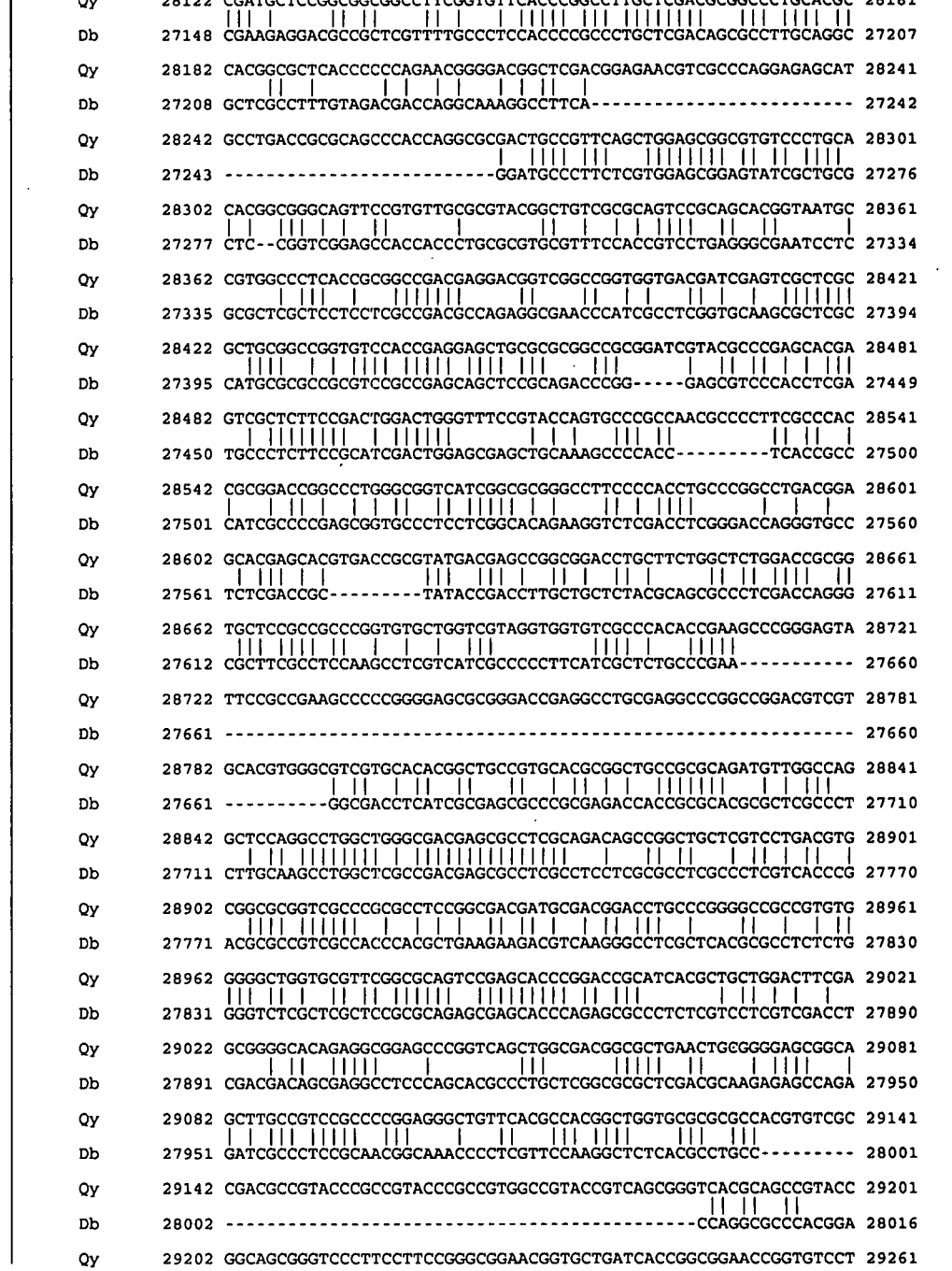



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RESULT 10
US-08-457-335A-6
; Sequence 6, Application US/08457335A
; Patent No. 5723759
;  GENERAL INFORMATION:
;    APPLICANT:  Schupp, Thomas
;    APPLICANT:  Ligon, James M.
;    APPLICANT:  Beck, James Joseph
;    APPLICANT:  Hill, Dwight Steven
;    APPLICANT:  Ryals, John Andrew
;    APPLICANT:  Gaffney, Thomas Deane
;    APPLICANT:  Lam, Stephen Ting
;    APPLICANT:  Hammer, Phillip E.
;    APPLICANT:  Uknes, Scott Joseph
;    TITLE OF INVENTION:  Genes for the synthesis of
;    TITLE OF INVENTION:  antipathogenic substances
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Ciba-Geigy Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,335A
;      FILING DATE:  01-JUN-1995
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/457,205
;      FILING DATE:  01-JUN-1995
;      APPLICATION NUMBER:  08/258,261
;      FILING DATE:  08-Jun-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elmer, James Scott
;      REGISTRATION NUMBER:  36,129
;      REFERENCE/DOCKET NUMBER:  CGC 1506/CIP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8614
;      TELEFAX:  919-541-8689
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28958 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-457-335A-6

  Query Match           10.2%;  Score 3140.6;  DB 1;  Length 28958;
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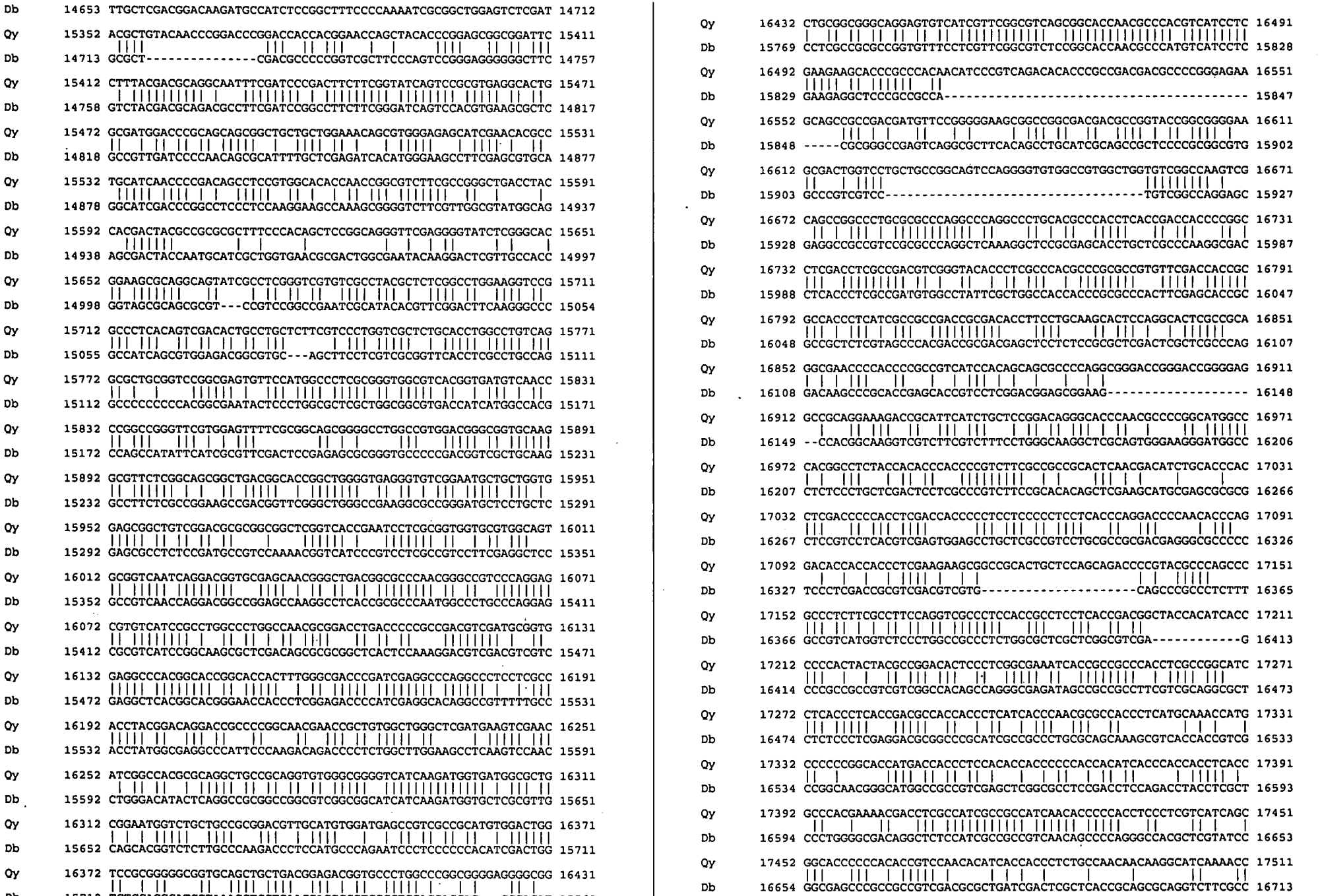
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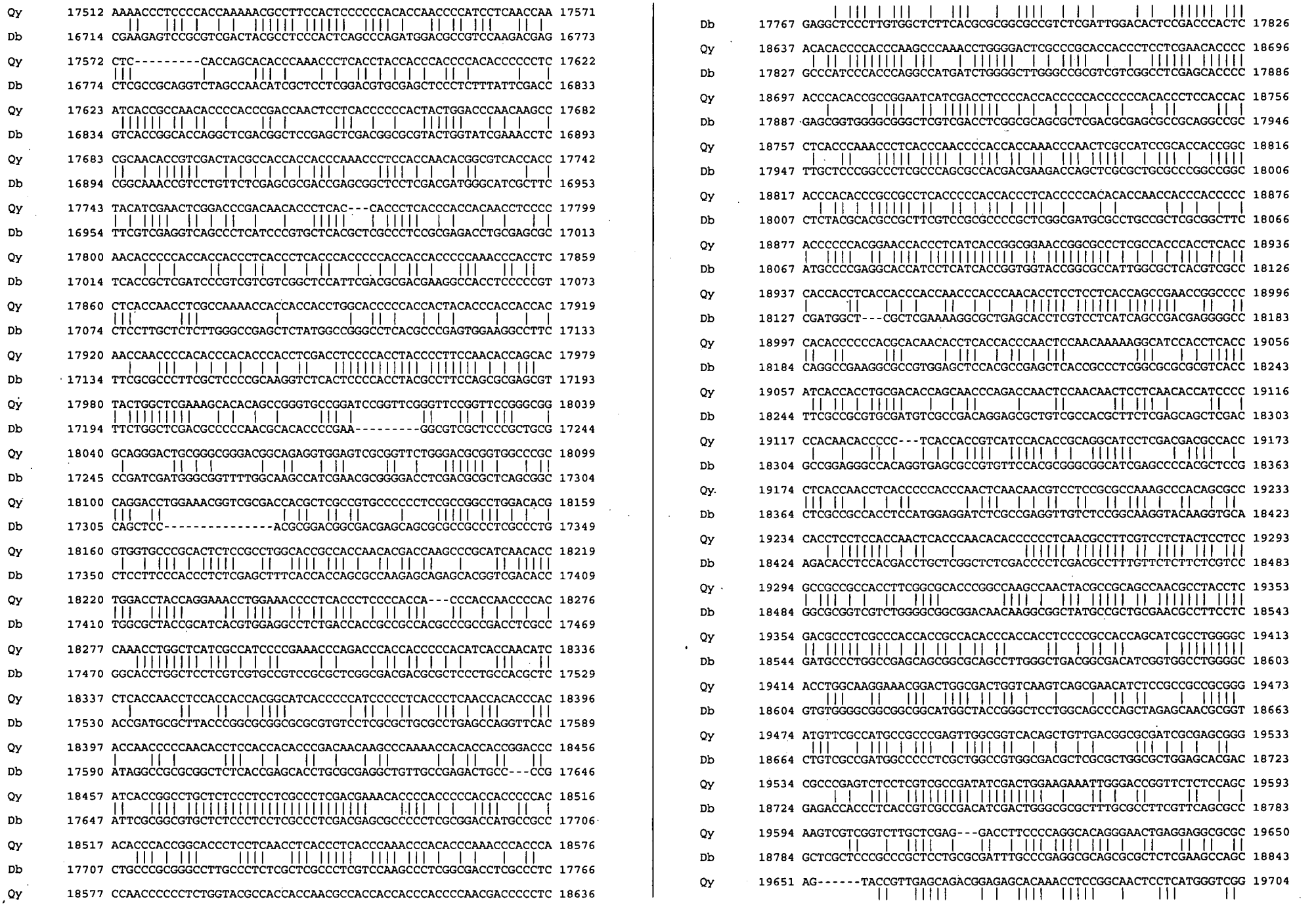
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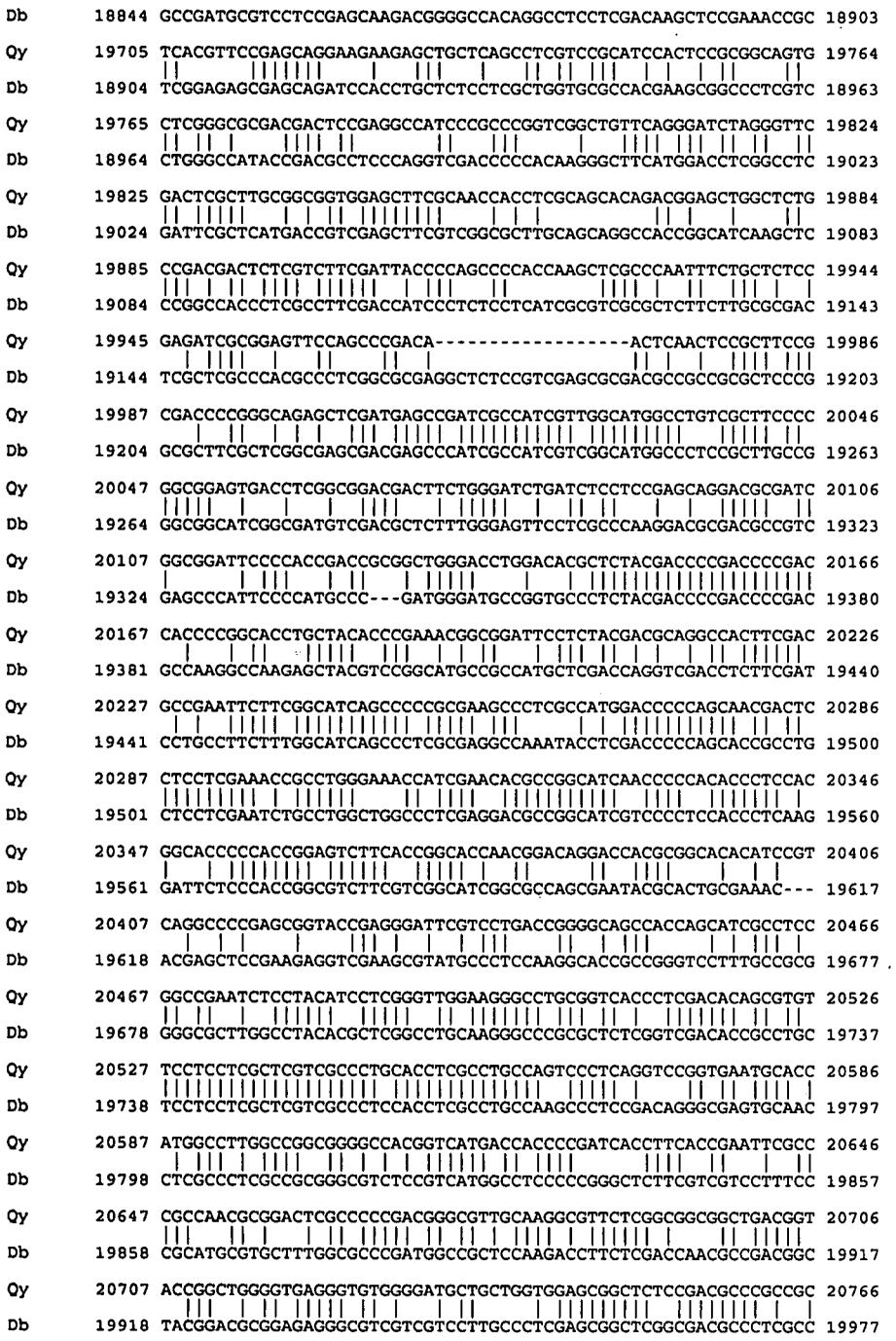
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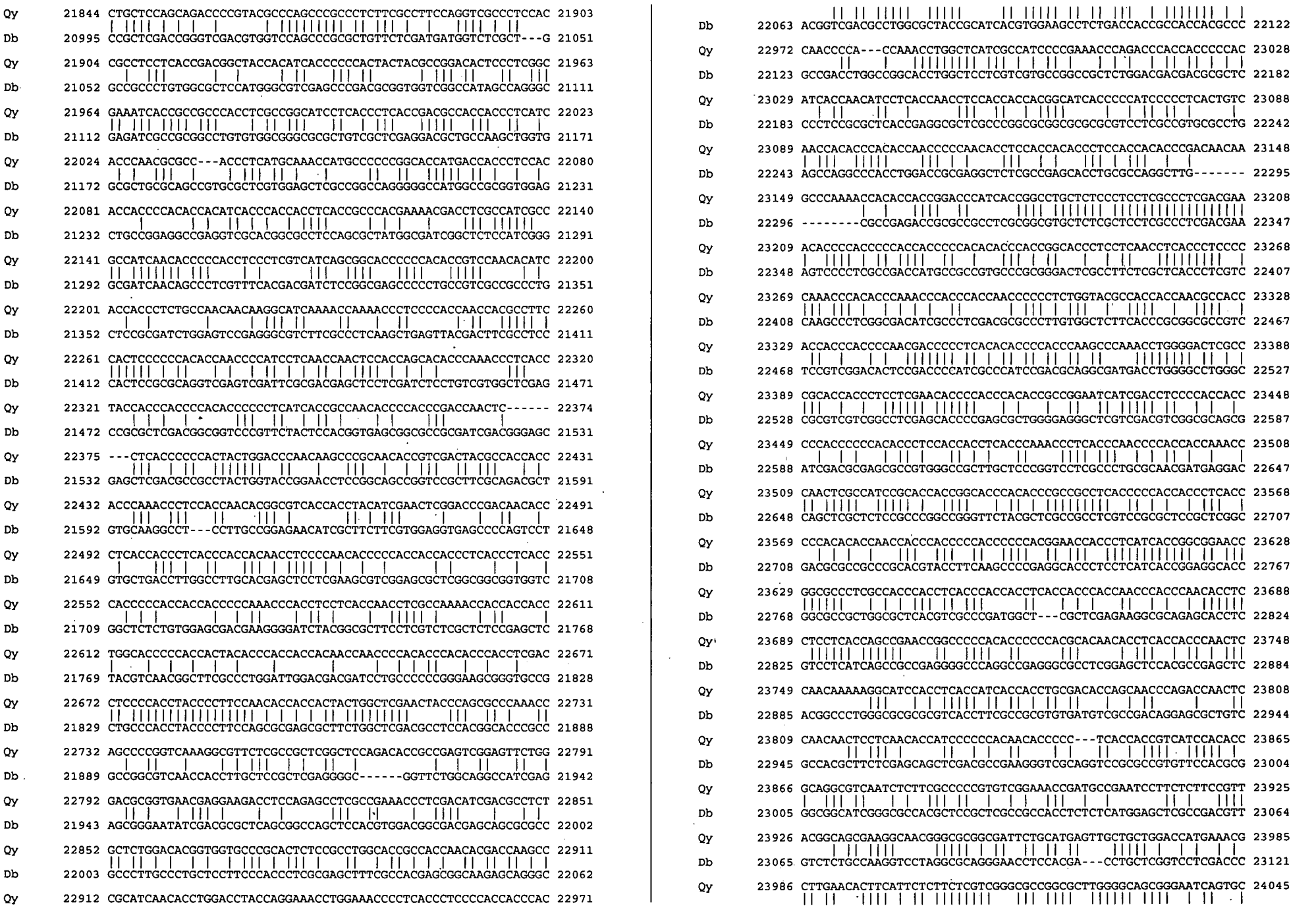
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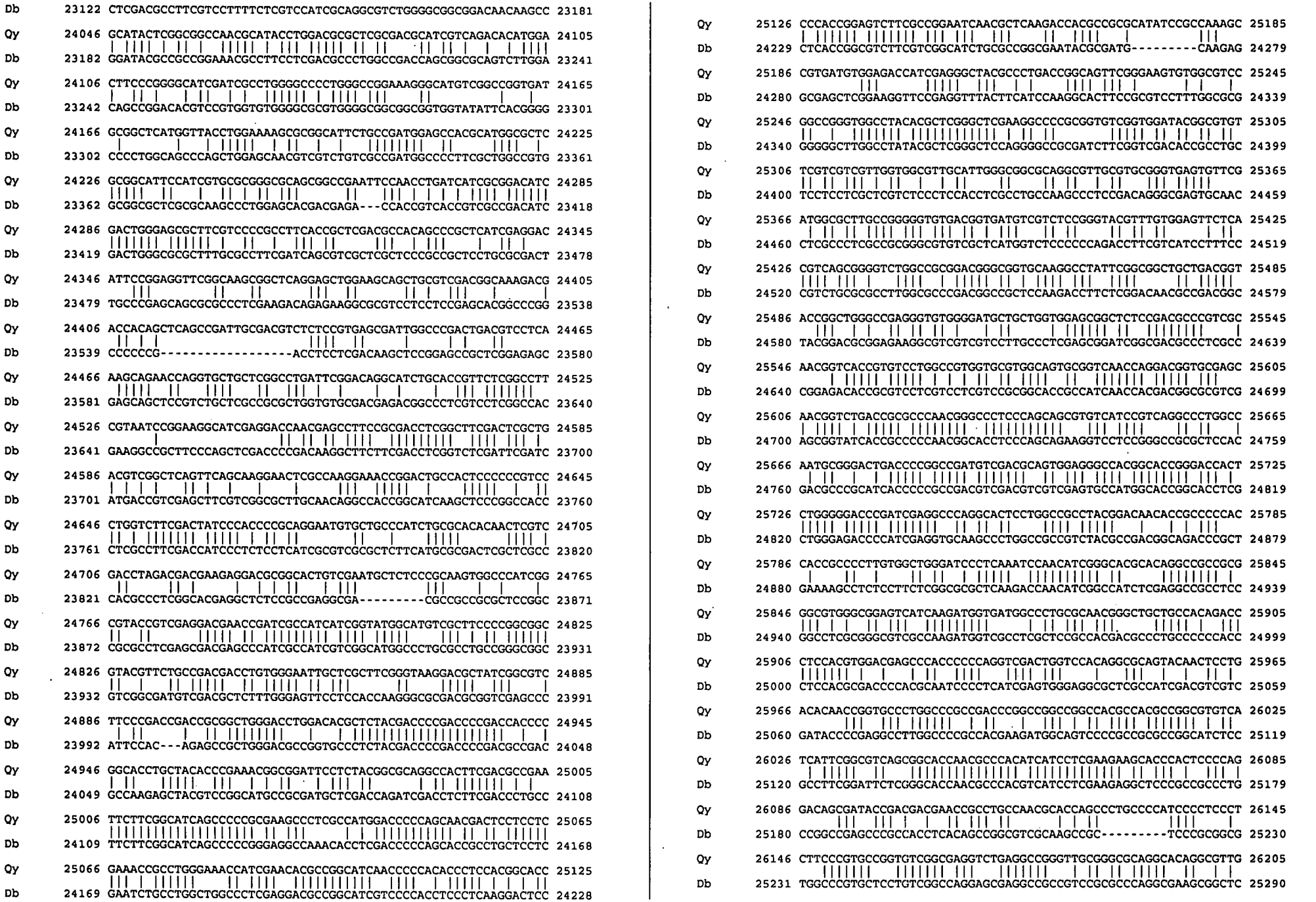
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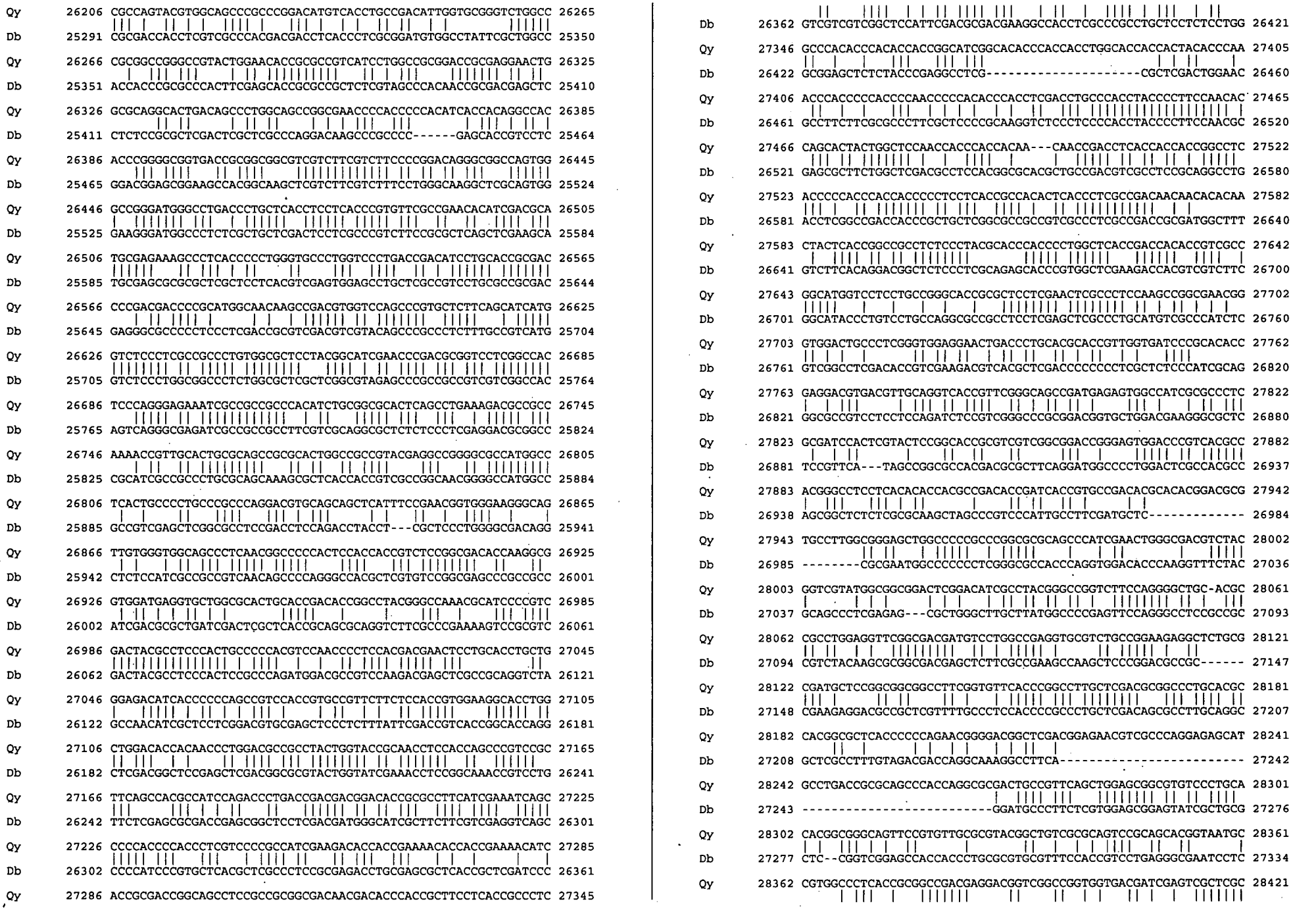


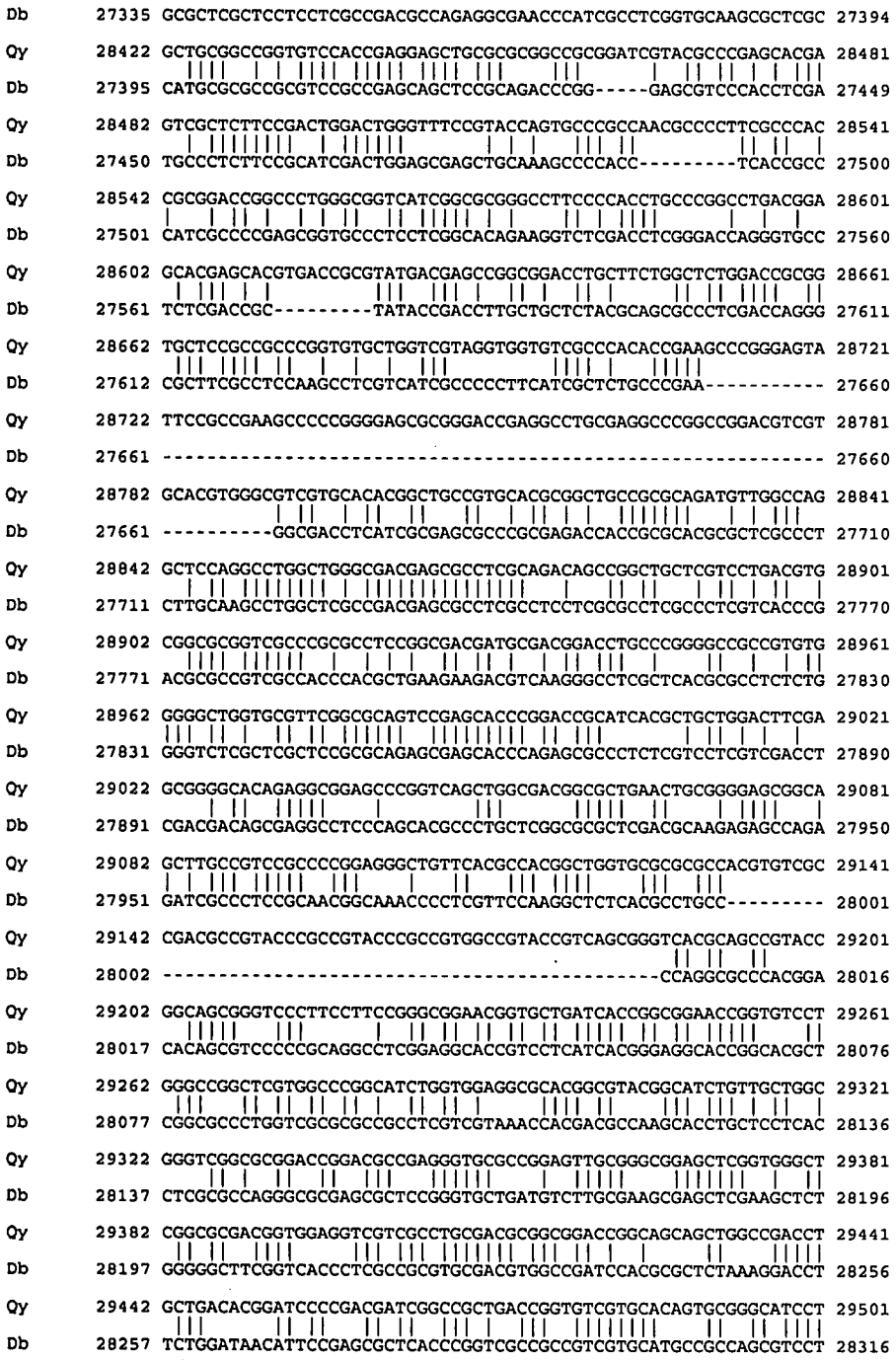



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RESULT 11
US-08-729-214-6
; Sequence 6, Application US/08729214
; Patent No. 5817502
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Hammer, Phillip E.
; APPLICANT: van Pee, Karl-Heinz
; APPLICANT: Kirner, Sabine
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,214
; FILING DATE: TBA
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP5
; TELECOMMUNICATION INFORMATION:

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;      TELEPHONE:  919-541-8587
;      TELEFAX:  919-541-8689
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28958 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-729-214-6

  Query Match             10.2%;  Score 3140.6;  DB 1;  Length 28958;
  Best Local Similarity   54.1%;  Pred. No. 0;
  Matches 8239;  Conservative    0;  Mismatches 6284;  Indels  698;  Gaps   63;

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              |||  | ||| |||   |     |  |  |||||||  ||  | |||||  |||     ||  |
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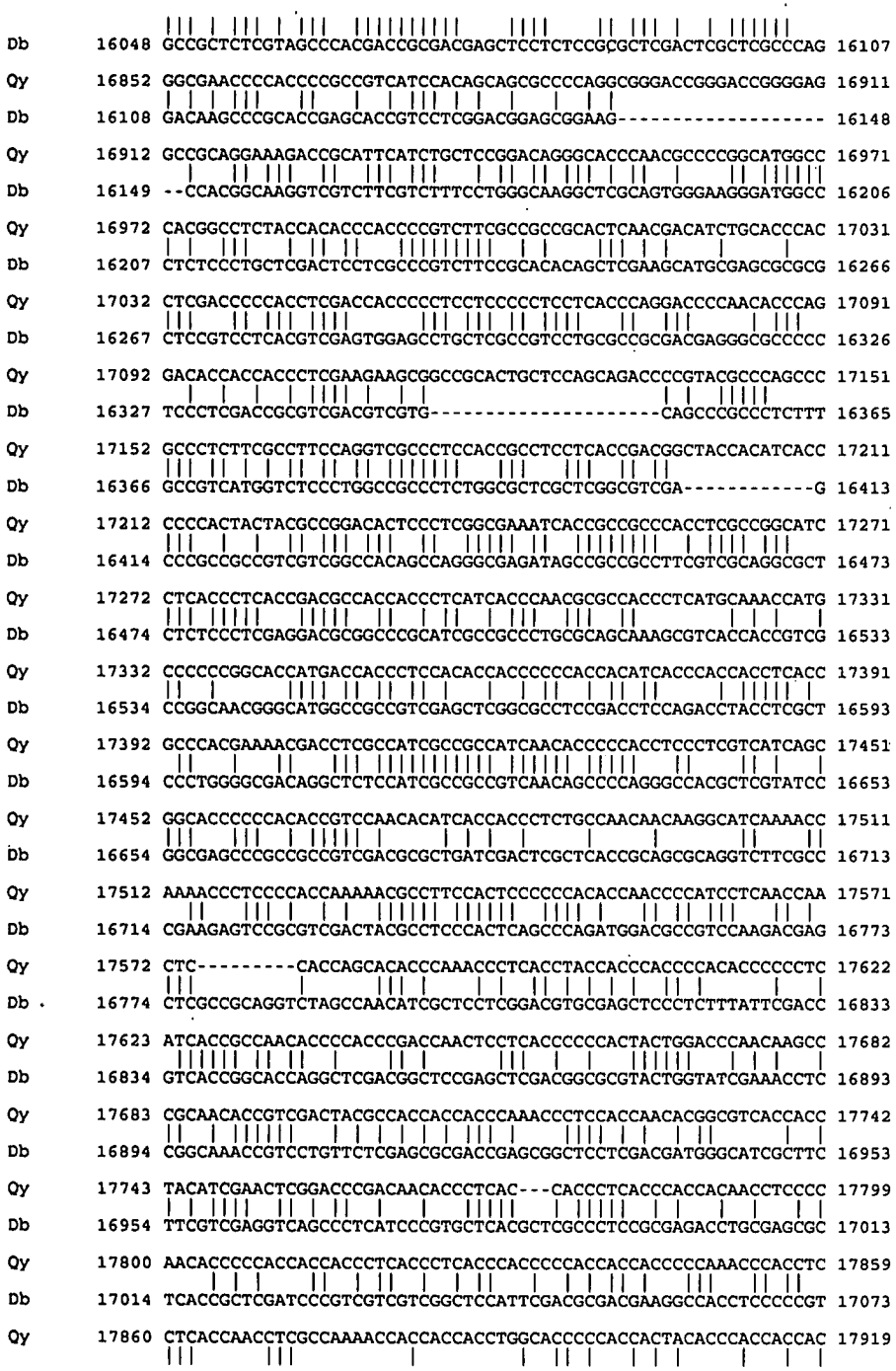
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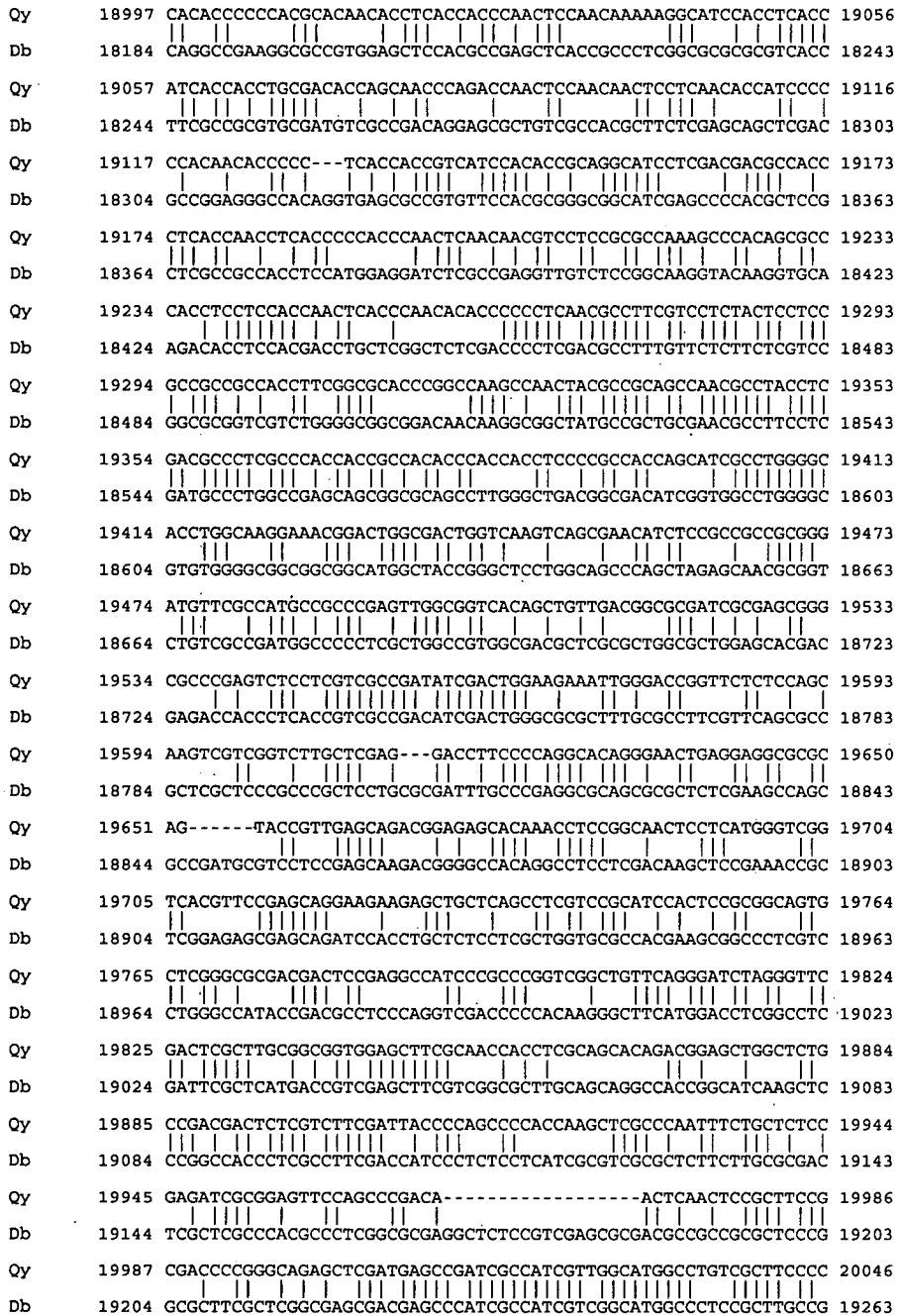
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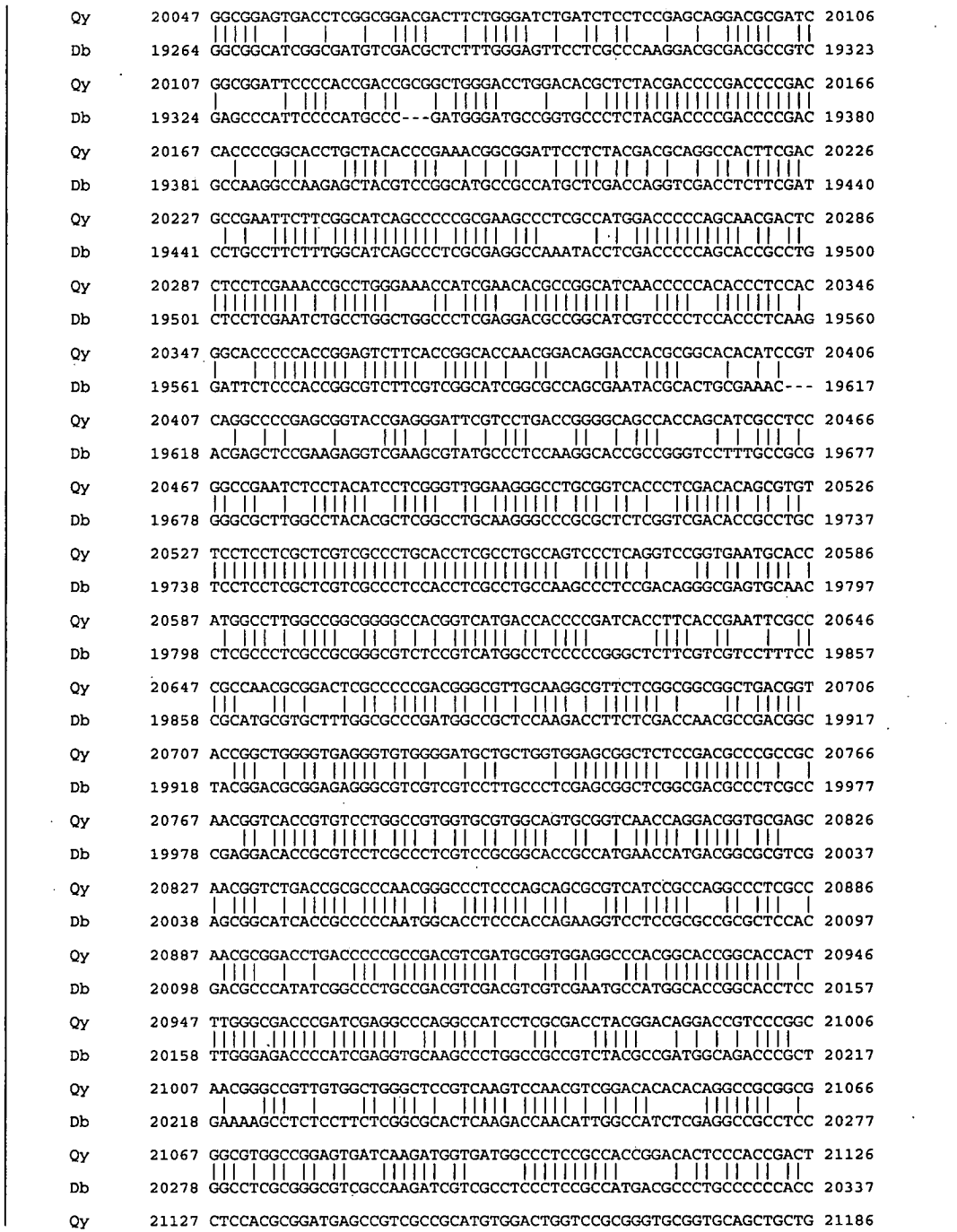
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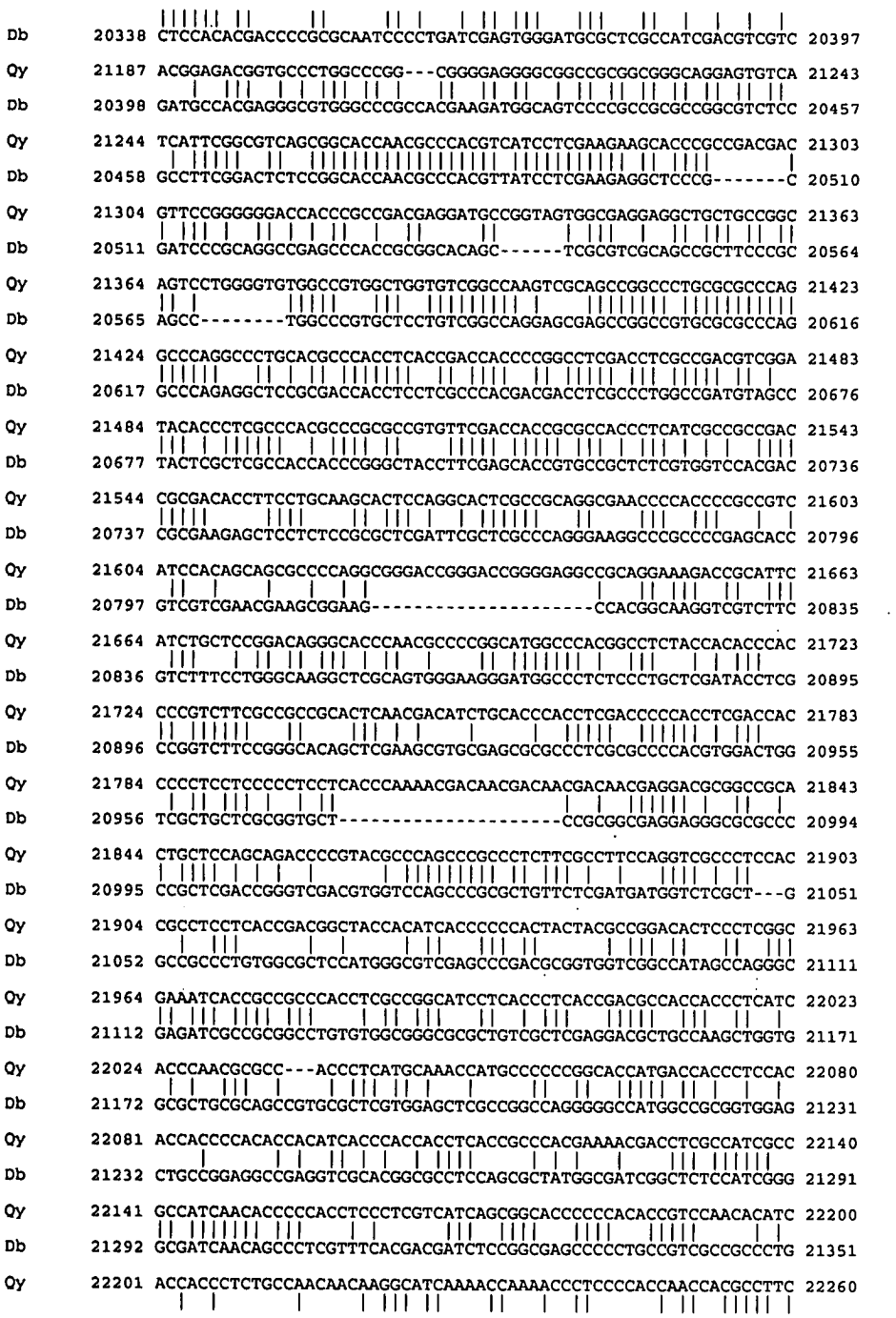
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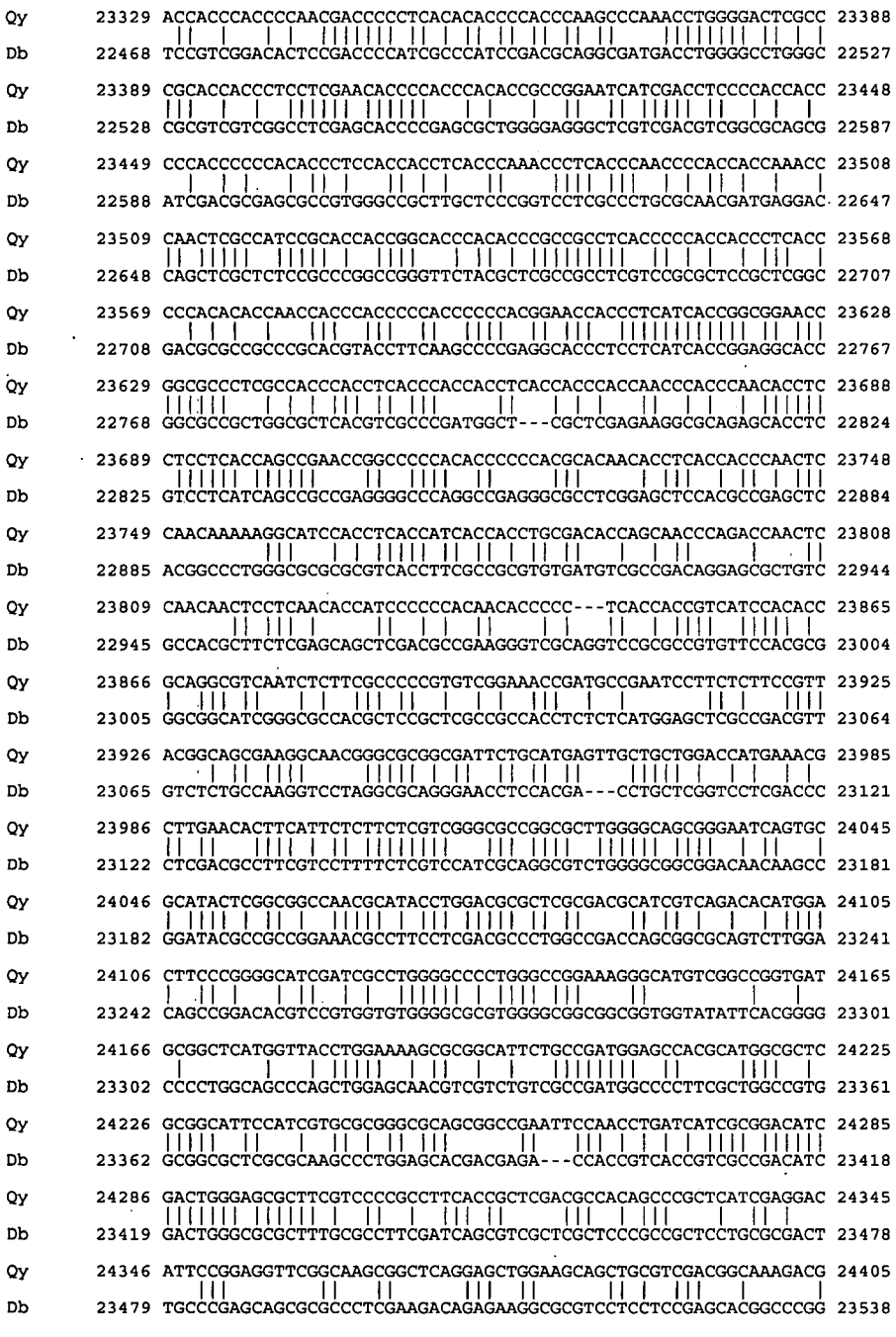
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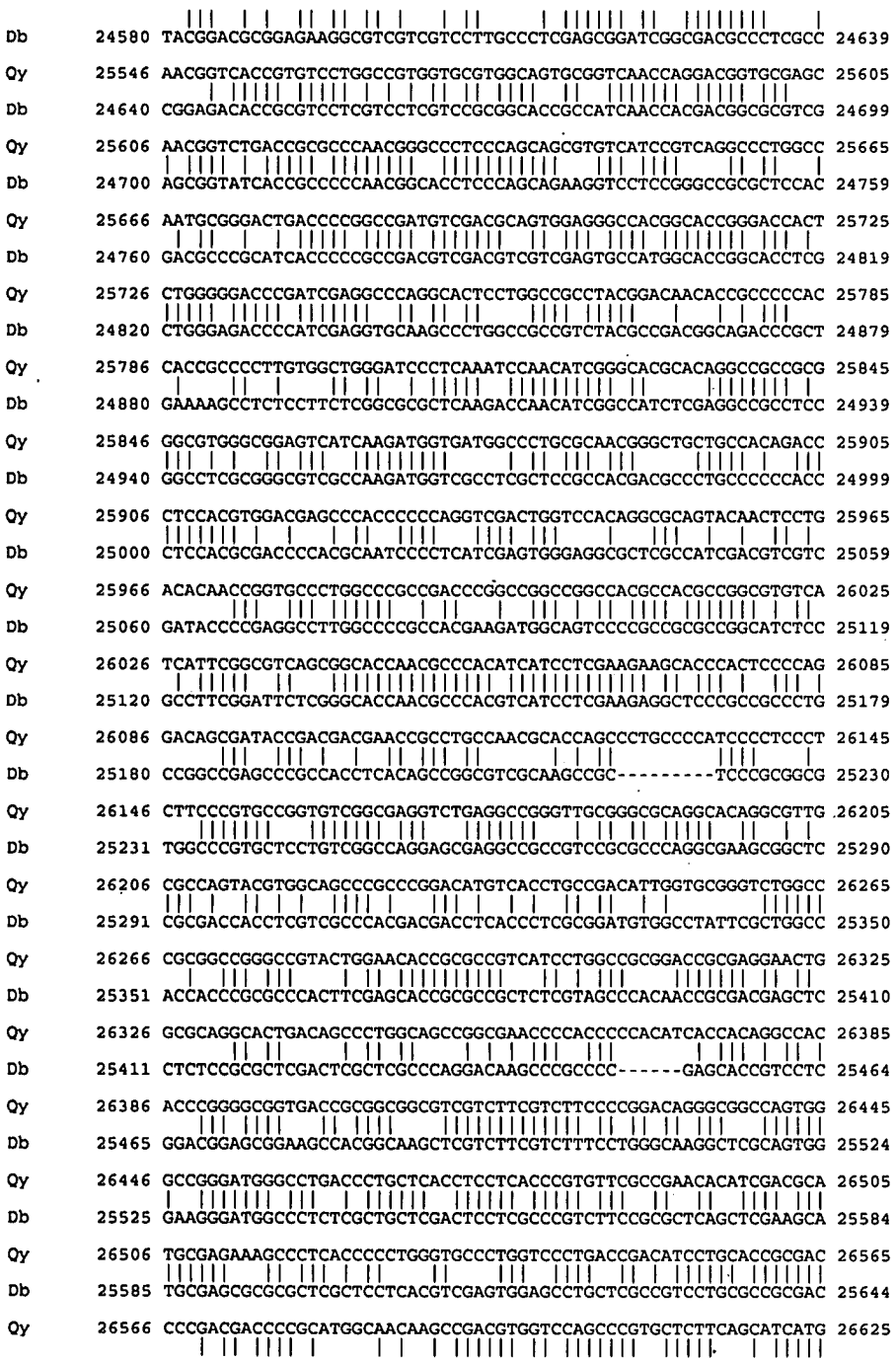

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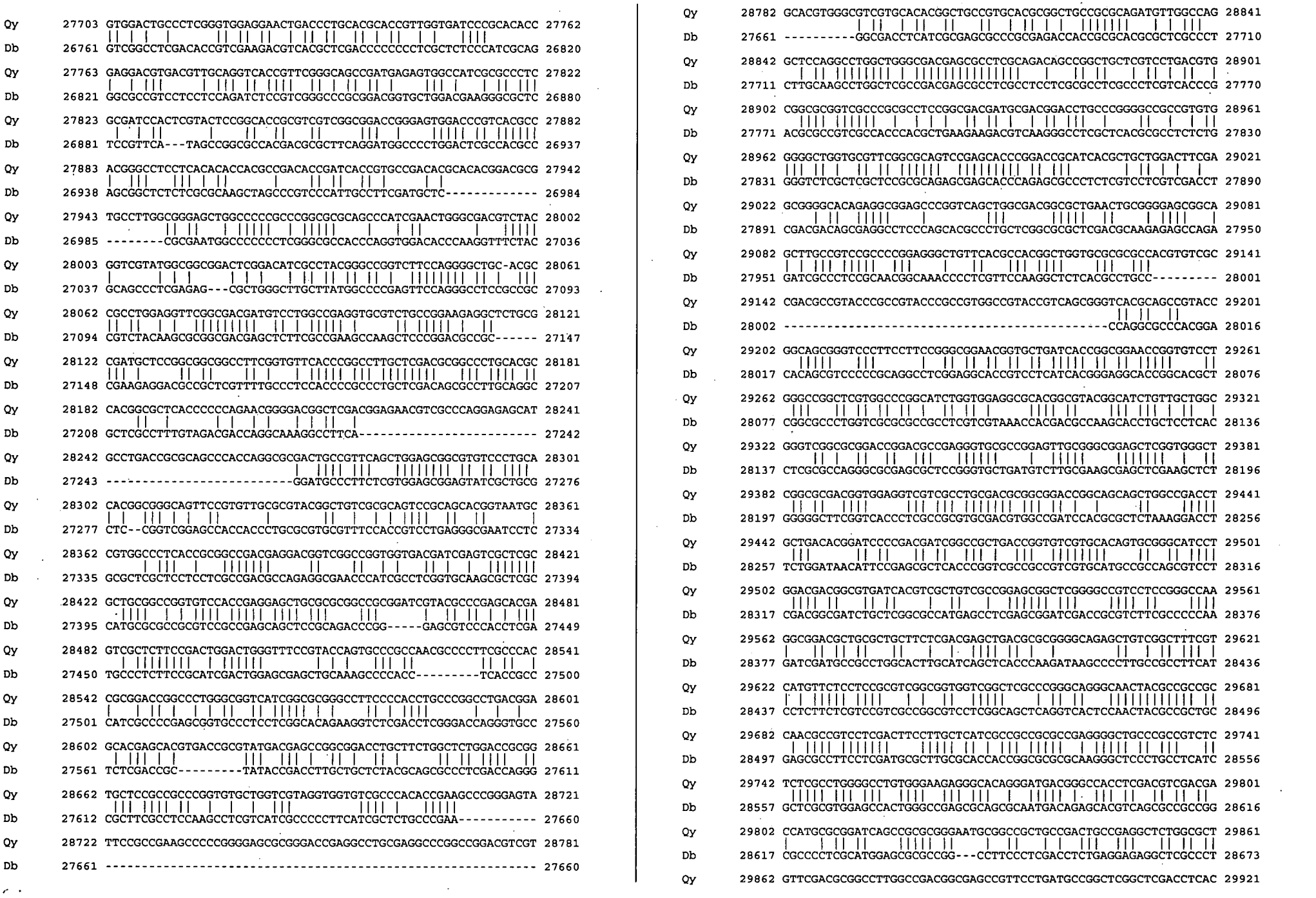





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RESULT 12
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; Sequence 6, Application US/09028934
; Patent No. 6117670
;  GENERAL INFORMATION:
;    APPLICANT:  Ligon, James M.
;    APPLICANT:  Hill, Dwight S.
;    APPLICANT:  Lam, Steven T.
;    APPLICANT:  Hammer, Philip E.
;    APPLICANT:  van Pee, Karl-Heinz
;    APPLICANT:  Kirner, Sabine
;    APPLICANT:  Young, Thomas R.
;    TITLE OF INVENTION:  Pyrrolnitrin Biosynthesis Genes and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6117670artis Corporation
;      STREET:  3054 Cornwallis Road
;      CITY:  Research Triangle Park
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/028,934
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/729,214
;      FILING DATE:  09-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/258,261
;      FILING DATE:  08-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meigs, J. Timothy
;      REGISTRATION NUMBER:  38,241
;      REFERENCE/DOCKET NUMBER:  CGC1506/CIP7
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8587
;      TELEFAX:  919-541-8689
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28958 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-028-934-6

  Query Match             10.2%;  Score 3140.6;  DB 3;  Length 28958;
  Best Local Similarity   54.1%;  Pred. No. 0;
  Matches 8239;  Conservative    0;  Mismatches 6284;  Indels  698;  Gaps   63;

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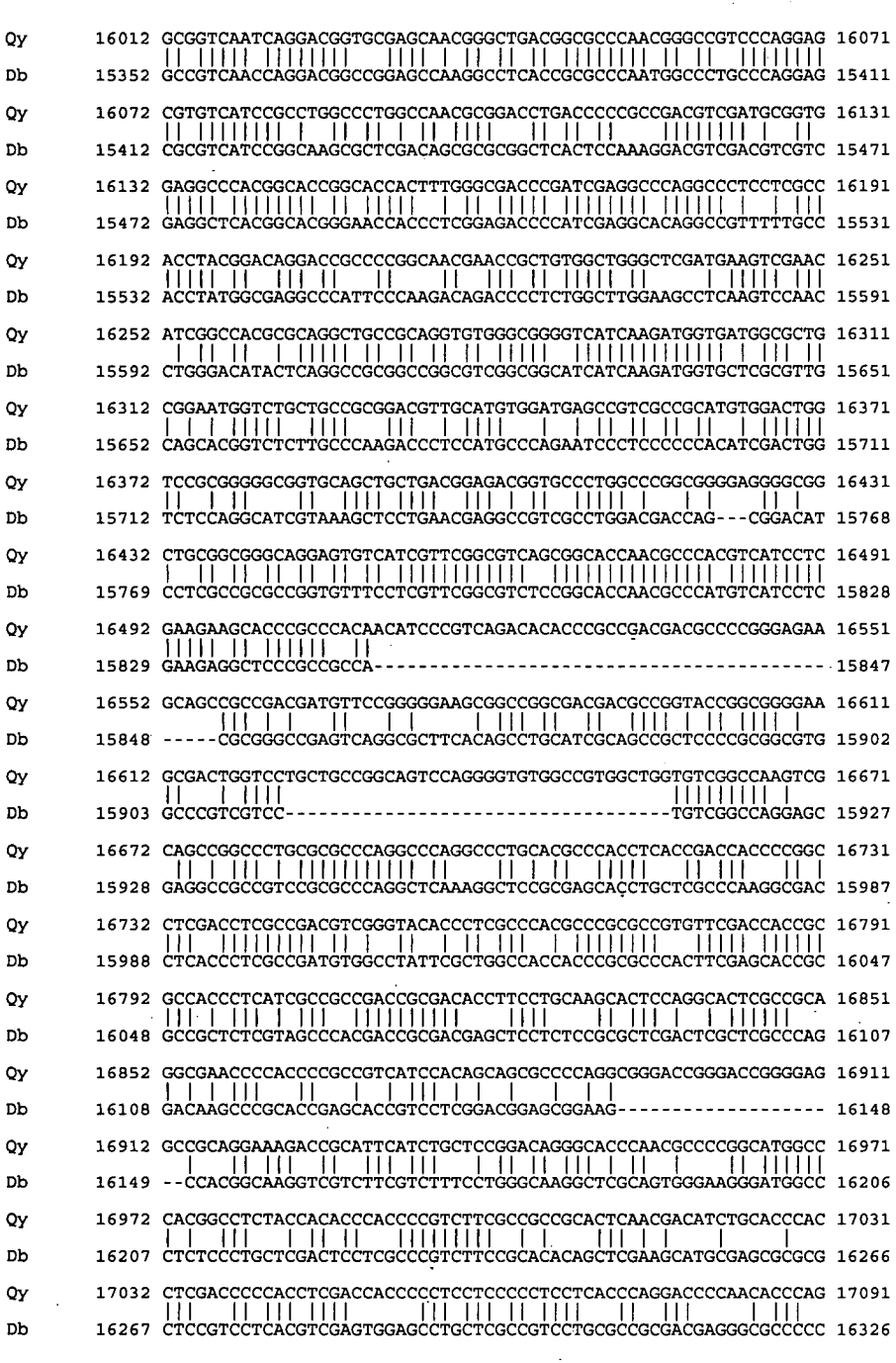
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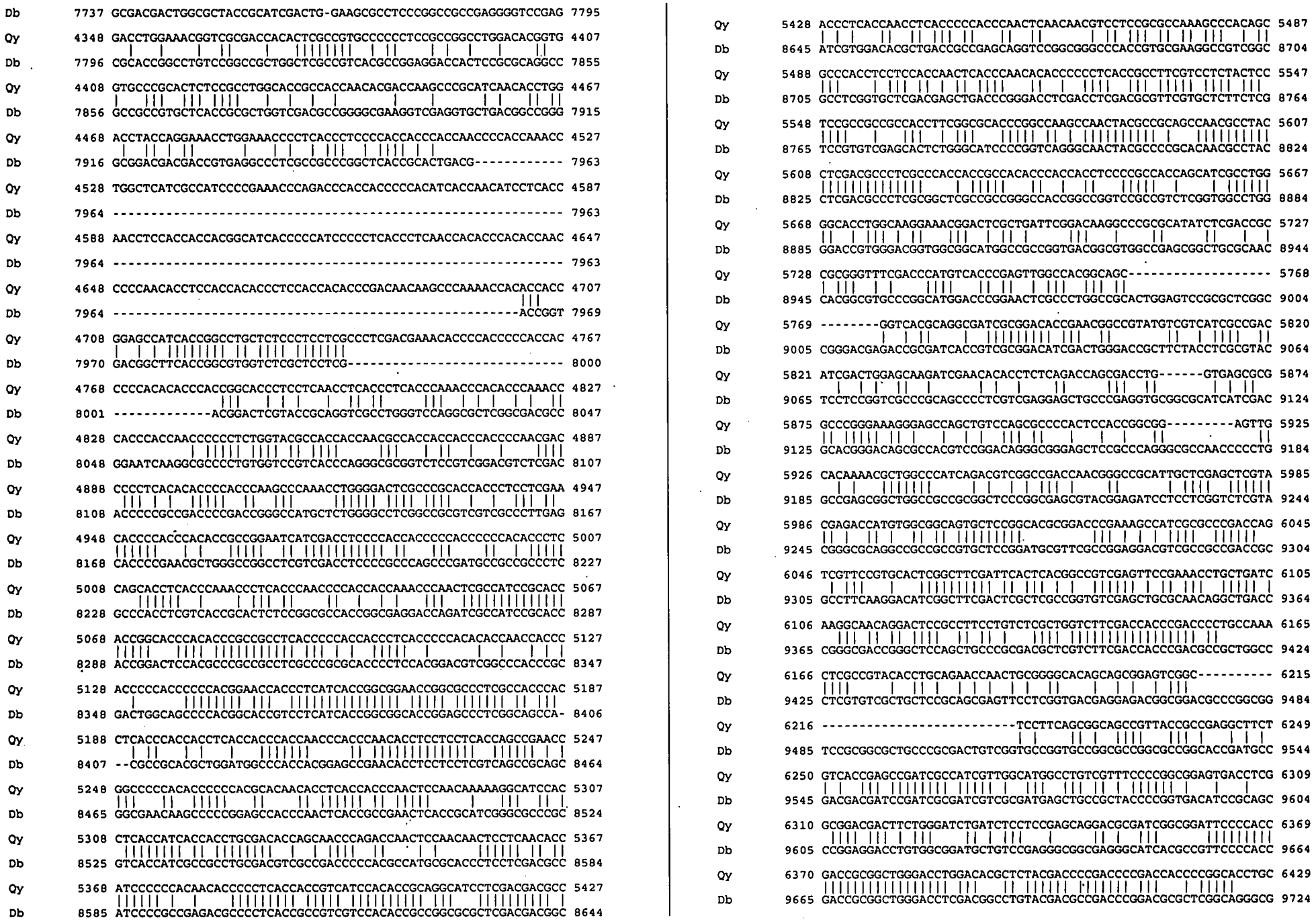
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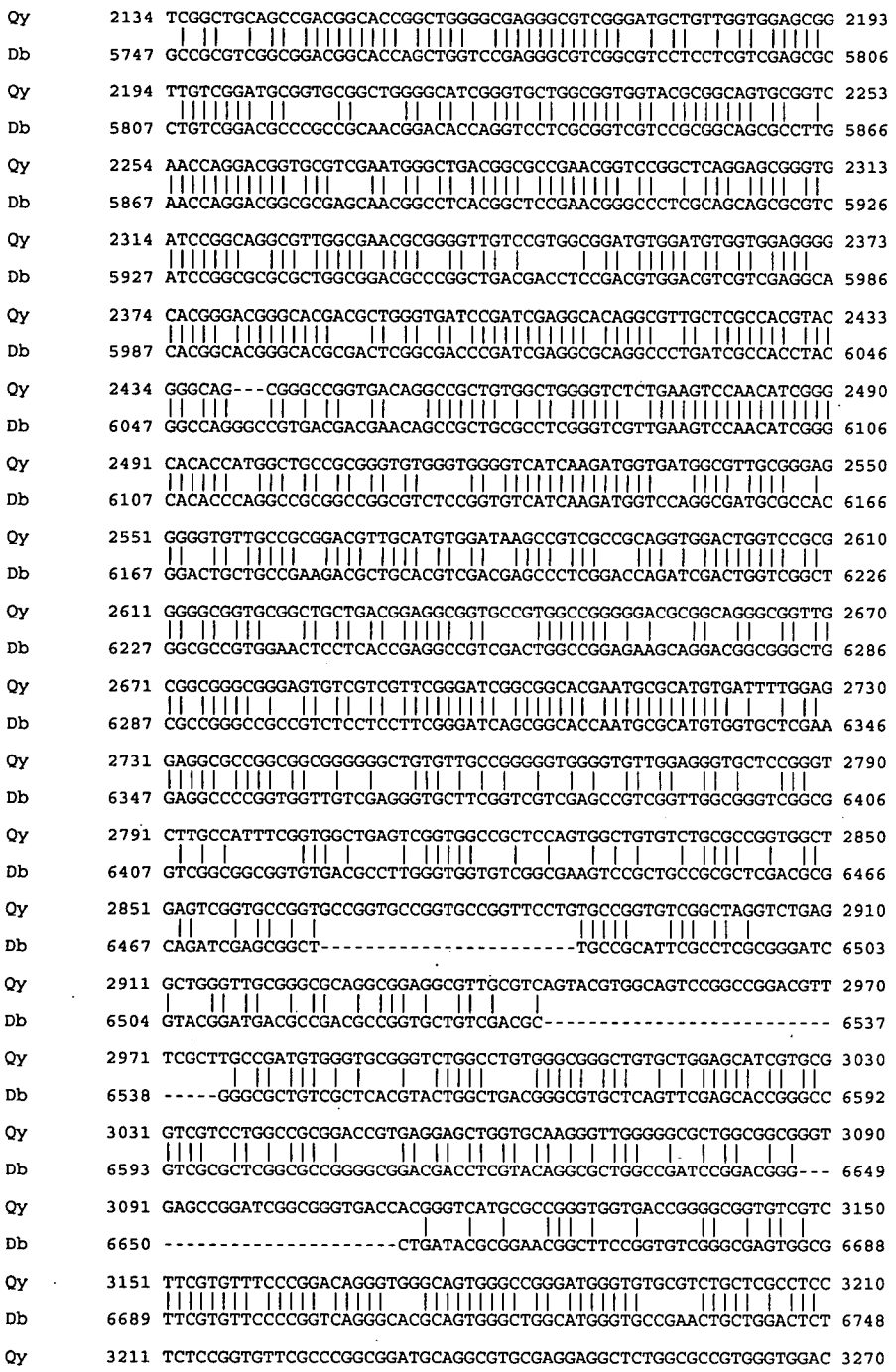
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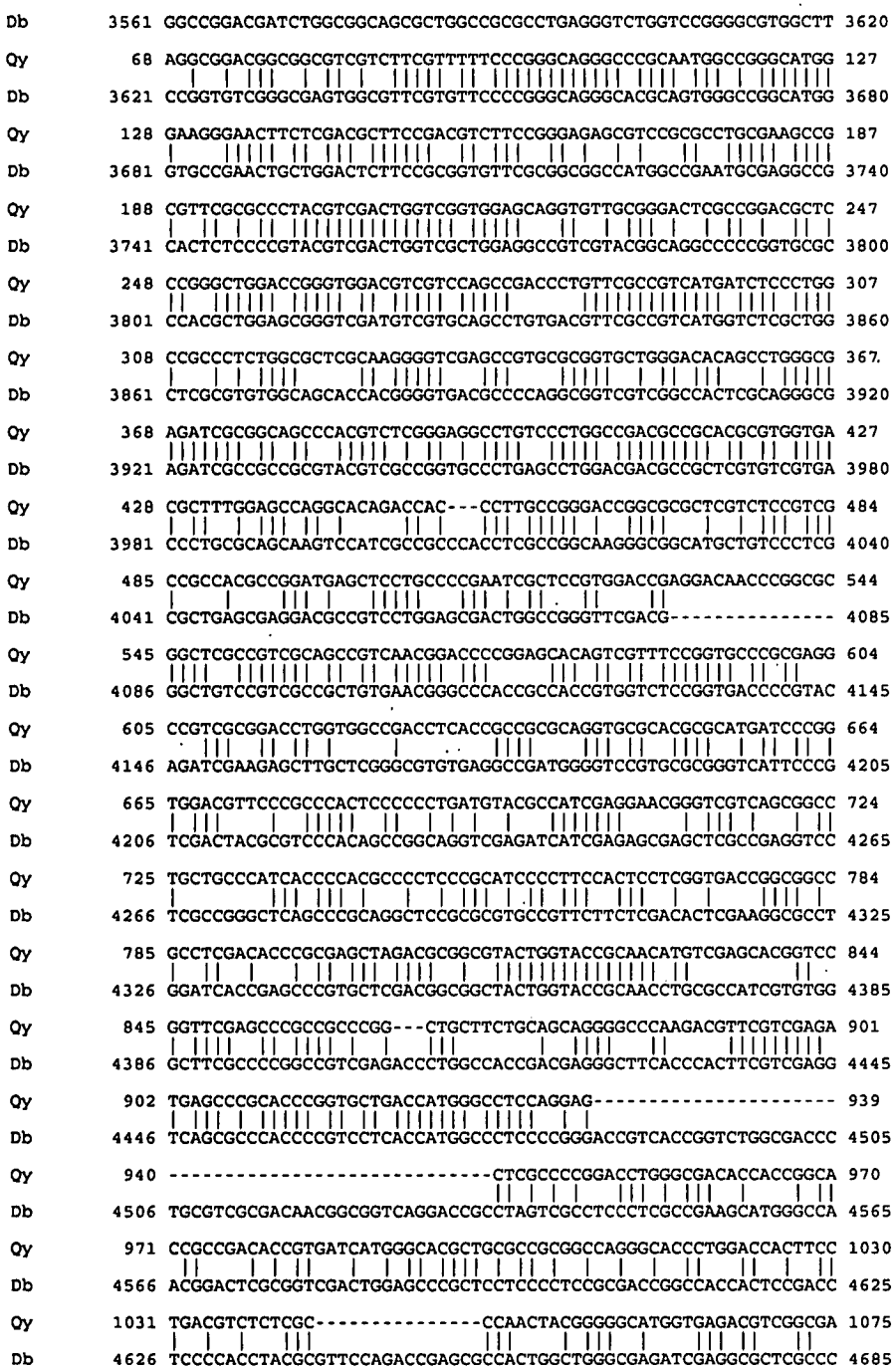
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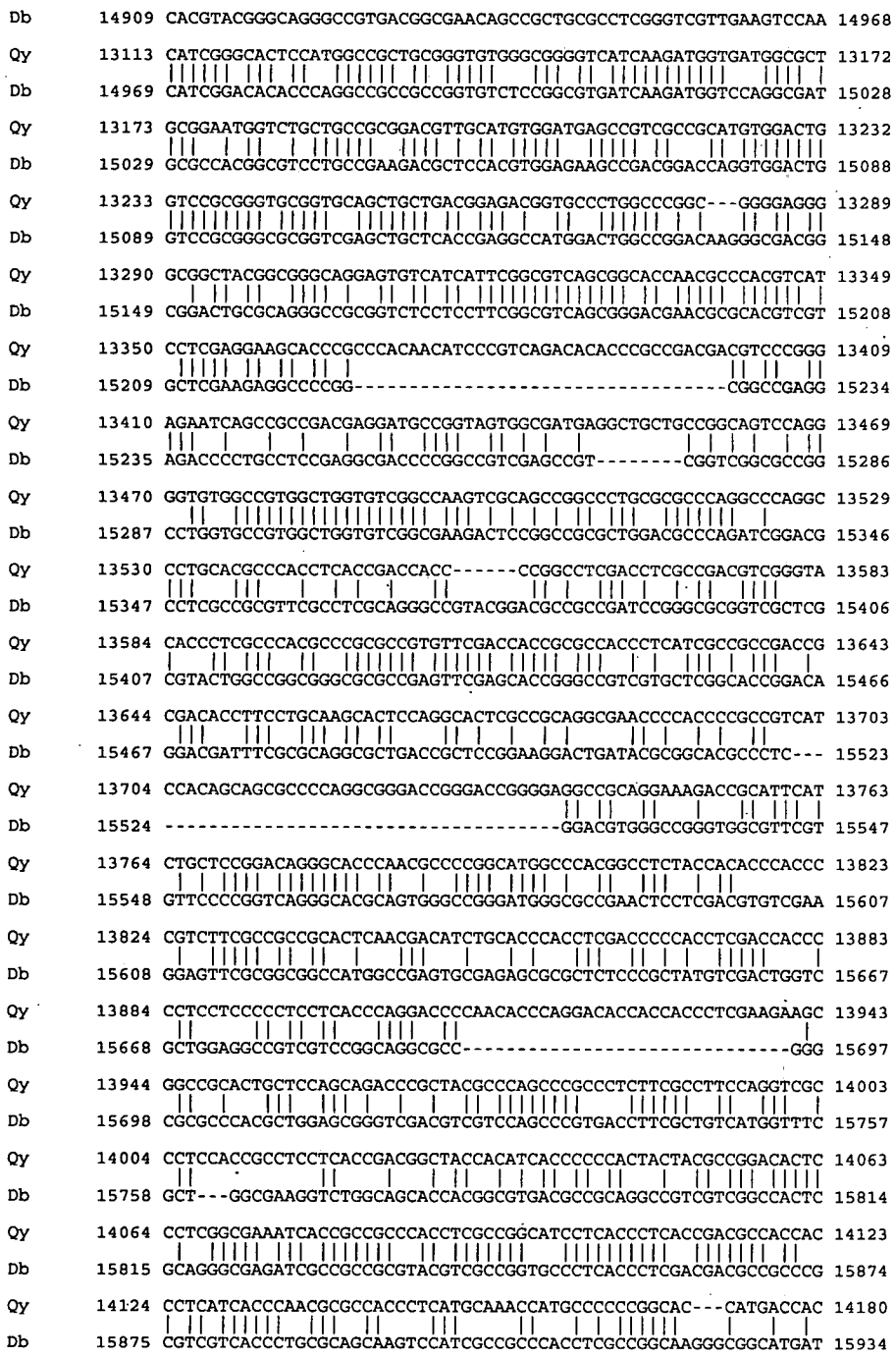
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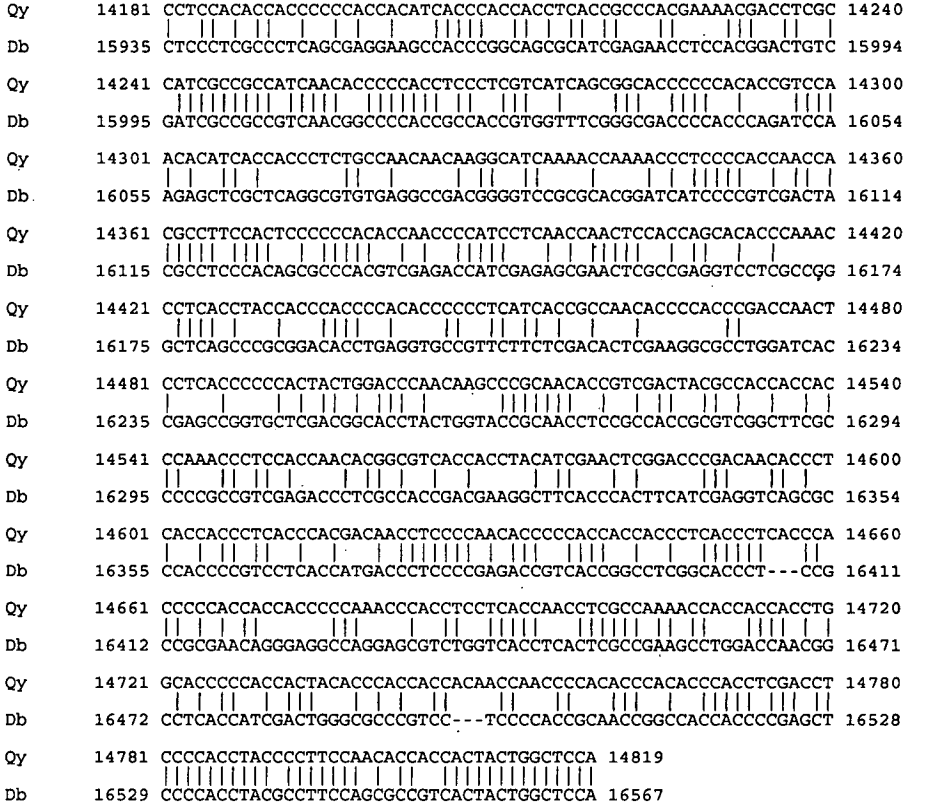

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Qy 16072 CGTGTCATCCGCCTGGCCCTGGCCAACGCGGACCTGACCCCCGCCGACGTCGATGCGGTG 16131
Db 15412 CGCGTCATCCGGCAAGCGCTCGACAGCGCGCGGCTCACTCCAAAGGACGTCGACGTCGTC 15471
Qy 16132 GAGGCCCACGGCACCGGCACCACTTTGGGCGACCCGATCGAGGCCCAGGCCCTCCTCGCC 16191
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Qy 16192 ACCTACGGACAGGACCGCCCCGGCAACGAACCGCTGTGGCTGGGCTCGATGAAGTCGAAC 16251
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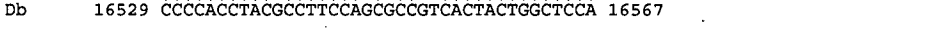

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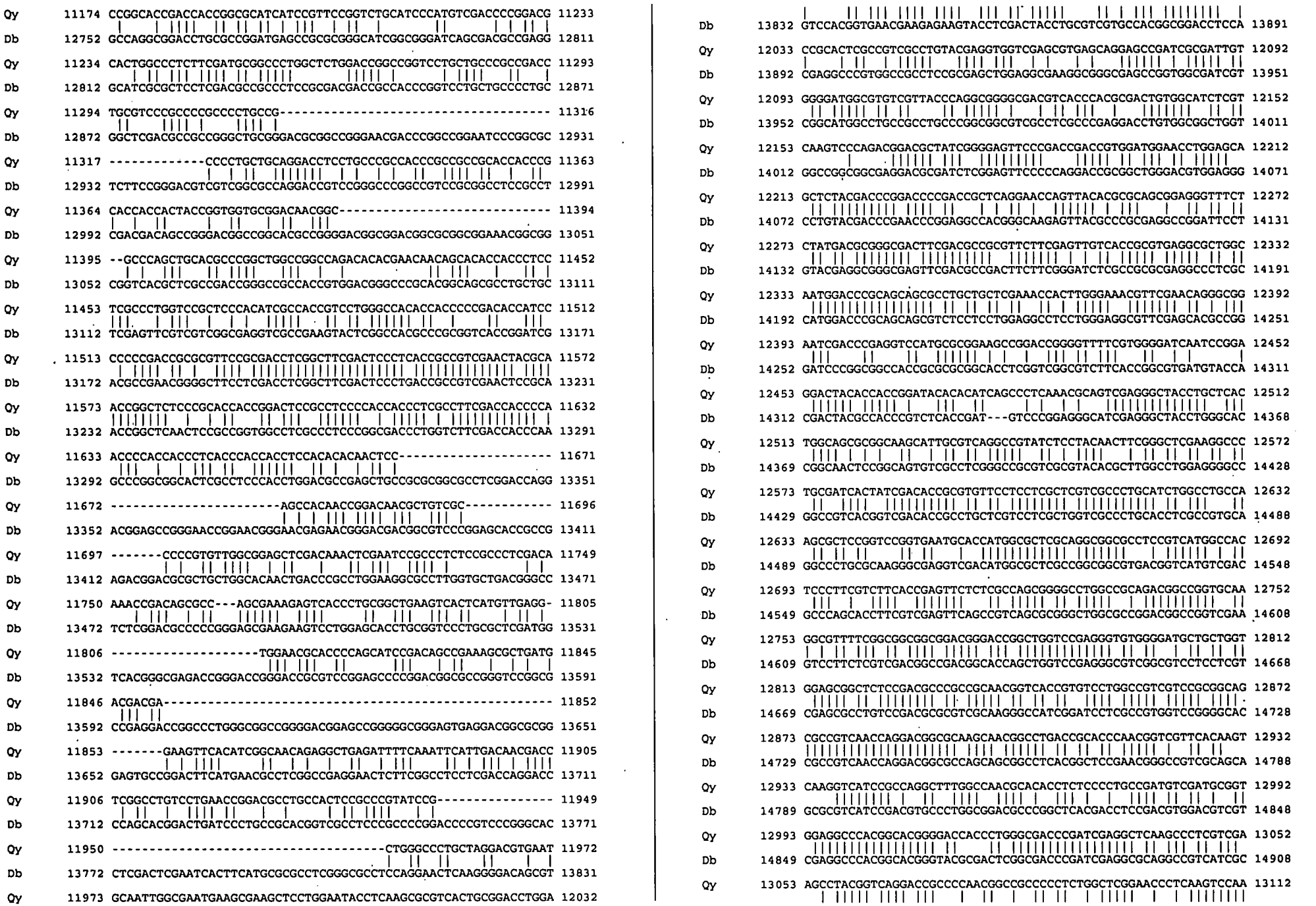


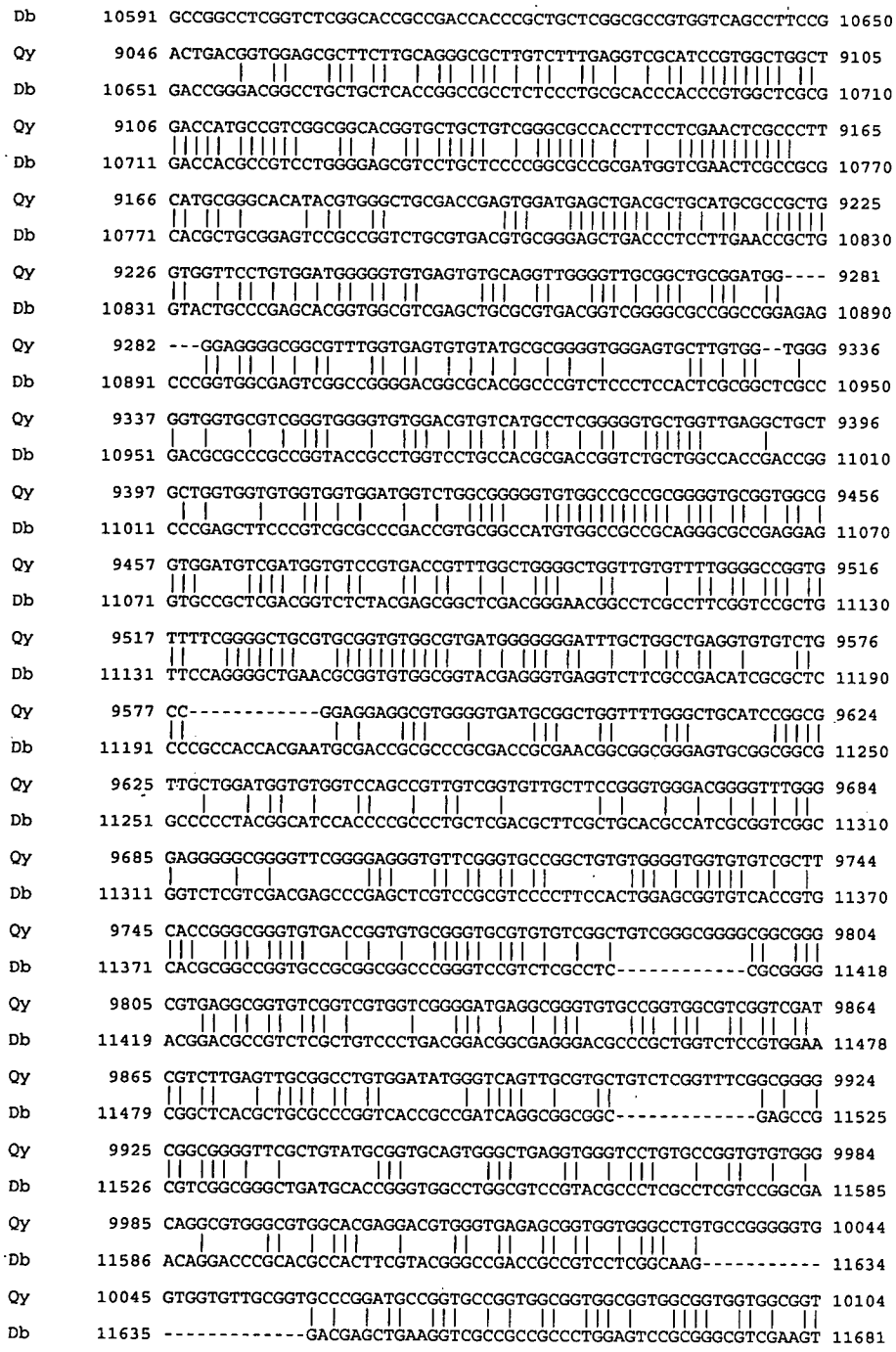


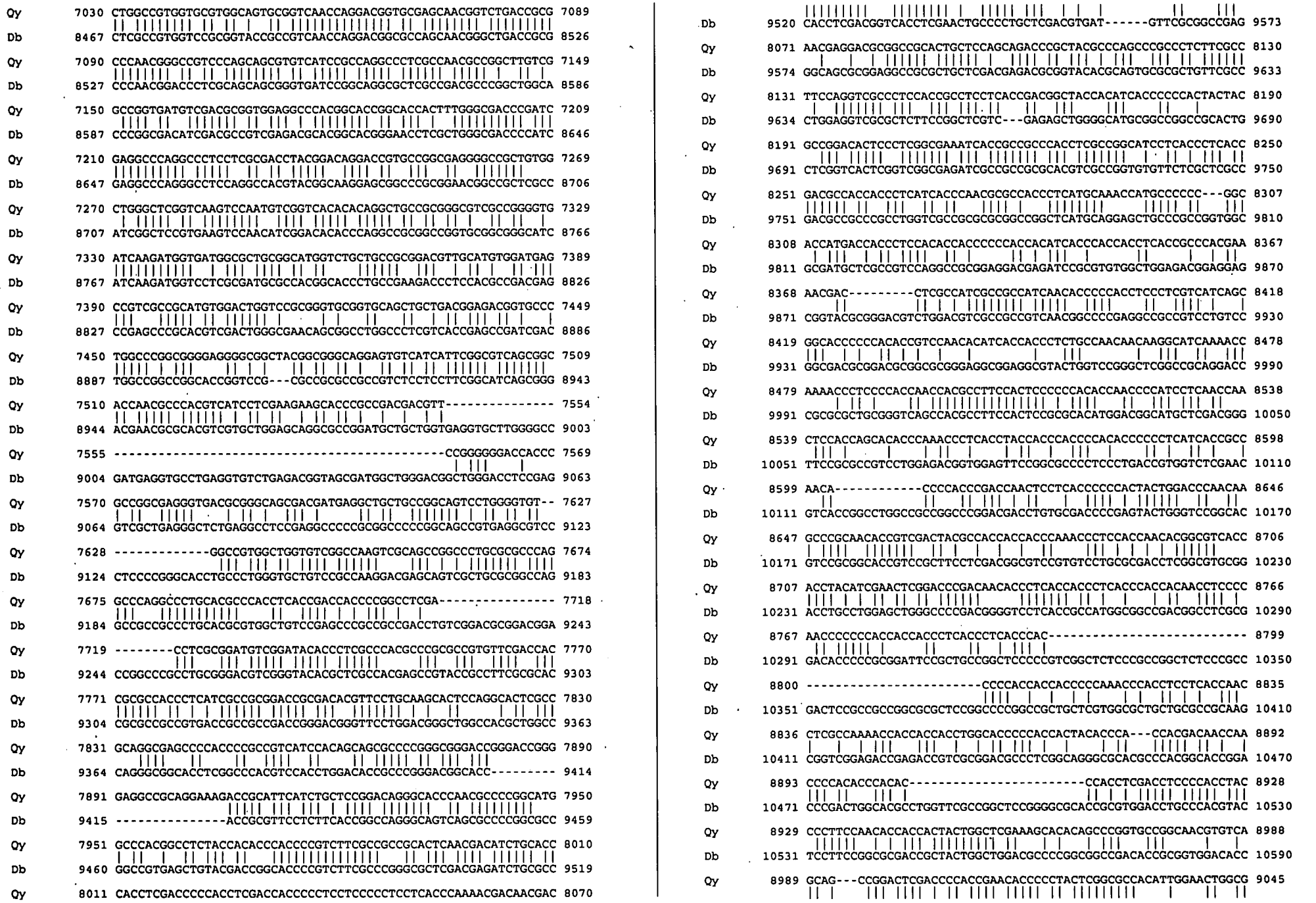
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; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
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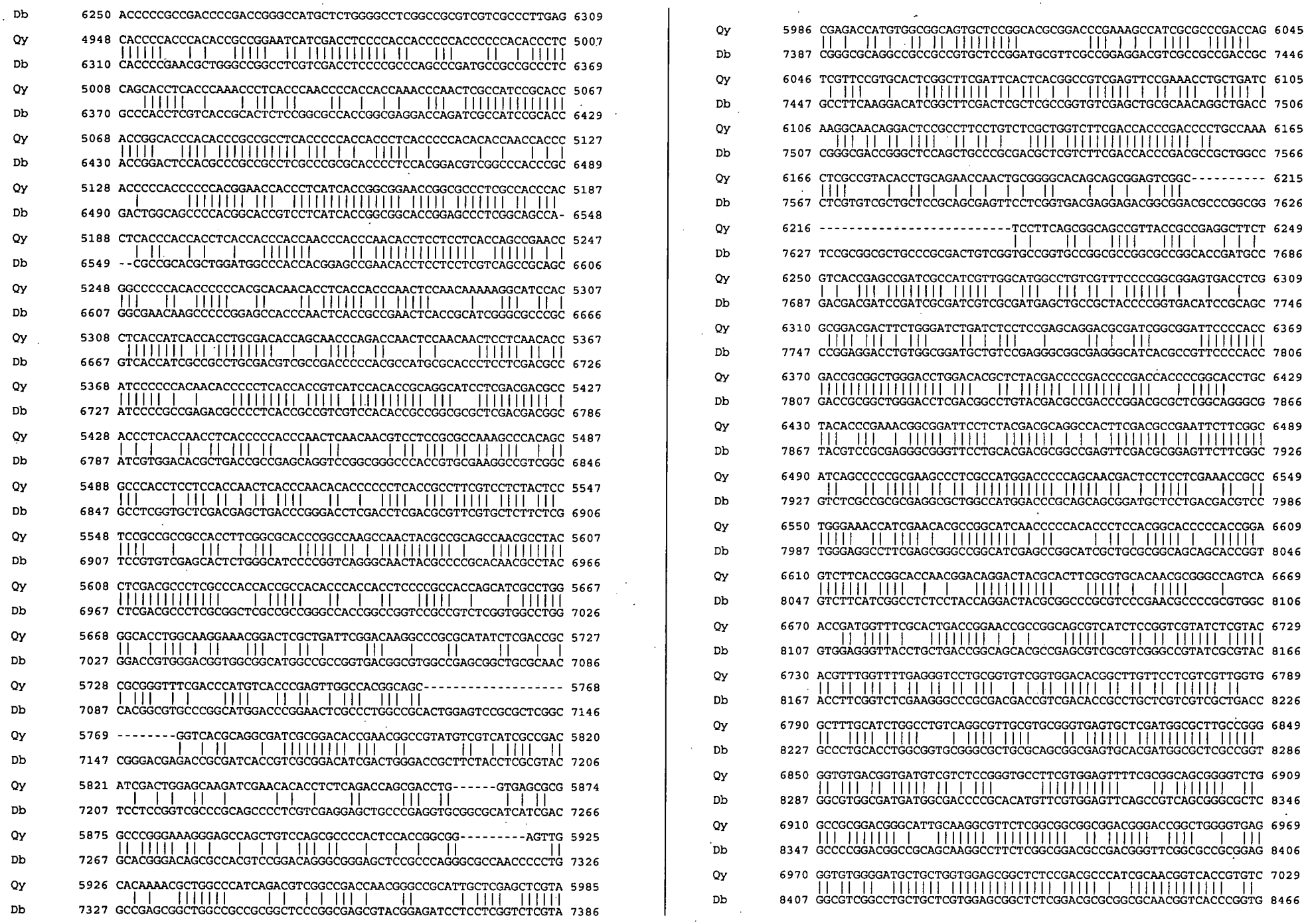
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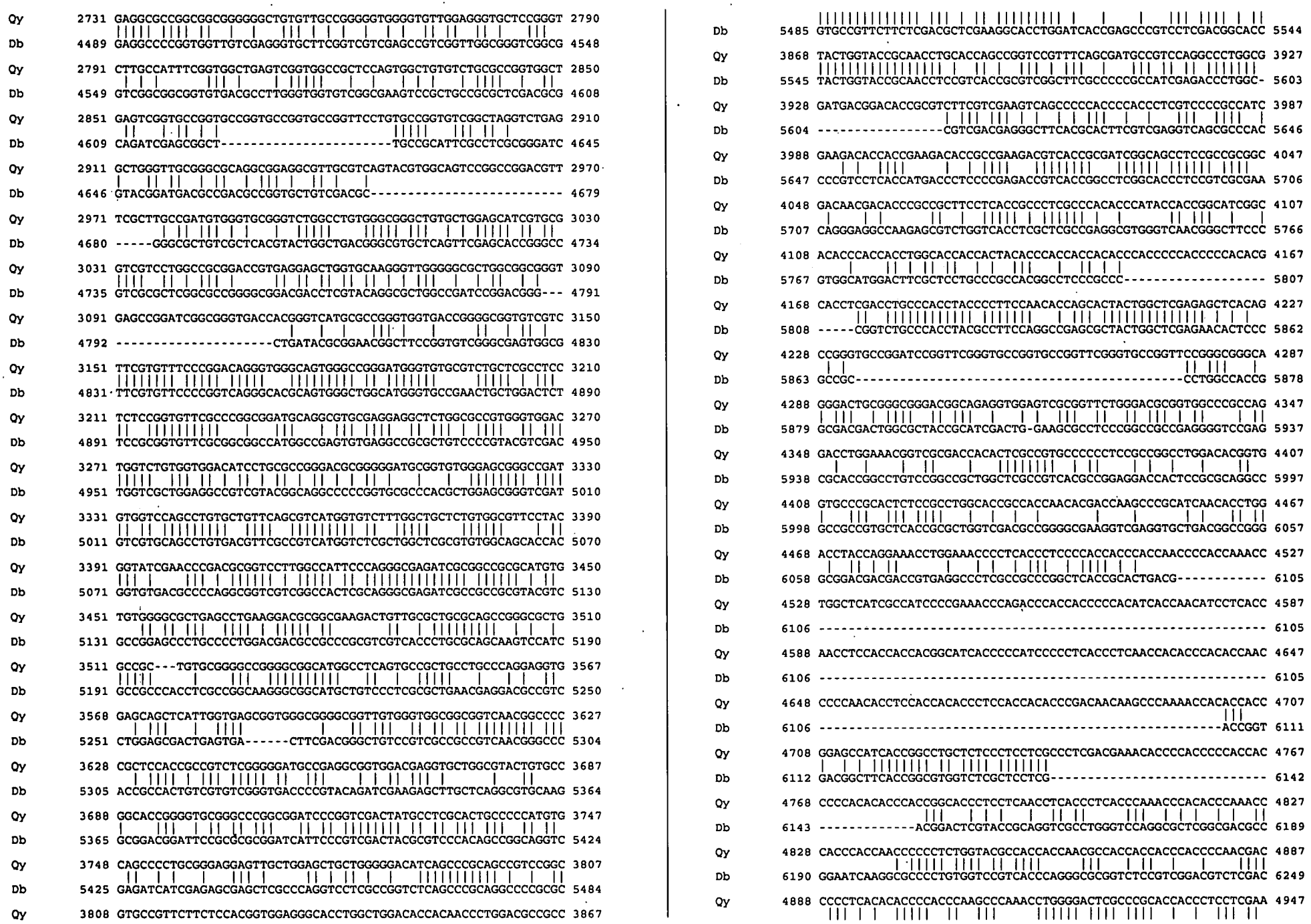


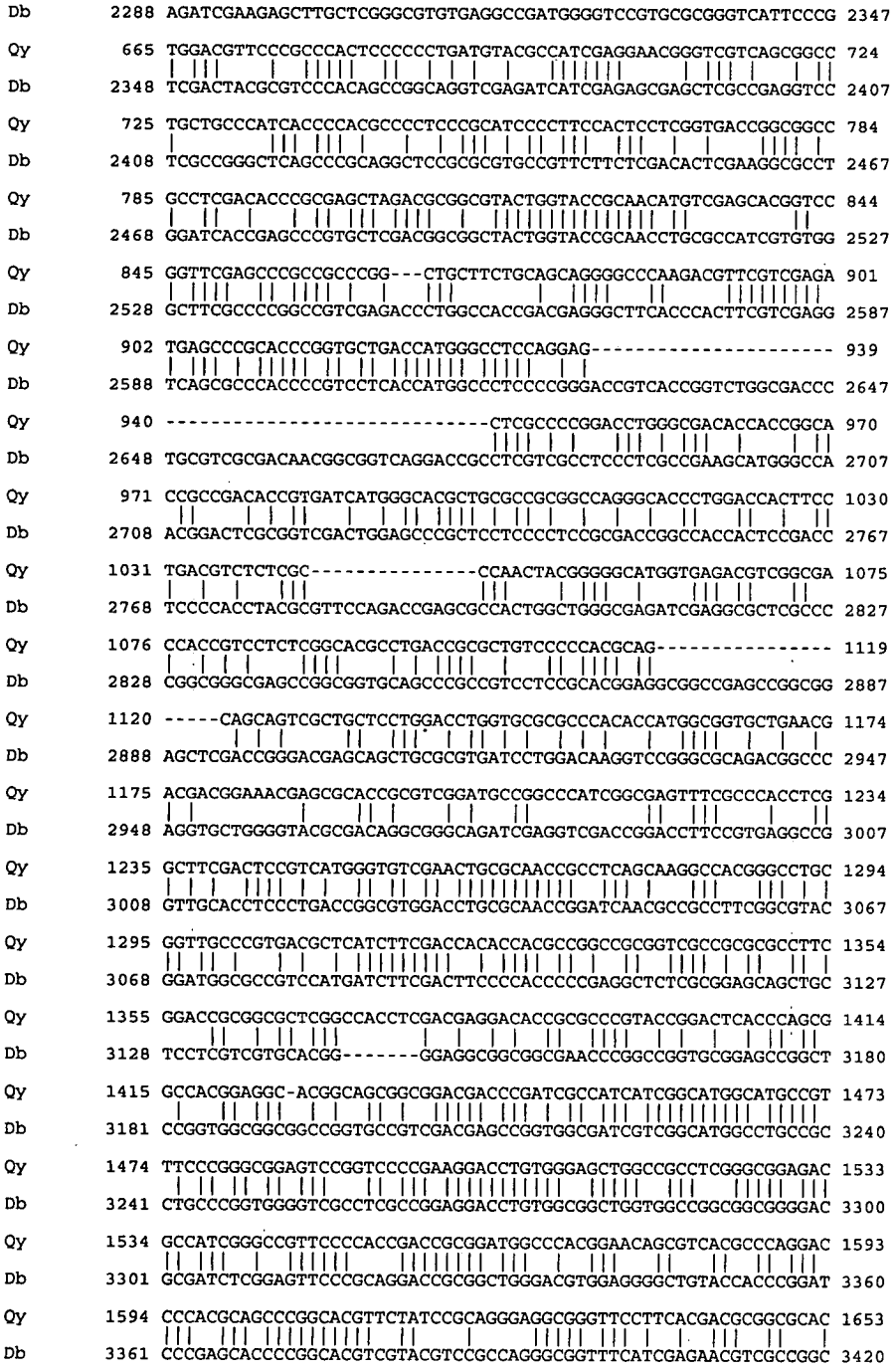


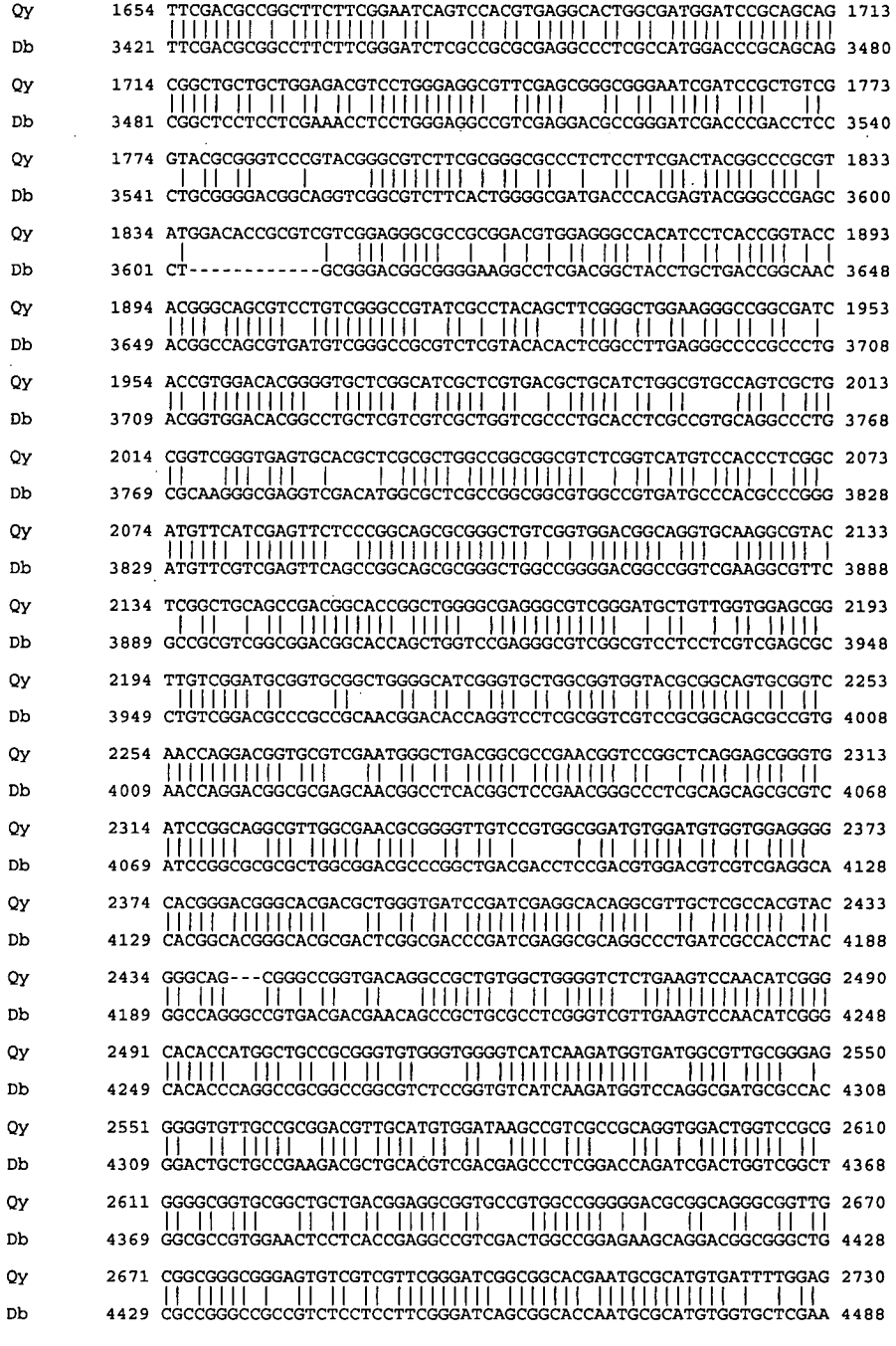

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; Patent No. 6117659
; GENERAL INFORMATION:
;  APPLICANT: ASHLEY, Gary
;  APPLICANT: BETLACH, Melanie C.
;  APPLICANT: BETLACH, Mary C.
;  APPLICANT: McDANIEL, Robert
;  APPLICANT: TANG, Li
;  TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
;  FILE REFERENCE: 300622002120
;  CURRENT APPLICATION NUMBER: US/09/320,878A
;  CURRENT FILING DATE: 1999-05-27
;  EARLIER APPLICATION NUMBER: CIP OF 09/141,908
;  EARLIER FILING DATE: 1998-08-28
;  EARLIER APPLICATION NUMBER: CIP OF 09/073,538
;  EARLIER FILING DATE: 1998-05-06
;  EARLIER APPLICATION NUMBER: CIP OF 08/846,247
;  EARLIER FILING DATE: 1997-04-30
;  EARLIER APPLICATION NUMBER: 60/119,139
;  EARLIER FILING DATE: 1999-02-08
;  EARLIER APPLICATION NUMBER: 60/100,880
;  EARLIER FILING DATE: 1998-09-22
;  EARLIER APPLICATION NUMBER: 60/087,080
;  EARLIER FILING DATE: 1998-05-28
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 38506
;   TYPE: DNA
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US-09-320-878-19

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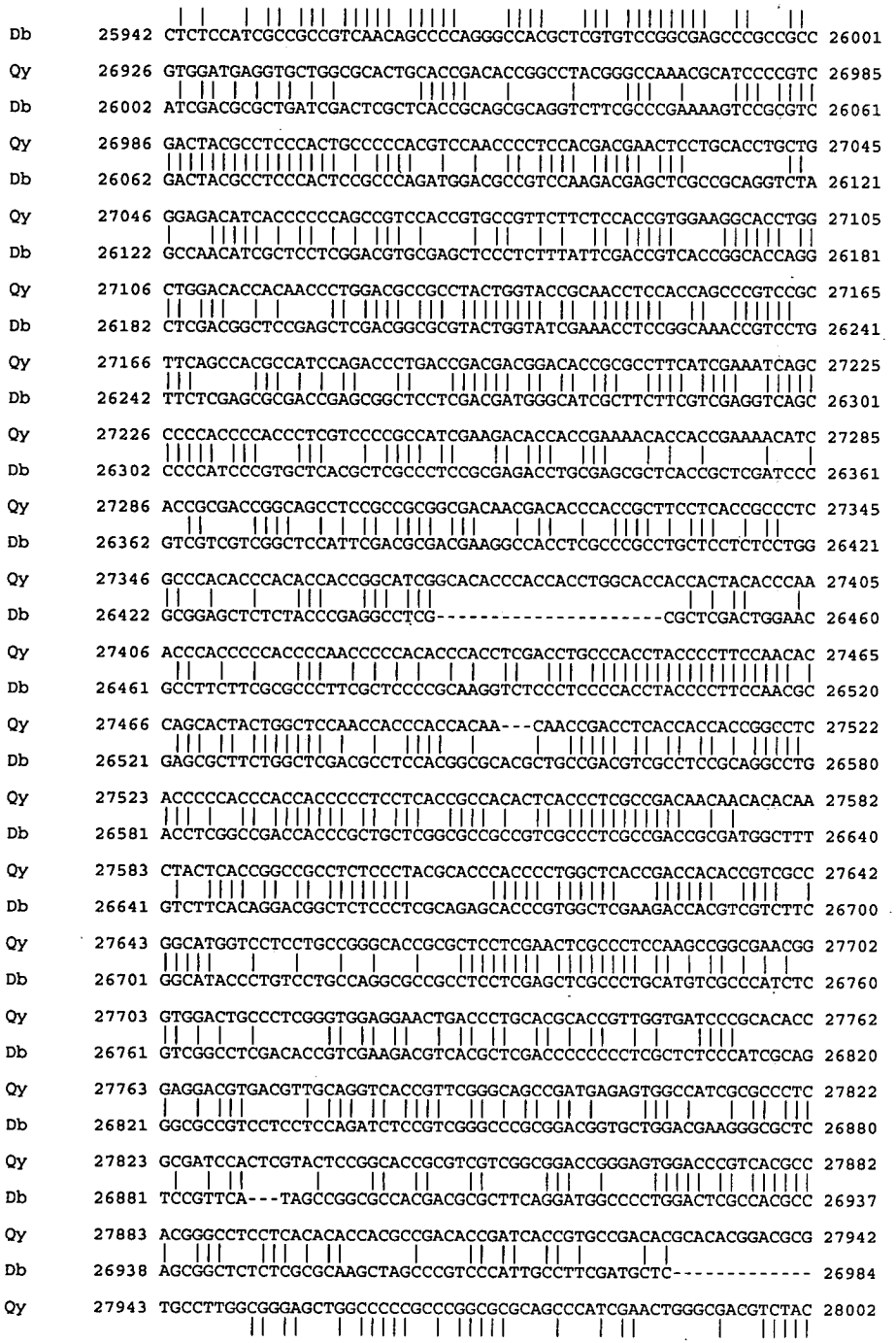
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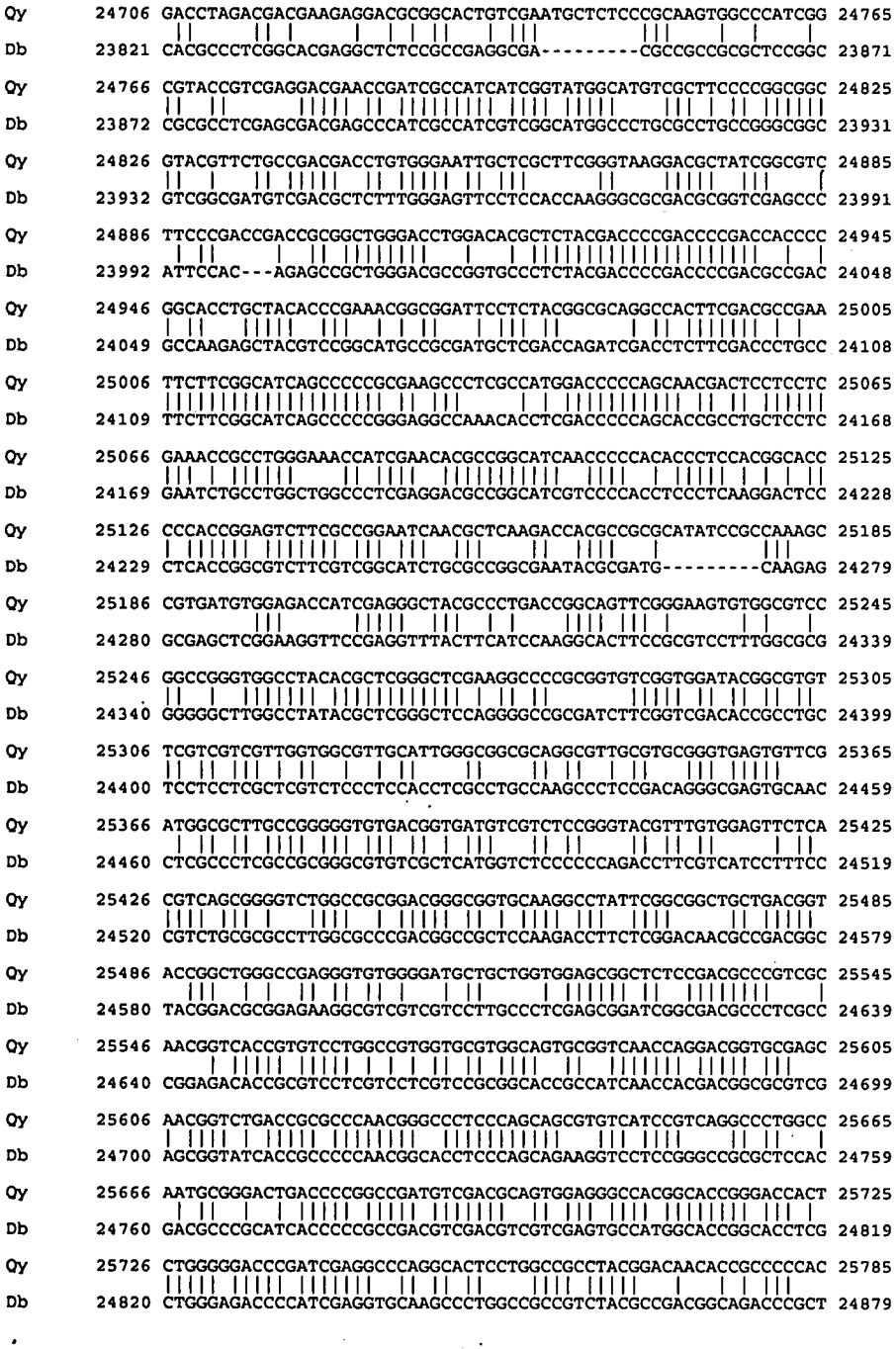
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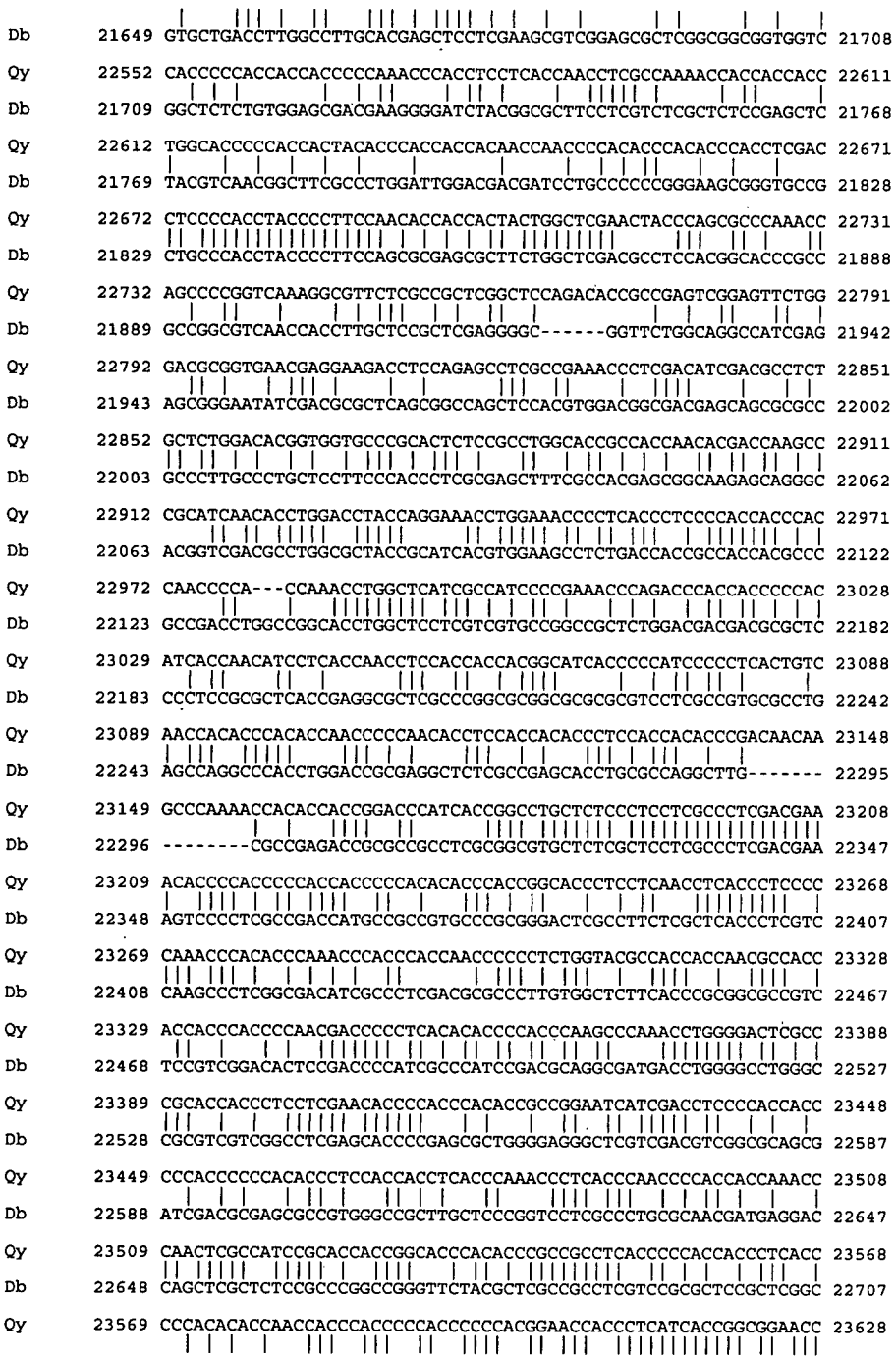
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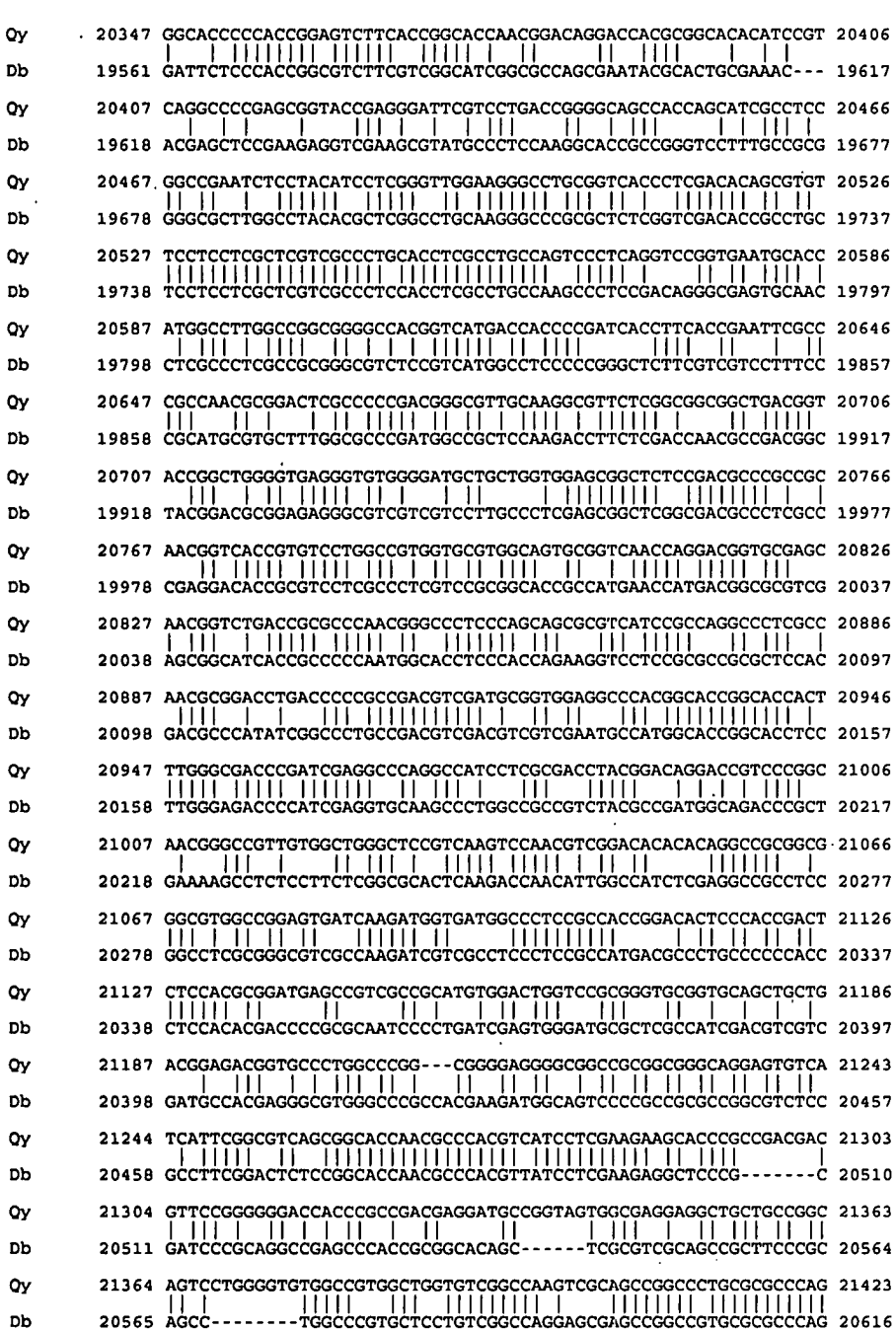
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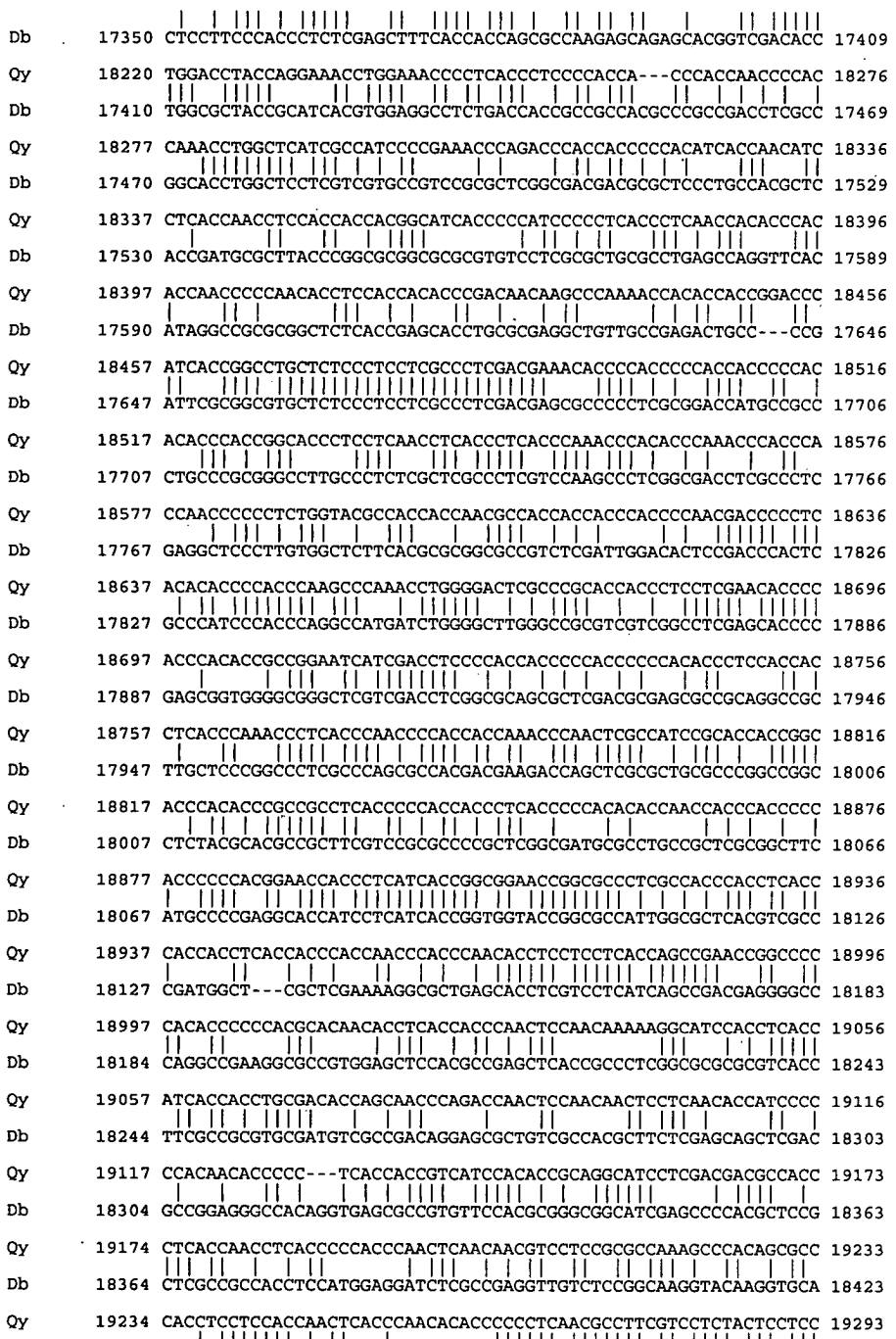
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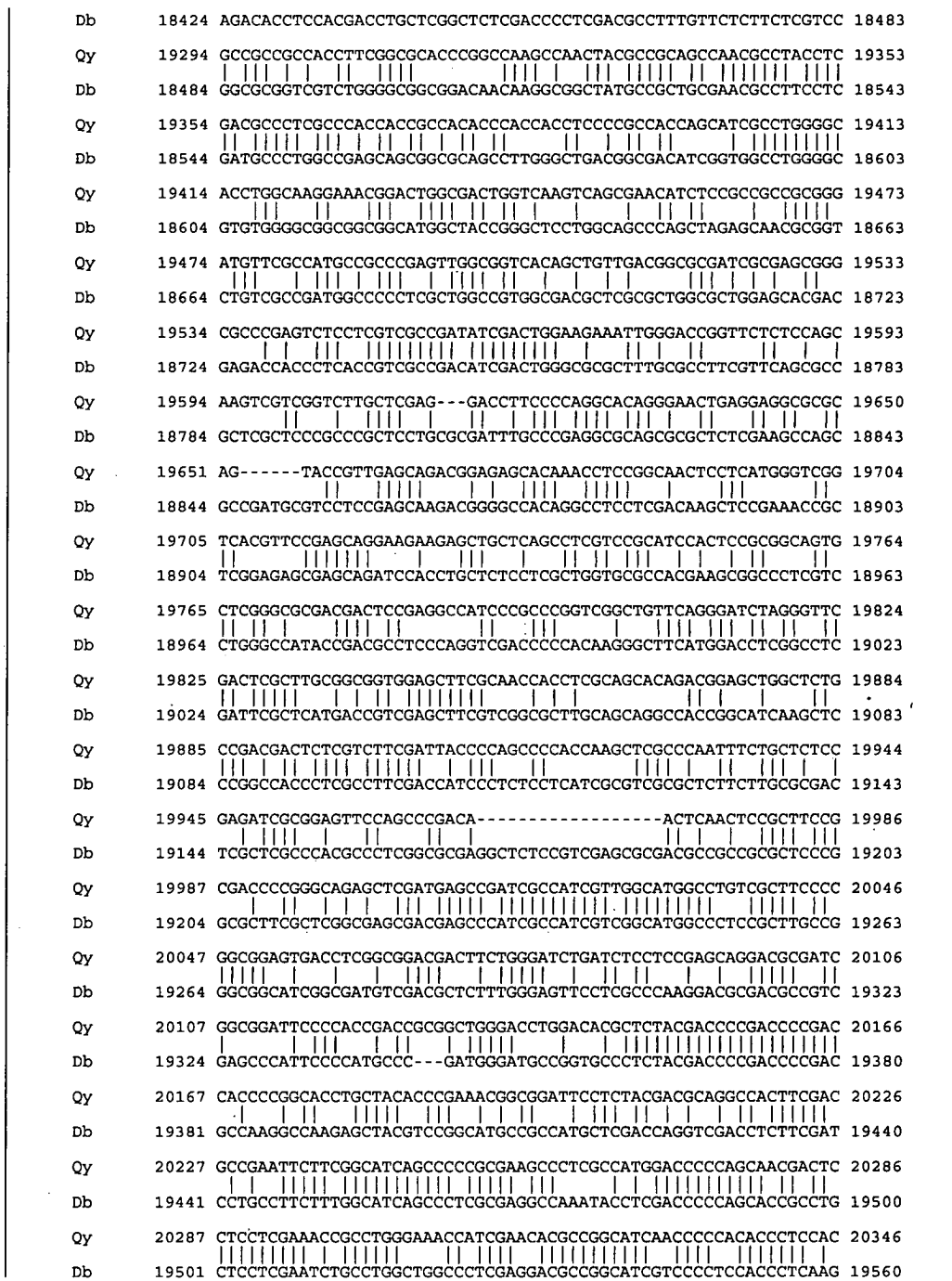

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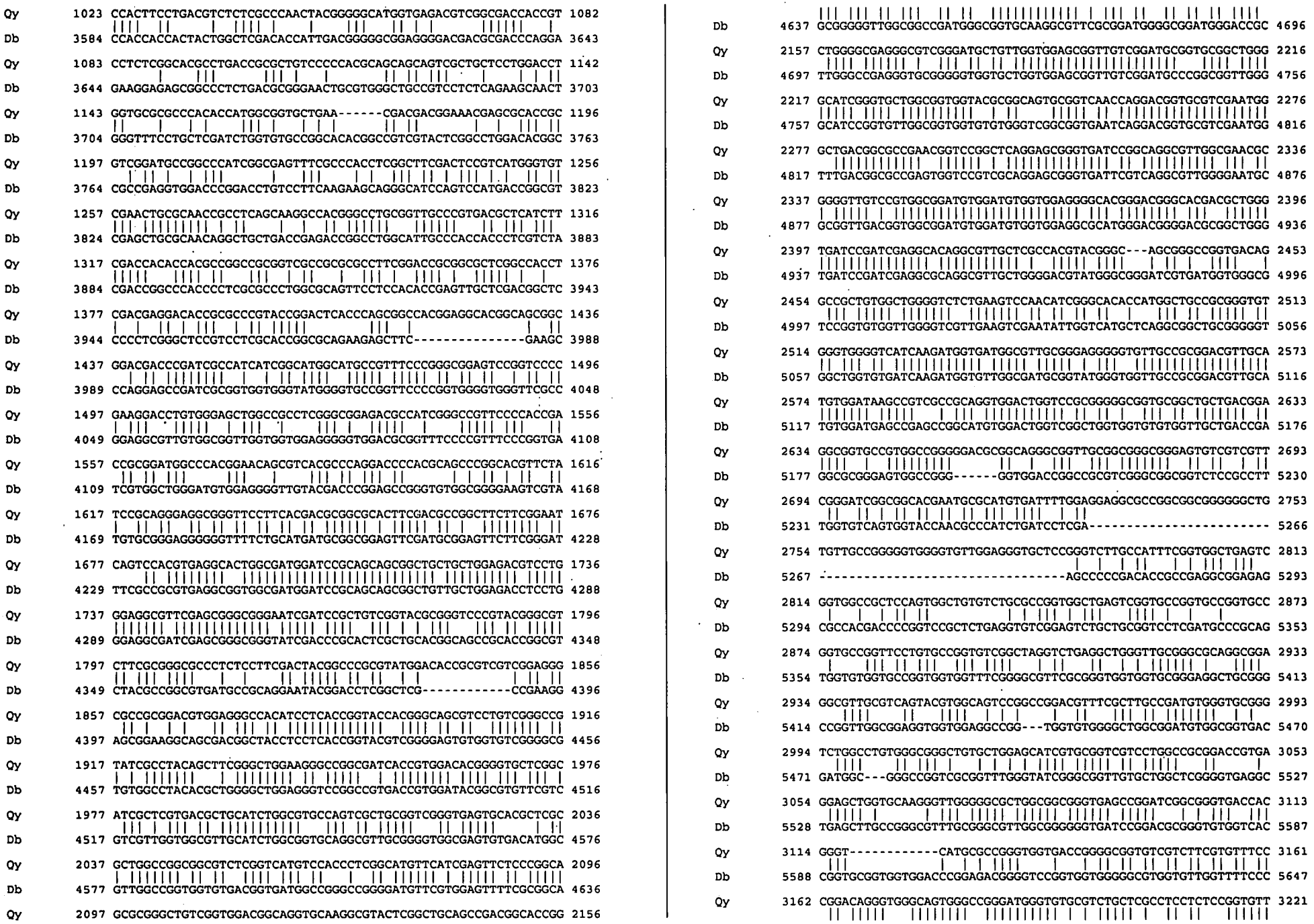

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RESULT 15
US-08-804-227C-1
; Sequence 1, Application US/08804227C
; Patent No. 5876991
;  GENERAL INFORMATION:
;    APPLICANT:  DeHoff, Bradley S.
;    APPLICANT:  Kuhstoss, Stuart A.
;    APPLICANT:  Rosteck, Paul R., Jr.
;    APPLICANT:  Sutton, Kimberly L.
;    TITLE OF INVENTION:  POLYKETIDE SYNTHASE GENES
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  THOMAS G. PLANT  1501
;      STREET:  LILLY CORPORATE CENTER
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  ASCI(DOS) Text only
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/804,227C
;      FILING DATE:  February 21, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plant, Thomas, G.
;      REGISTRATION NUMBER:  35,784
;      REFERENCE/DOCKET NUMBER:  X-8231
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-2459
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  43280 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  816..14234
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;      NAME/KEY:  CDS
;      LOCATION:  14351..19945
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;      LOCATION:  31232..36067
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;      NAME/KEY:  CDS
;      LOCATION:  36249..41774
US-08-804-227C-1

  Query Match             9.6%;  Score 2939.8;  DB 2;  Length 43280;
  Best Local Similarity   53.9%;  Pred. No. 0;
  Matches 8131;  Conservative    0;  Mismatches 6077;  Indels  885;  Gaps   66;
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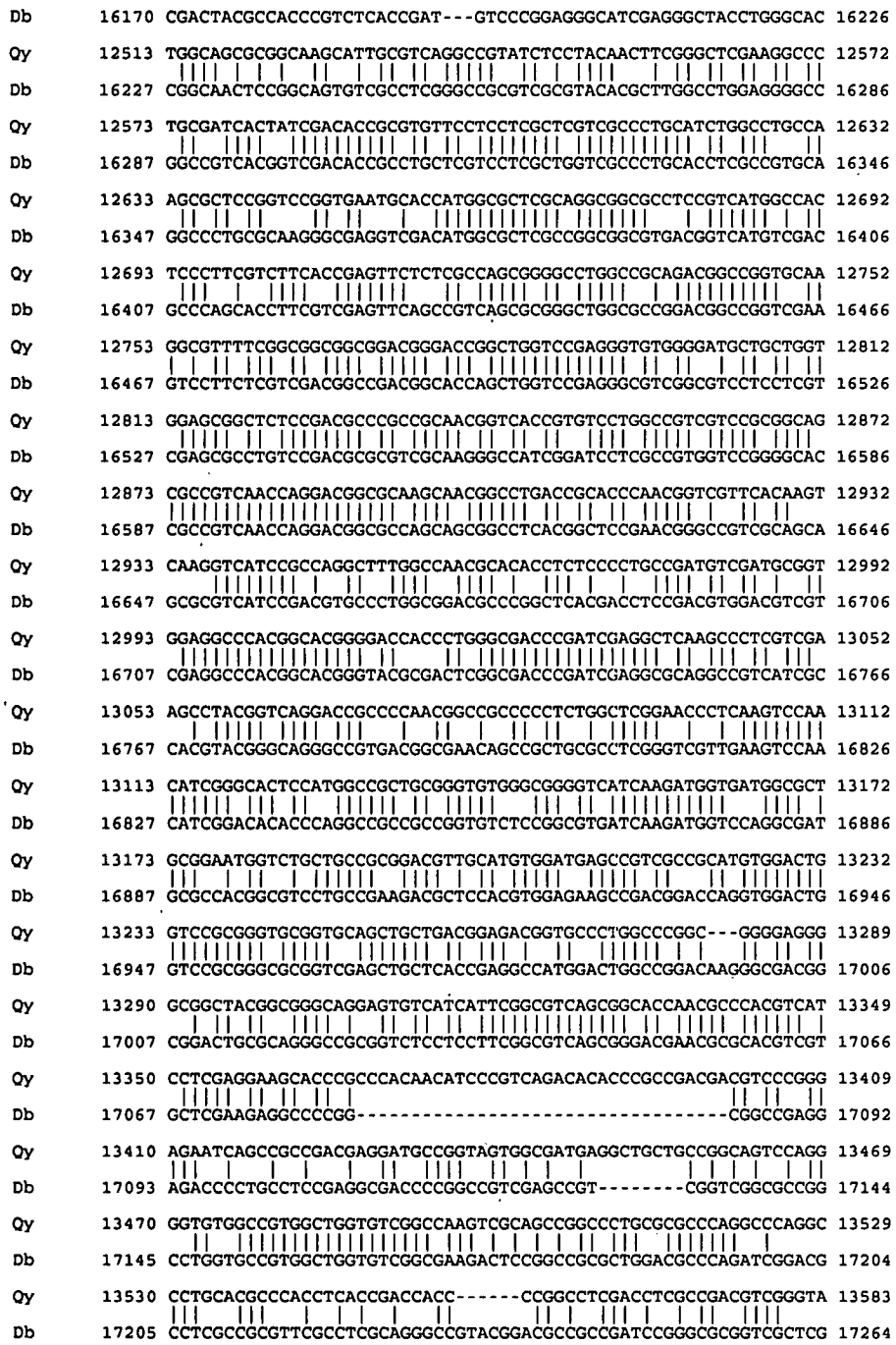
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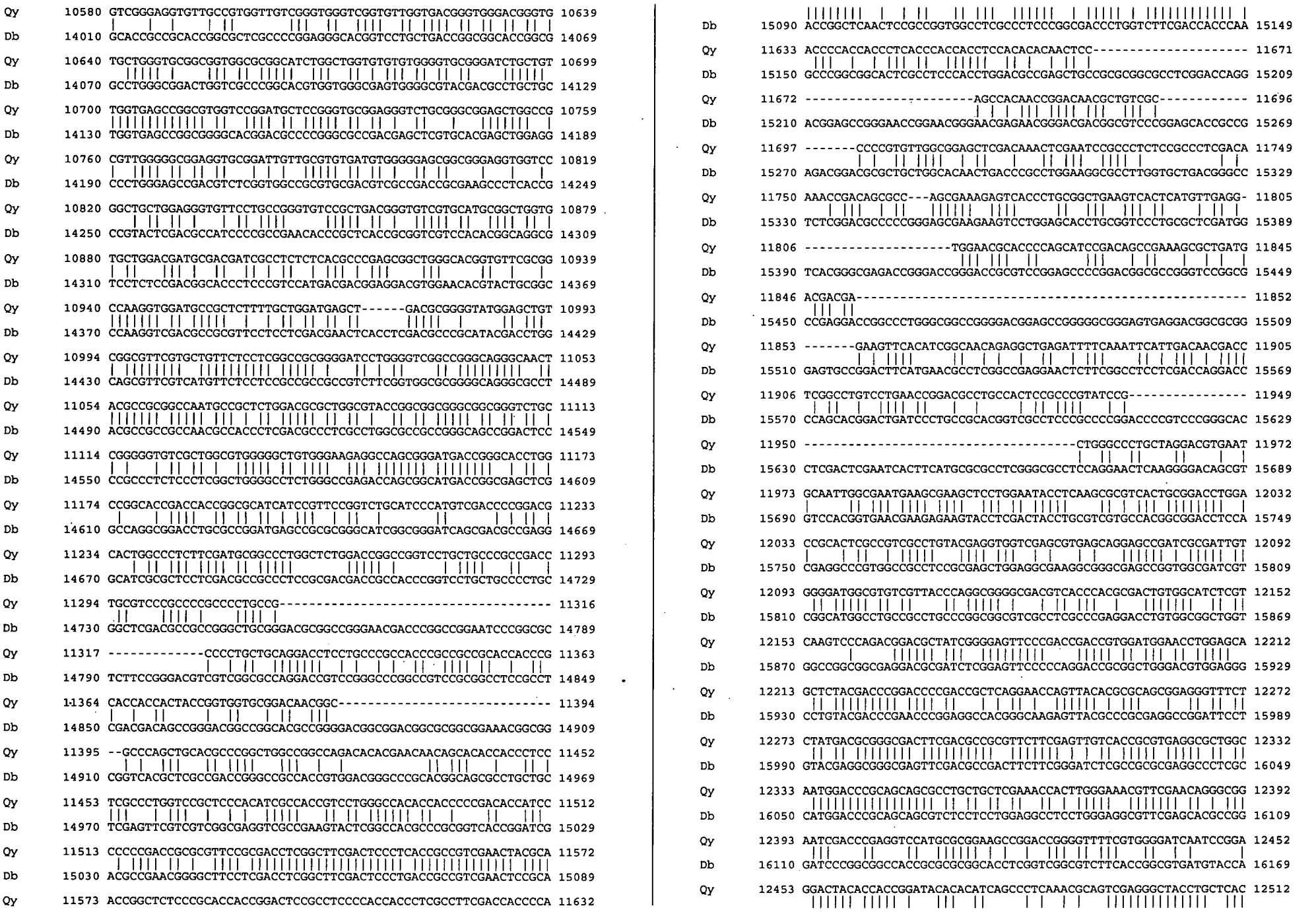
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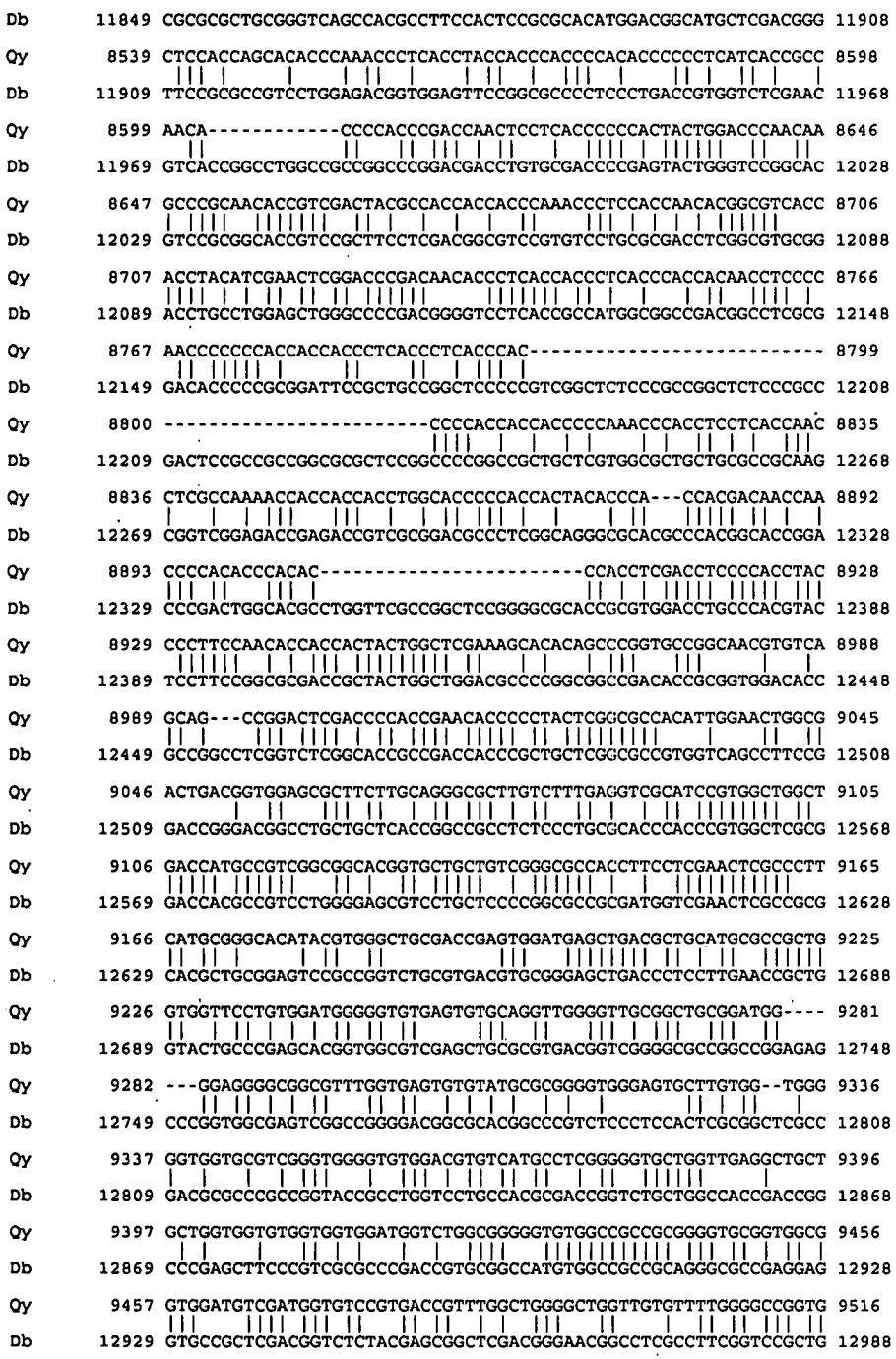
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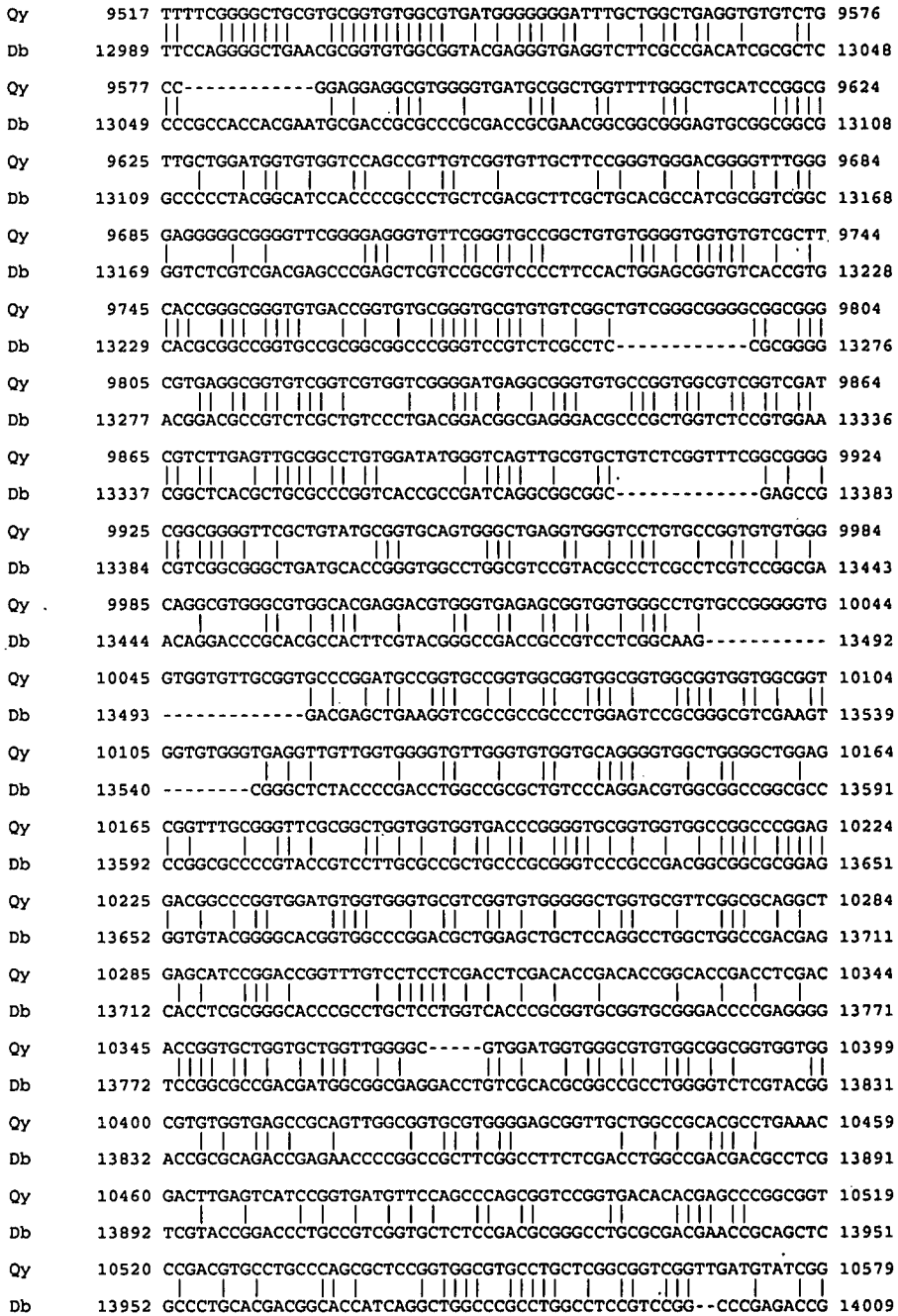
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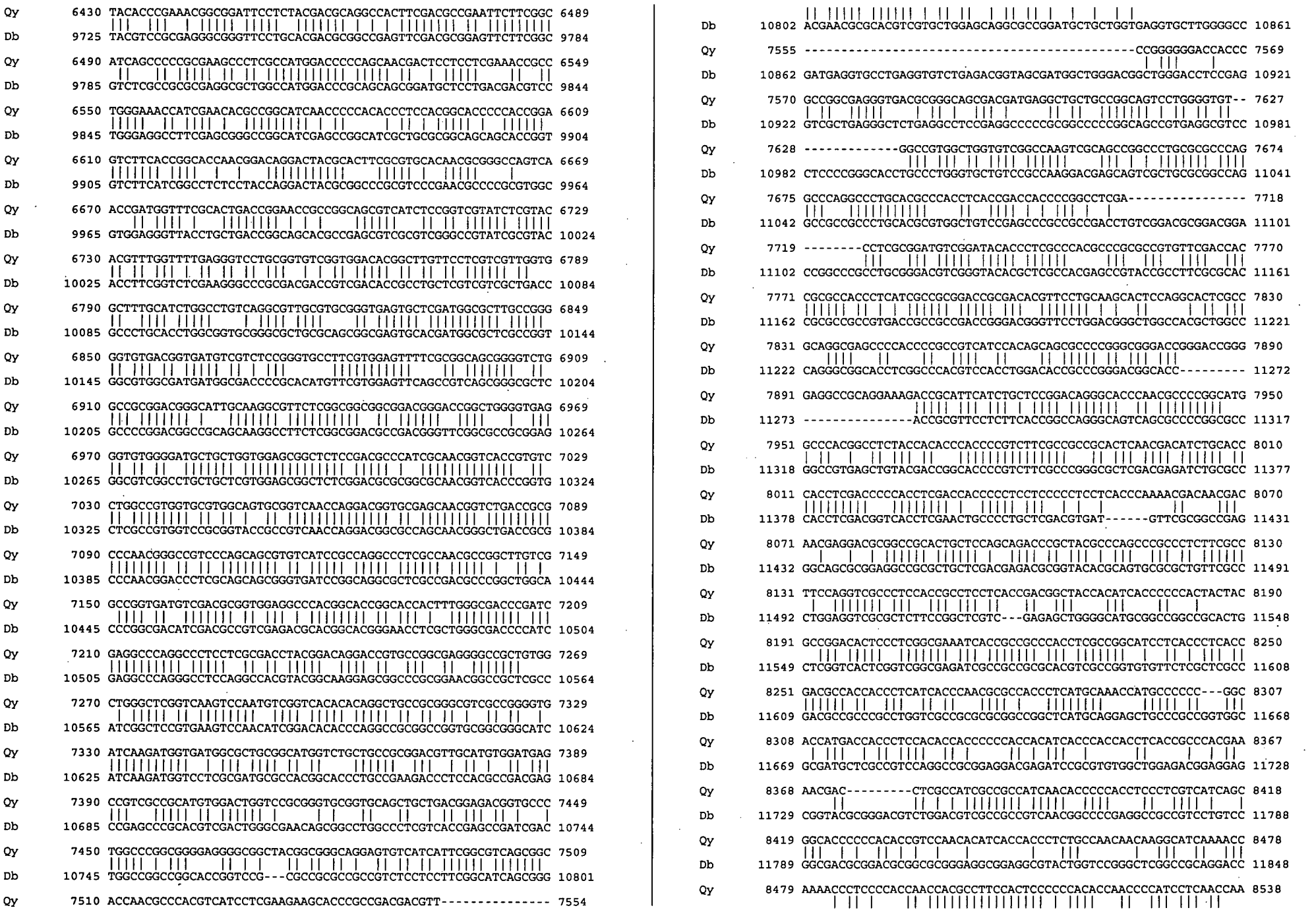
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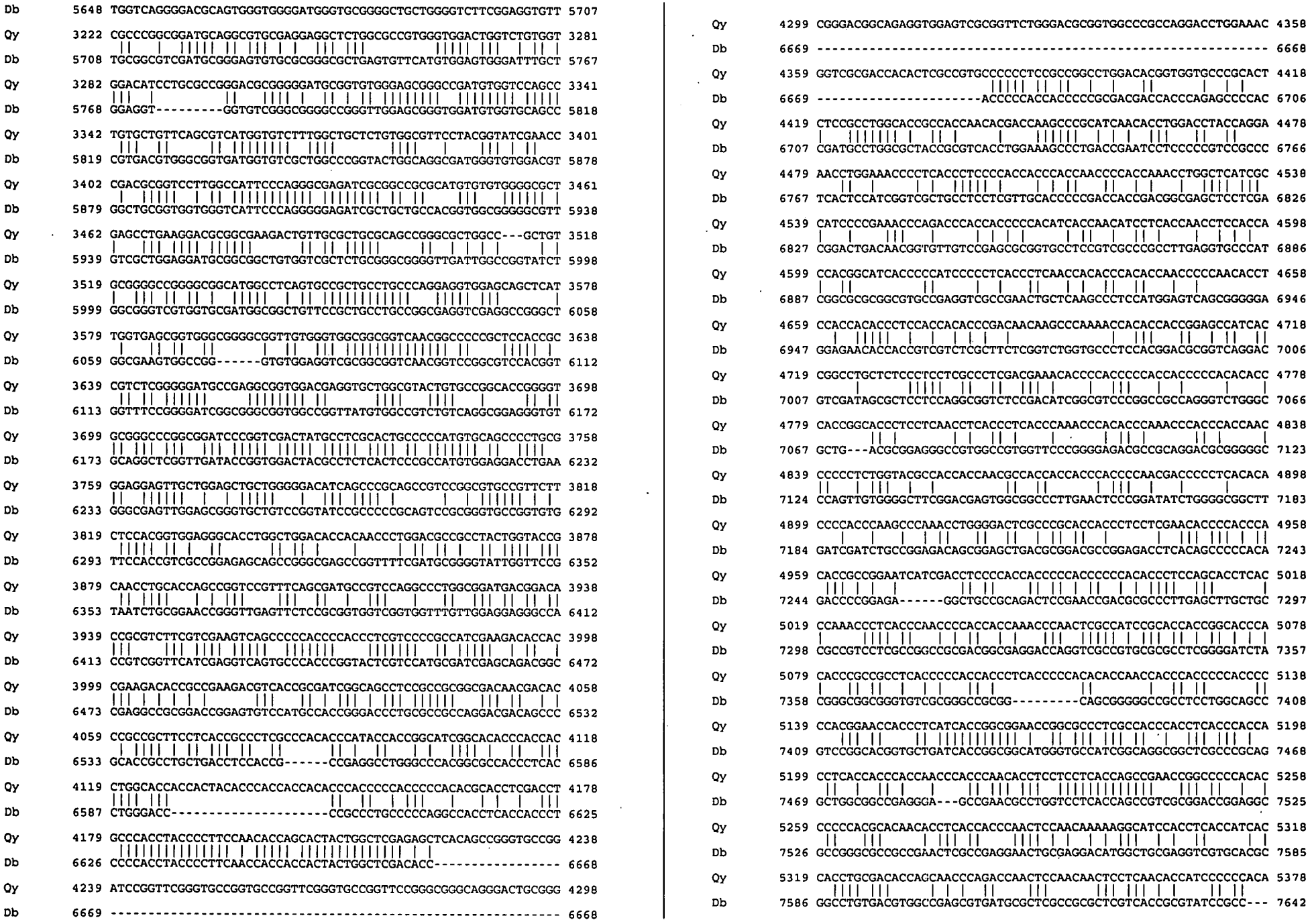

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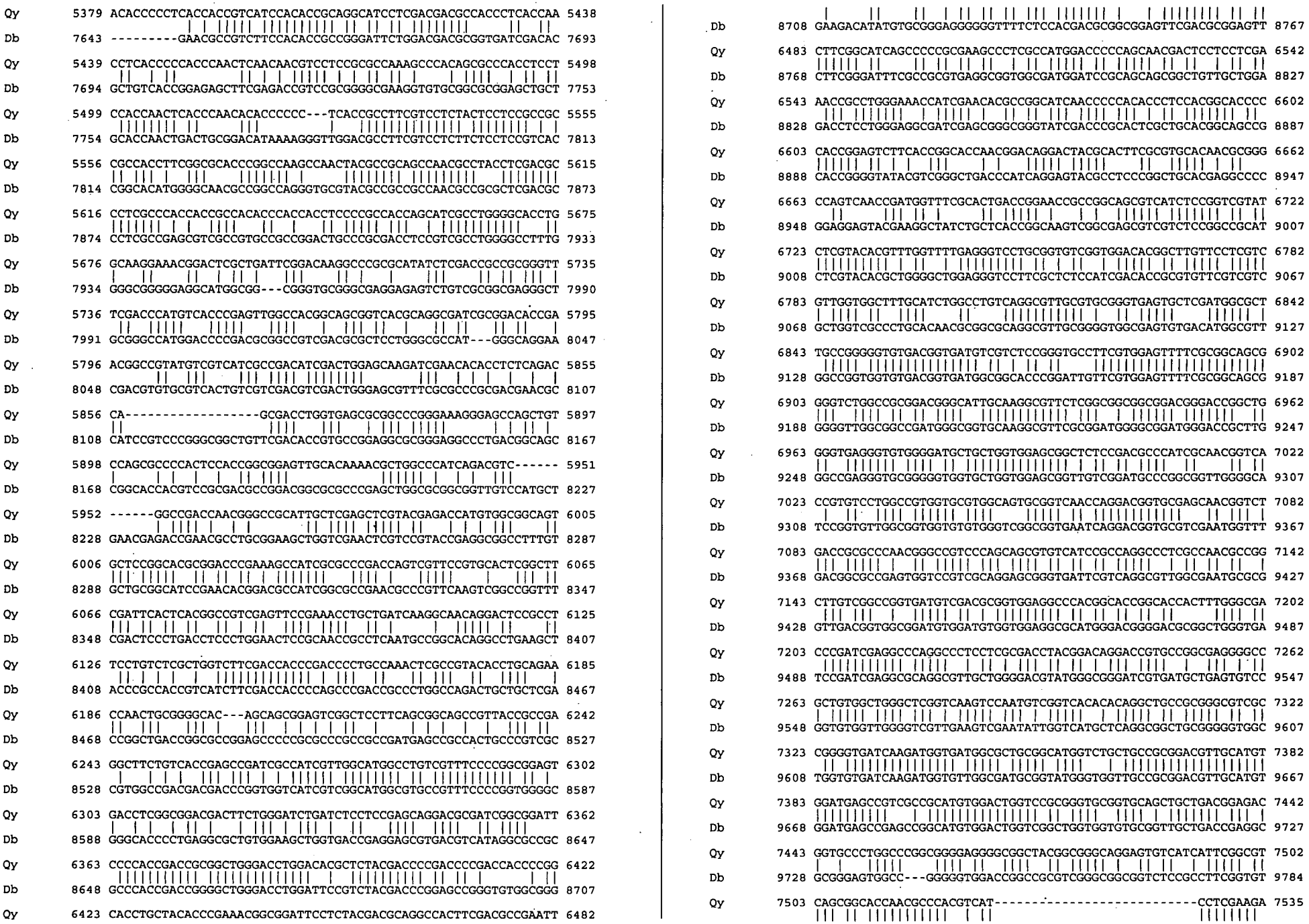


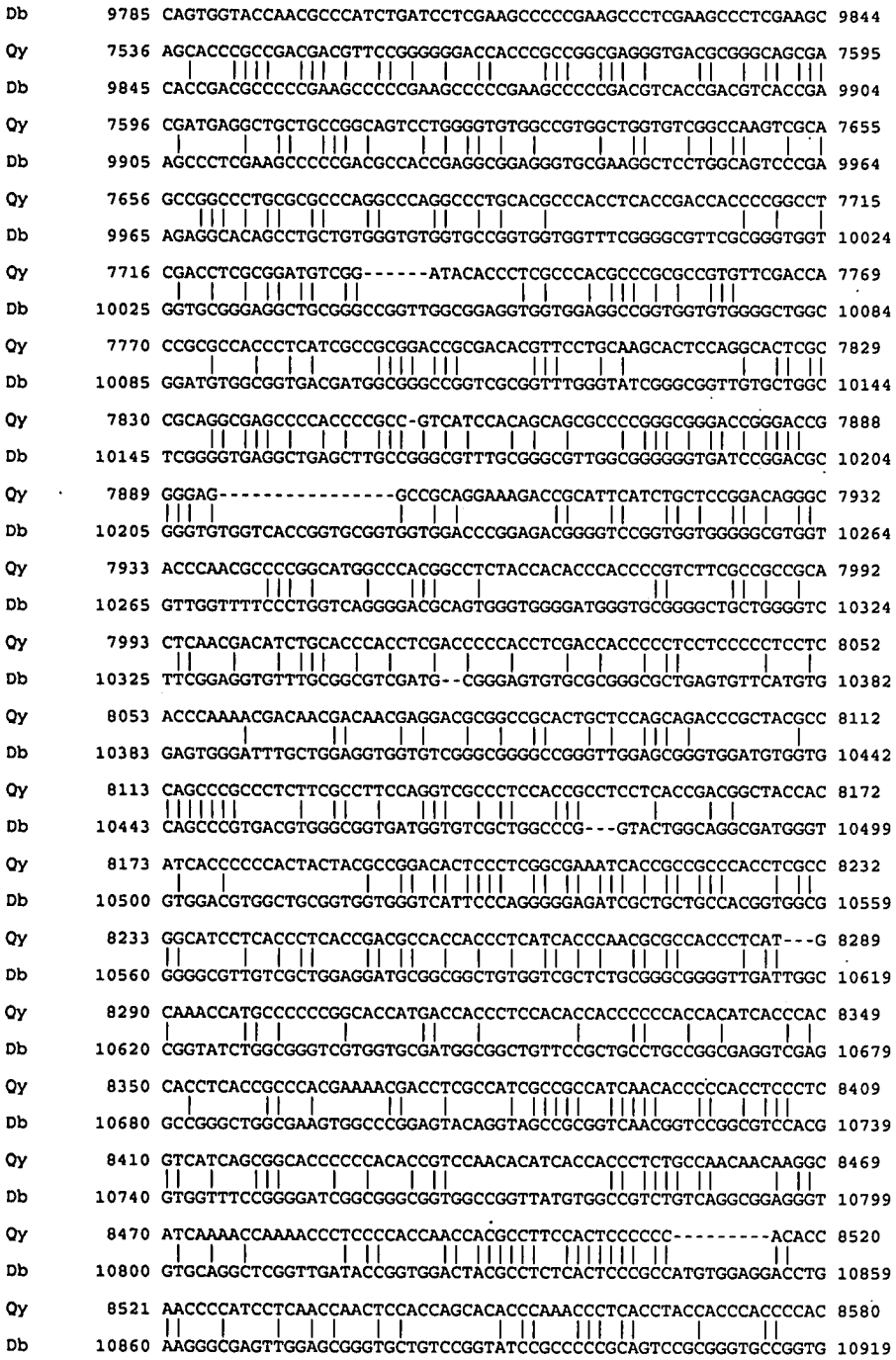


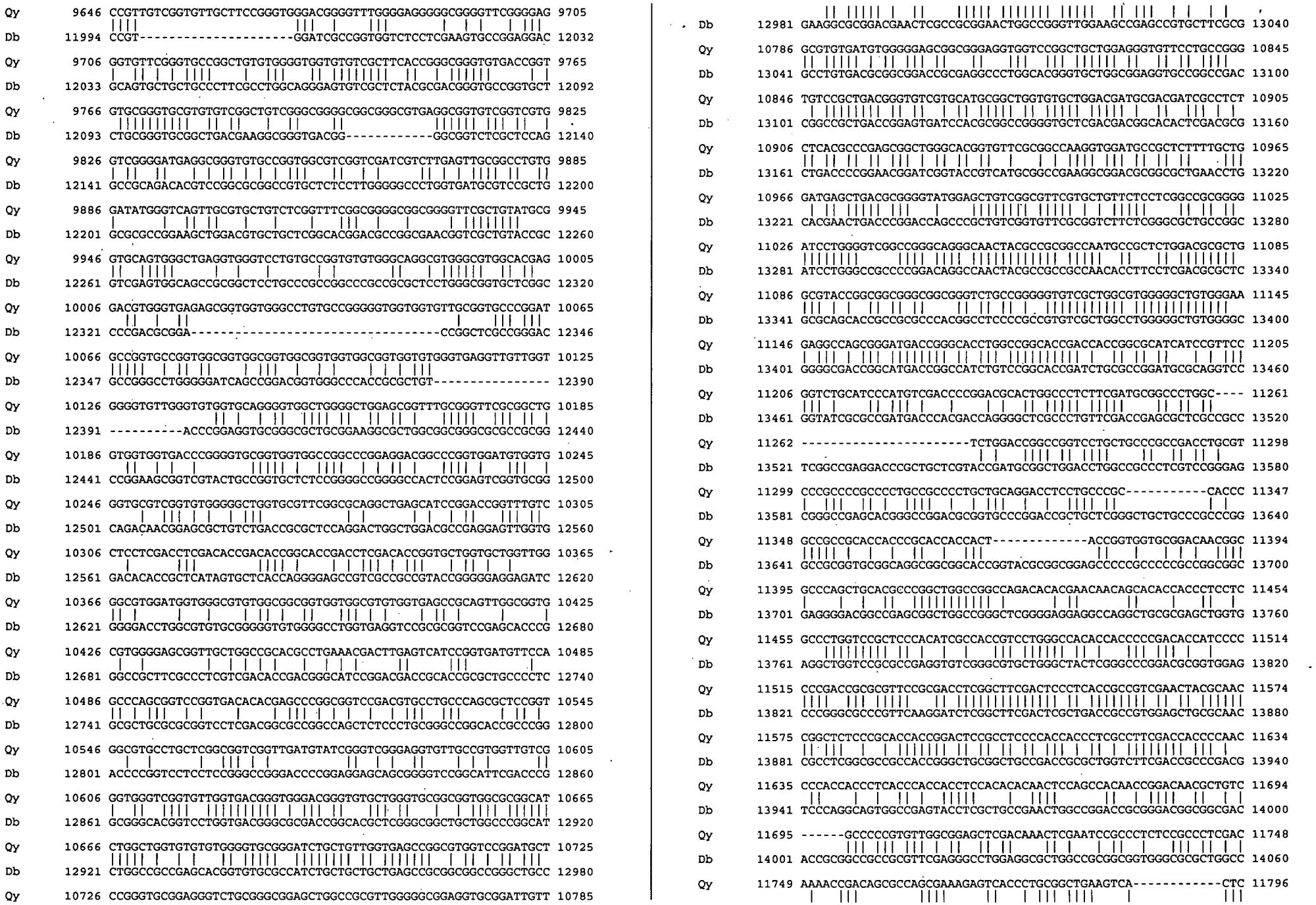


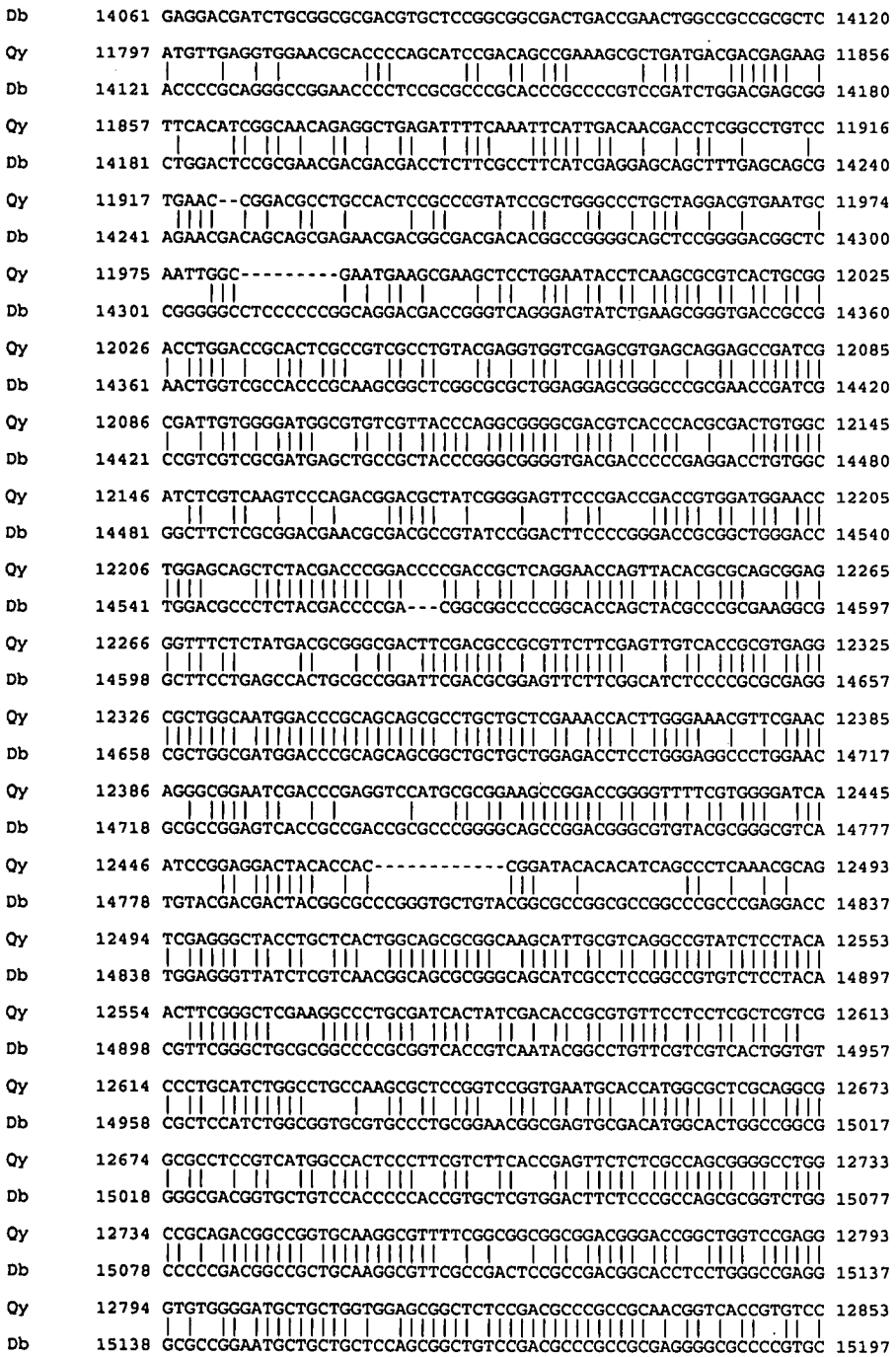







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Search completed: June 19, 2003, 07:33:04
Job time : 5051 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 17, 2003, 12:54:32 ; Search time 72.1932 Seconds
(without alignments)
1618.821 Million cell updates/sec

Title: US-09-914-286-3
Perfect score: 20829
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Scoring table: BLOSUM62
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8151	39.1	4551	3	US-09-320-878-1	Sequence 1, Appli
2	8148	39.1	4613	4	US-09-105-537-31	Sequence 31, Appl
3	8148	39.1	11877	4	US-09-105-537-6	Sequence 6, Appli
4	7705.5	37.0	4472	2	US-08-804-227C-2	Sequence 2, Appli
5	7281.5	35.0	5588	4	US-09-036-987A-6	Sequence 6, Appli
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7	7255	34.8	4545	2	US-08-804-227C-14	Sequence 14, Appl
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9	7041.5	33.8	3816	4	US-09-428-517-3	Sequence 3, Appli
10	7017	33.7	3739	4	US-09-105-537-33	Sequence 33, Appl
11	6941.5	33.3	4550	2	US-08-804-227C-8	Sequence 8, Appli
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13	6912.5	33.2	4150	4	US-09-428-517-2	Sequence 2, Appli
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ALIGNMENTS

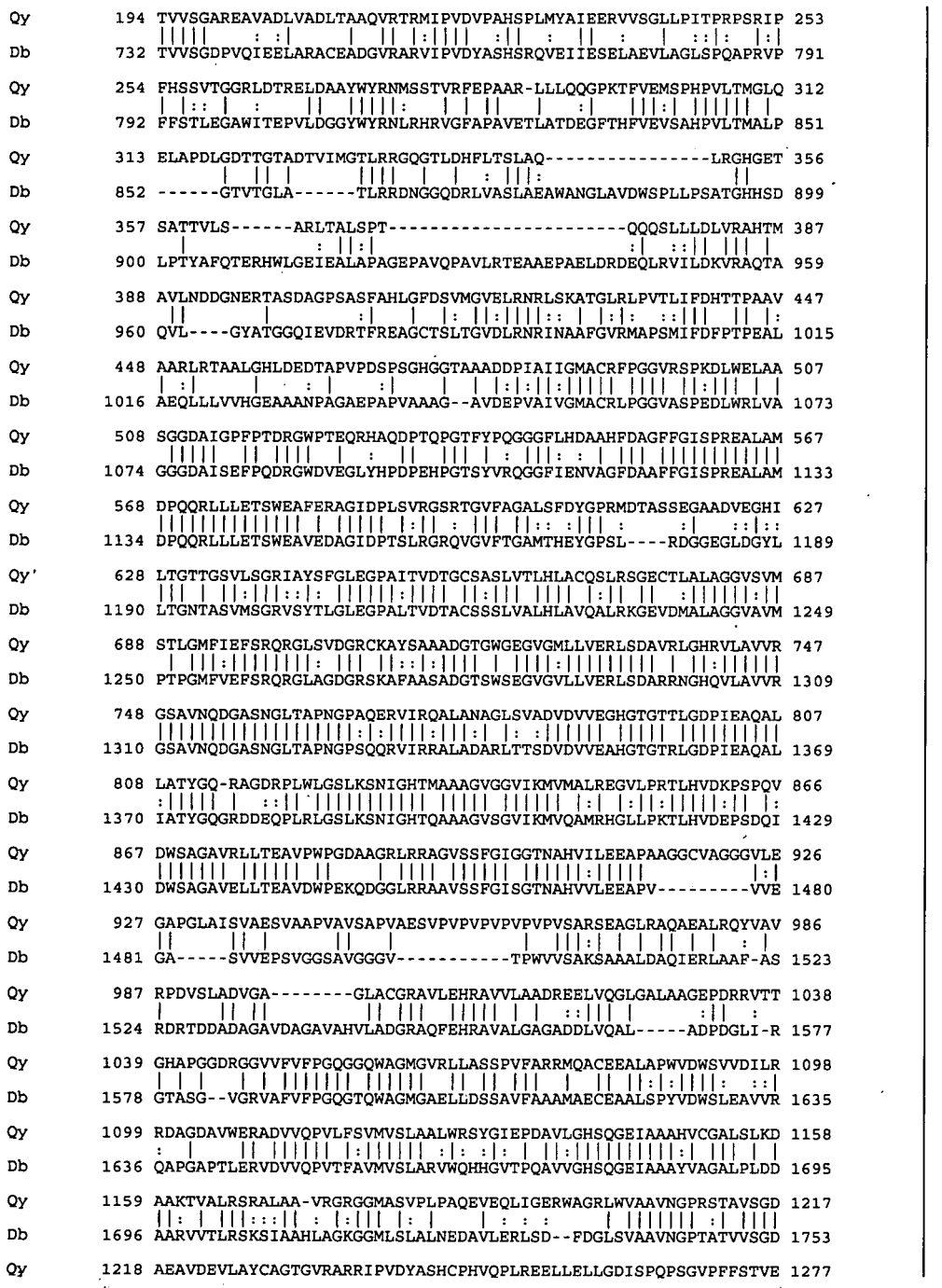
RESULT 1
US-09-320-878-1
; Sequence 1, Application US/09320878A
; Patent No. 6117659
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: McDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4551
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-320-878-1

Query Match 39.1%; Score 8151; DB 3; Length 4551;
Best Local Similarity 44.8%; Pred. No. 0;
Matches 1910; Conservative 462; Mismatches 1307; Indels 586; Gaps 94;

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Qy 1571 AITGLLSLLALDETPHPHHPHTPTGTLLNLTLTQTHTQTHPPTPLWYATTNATTTHPNDP 1630
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Qy 1631 LTHPTQAQTWGLARTTLLEHPTHTAGIIDLPTTPTPHTLQHLTQTLTQPHHQTQLAIRTT 1690
Db 2062 PADPDRAMLWGLGRVVALEHPERWAGLVDLPAQPDAAALAHLVTALSGATGEDQIAIRTT 2121
Qy 1691 GTHTRRLTPTTLTPTH-QPPTP--TPHGTTLITGGTGALATHLTHHLTTHQPTQHLLLTS 1747
Db 2122 GLHARRL---ARAPLHGRRPTRDWQPHGTVLITGGTGALGSHAARWM-AHHGAEHLLLVS 2177
Qy 1748 RTGPHTPHAQHLTTQLQQKGIHLTITTCDTSNPDQLQQLLNTIPPQHPLTTVIHTAGILD 1807
Db 2178 RSGEQAPGATQLTAELTASGARVTIAACDVADPHAMRTLLDAIPAETPLTAVVHTAGALD 2237
Qy 1808 DATLTNLTPTQLNNVLRAKAHSAHLLHQLTQHTPLTAFVLYSSAAATFGAPGQANYAAAN 1867
Db 2238 DGIVDTLTAEQVRRAHRAKAVGASVLDELTRDLDLDAFVLFSSVSSTLGIPGQGNYAPHN 2297
Qy 1868 AYLDALAHHRHTHHLPATSIAWGTWQGNGLADSDKARAYLDRRGFRPMSPELATAAVTQA 1927
Db 2298 AYLDALAARRRATGRSAVSVAWGPWDGGGMAAGDGVAERLRNHGVPGMDPELALAALESA 2357
Qy 1928 IADTERPYVVIADIDWSK-------------IEHTSQTSDLVSA-----ARELREPAVQRP 1969
Db 2358 LGRDETA-ITVADIDWDRFYLAYSSGRPQPLVEELPEVRRIIDARDSATSGQGGSSAQGA 2416
Qy 1970 TPPAELHKTLAHQTSADQRAALLELVRDHVAAVLRHADPKAIAPDQSFRALGFDSLTAVE 2029
Db 2417 NPLAE---RLAAAAPGERTEILLGLVRAQAAAVLRMRSPEDVAADRAFKDIGFDSLAGVE 2473
Qy 2030 FRNLLIKATGLRLPVSLVFDHPTPAKLAVHLQNQLRG-----TAAESAPSAAAVTAEASV 2084
Db 2474 LRNRLTRATGLQLPATLVFDHPTPLALVSLLRSEFLGDEETADARRSAALPATVGAGAGA 2533
Qy 2085 -------TEPIAIVGMACRFPGGVTSADDFWDLISSEQDAIGGFPTDRGWDLDTLYDPDP 2137
Db 2534 GAGTDADDDPIAIVAMSCRYPGDIRSPEDLWRMLSEGGEGITPFPTDRGWDLDGLYDADP 2593
Qy 2138 DHPGTCYTRNGGFLYDAGHFDAEFFGISPREALAMDPQQRLLLETAWETIEHAGINPHTL 2197
Db 2594 DALGRAYVREGGFLHDAAEFDAEFFGVSPREALAMDPQQRMLLTTSWEAFERAGIEPASL 2653
Qy 2198 HGTPTGVFTGTNGQDYALRVHNAGQSTDGFALTGTAGSVISGRISYTFGFEGPAVSVDTA 2257
Db 2654 RGSSTGVFIGLSYQDYAARVPNAPRGVEGYLLTGSTPSVASGRIAYTFGLEGPATTVDTA 2713
Qy 2258 CSSSLVALHLACQALRAGECSMALAGGVTVMSSPGAFVEFSRQRGLAADGHCKAFSAAAD 2317

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Db       2714 CSSSLTALHLAVRALRSGECTMALAGGVAMMATPHMFVEFSRQRALAPDGRSKAFSADAD 2773

Qy       2318 GTGWGEGVGMLLVERLSDAHRNGHRVLAVVRGSAVNQDGASNGLTAPNGPSQQRVIRQAL 2377

Db       2774 GFGAAEGVGLLLVERLSDARRNGHPVLAVVRGTAVNQDGASNGLTAPNGPSQQRVIRQAL 2833

Qy       2378 ANAGLSAGDVDAVEAHGTGTTLGDPIEAQALLATYGQDRAGEGPLWLGSVKSNVGHTQAA 2437

Db       2834 ADARLAPGDIDAVETHGTGTSLGDPIEAQGLQATYGKERPAERPLAIGSVKSNIGHTQAA 2893

Qy       2438 AGVAGVIKMVMALRHGLLPRTLHVDEPSPHVDWSAGAVQLLTETVPWPGGEGRLRRAGVS 2497

Db       2894 AGAAGIIKMVLAMRHGTLPKTLHADEPSPHVDWANSGLALVTEPIDWPAGTGP-RRAAVS 2952

Qy       2498 SFGVSGTNAHVILEEAP--------ADDVP-----------GGPPAGEGDAGSDDEAAA 2537

Db       2953 SFGISGTNAHVVLEQAPDAAGEVLGADEVPEVSETVAMAGTAGTSEVAEGSEASEAPAAP 3012

Qy       2538 GS-----PGVWPWLVSAKSQPALRAQAQALHAHLTDHPGLDLA---------DVGYTLAH 2583

Db       3013 GSREASLPGHLPWVLSAKDEQSLRGQAAALHAWLSE-PAADLSDADGPARLRDVGYTLAT 3071

Qy       2584 ARAVFDHRATLIAADRDTFLQALQALAAGEPHPAVIHSSAPGGTGTGEAAGKTAFICSGQ 2643

Db       3072 SRTAFAHRAAVTAADRDGFLDGLATLAQGGTSAHVHLDTARDGT--------TAFLFTGQ 3123

Qy       2644 GTQRPGMAHGLYHTHPVFAAALNDICTHLDPHLDHPLLPLLTQNDNDNEDAAALLQQTRY 2703

Db       3124 GSQRPGAGRELYDRHPVFARALDEICAHLDGHLELPLLDVMFAAEGSAE--AALLDETRY 3181

Qy       2704 AQPALFAFQVALHRLLTDGYHITPHYYAGHSLGEITAAHLAGILTLTDATTLITQRATLM 2763

Db       3182 TQCALFALEVALFRLV-ESWGMRPAALLGHSVGEIAAAHVAGVFSLADAARLVAARGRLM 3240

Qy       2764 QTMPP-GTMTTLHTTPHHITHHLTAHE---NDLAIAAINTPTSLVISGTPHTVQHITTLC 2819

Db       3241 QELPAGGAMLAVQAAEDEIRVWLETEERYAGRLDVAAVNGPEAAVLSGDADAAREAEAYW 3300

Qy       2820 QQQGIKTKTLPTNHAFHSPHTNPILNQLHQHTQTLTYHPPHTPLITANT----PPDQLLT 2875

Db       3301 SGLGRRTRALRVSHAFHSAHMDGMLDGFRAVLETVEFRRPSLTVVSNVTGLAAGPDDLCD 3360

Qy       2876 PHYWTQQARNTVDYATTTQTLHQHGVTTYIELGPDNTLTTLTHHNLPNPPTTTLT---LT 2932

Db       3361 PEYWVRHVRGTVRFLDGVRVLRDLGVRTCLELGPDGVLTAMAADGLADTPADSAAGSPVG 3420

Qy       2933 HPHHHPQTH---------LLTNL-----AKTTTTWHPHHYTH-HDNQPHTHT-------- 2969

Db       3421 SPAGSPADSAAGALRPRPLLVALLRRKRSETETVADALGRAHAHGTGPDWHAWFAGSGAH 3480

Qy       2970 HLDLPTYPFQHHHYWLESTQPGAG---NVSAAGLDPTEHPLLGATLELATDGGALLAGRL 3026

Db       3481 RVDLPTYSFRRDRYWLDA--PAADTAVDTAGLGLGTADHPLLGAVVSLPDRDGLLLTGRL 3538

Qy       3027 SLRSHPWLADHAVGGTVLLSGATFLELALHAGTYVGCDRVDELTLHAPLVVPVDGGVSVQ 3086

Db       3539 SLRTHPWLADHAVLGSVLLPGAAMVELAAHAAESAGLRDVRELTLLEPLVLPEHGGVELR 3598

Qy       3087 VGVAAADGE--------GRRLVSVYARGGSACGGGGASGGVWTCHASGVLVEAAAGGVVV 3138

Db       3599 VTVGAPAGEPGGESAGDGARPVSLHSRLADA-----PAGTAWSCHATGLLATDRPELPVA 3653

Qy       3139 DGLAGVWPPRGAVAVDVDGVRDRLAGAGCVLGPVFSGLRAVWRDGGDLLAEVCLP----- 3193

Db       3654 PDRAAMWPPQGAEEVPLDGLYERLDGNGLAFGPLFQGLNAVWRYEGEVFADIALPATTNA 3713

Qy       3194 -----EEAWGDAAG--FGLHPALLDGVVQPLSVLLPGGTGFGEGAGFGEGVRVPAVWGGV 3246

Db       3714 TAPATANGGGSAAAAPYGIHPALLDASLHAIAV---GGL-----VDEPELVRVPFHWSGV 3765

Qy       3247 SLHRAGVTGVRVRVSAVGRGGGREAVSVVVGDEAGVPVASVDRLELRPVDMGQLRAVSVS 3306

Db       3766 TVHAAGAAAARVRLAS----AGTDAVSLSLTDGEGRPLVSVERLTLRPVTADQAAASRVG 3821
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Qy       3307 AGRRGSLYAVQW----------AEVGPVPVCGQ----------A 3330

Db       3822 ----GLMHRVAWRPYALASSGEQDPHATSYGPTAVLGKDELKVAAALESAGVEVGLYPDL 3877

Qy       3331 WAWHEDVGESGGGPVPGVVVLRCPDAGAGGGGGGGGGGVGEVVGGVLGVVQGWLGLERF 3390

Db       3878 AALSQDV--AAGAPAPRTVLAPLP-----AGPADGGAEGVRGTVARTLELLQAWLADEHL 3930

Qy       3391 AGSRLVVVTRGAV----VAGPEDGPVDVVGASVWGLVRSAQAEHPDRFVLLDLDTDTGT- 3445

Db       3931 AGTRLLLVTRGAVRDPEGSGADDGGEDLSHAAAWGLVRTAQTENPGRFGLLDLADDASSY 3990

Qy       3446 ----DLDTGAGAGWGVDGGRVAAVVACGEPQLAVRGERLLAARLKRLESSGDVPAQRSGD 3501

Db       3991 RTLPSVLSDAGLR----------DEPQLALHDGTIRLARL---------- 4020

Qy       3502 TRARRSDVPAQRSGGVPARRSVDVSGREVLPWLSGGSVLVTGGTGVLGAAVARHLAGVCG 3561

Db       4021 -----ASVRPETGTAAPA----------LAP---EGTVLLTGGTGGLGGLVARHVVGEWG 4062

Qy       3562 VRDLLLVSRRGPDAPGAEGLRAELAALGAEVRIVACDVGERREVVRLLEGVPAGCPLTGV 3621

Db       4063 VRRLLLVSRRGTDAPGADELVHELEALGADVSVAACDVADREALTAVLDAIPAEHPLTAV 4122

Qy       3622 VHAAGVLDDATIASLTPERLGTVFAAKVDAALLLDELTR--GMELSAFVLFSSAAGILGS 3679

Db       4123 VHTAGVLSDGTLPSMTTEDVEHVLRPKVDAAFLLDELTSTPAYDLAAFVMFSSAAAVFGG 4182

Qy       3680 AGQGNYAAANAALDALAYRRRAAGLPGVSLAWGLWEEASGMTGHLAGTDHRRIIRSGLHP 3739

Db       4183 AGQGAYAAANATLDALAWRRRAAGLPALSLGWGLWAETSGMTGELGQADLRRMSRAGIGG 4242

Qy       3740 MSTPDALALFDAALALDR-PVLLP-----ADLRPA-----PPLPPLLQDLLPATRRR--- 3785

Db       4243 ISDAEGIALLDAALRDDRHPVLLPLRLDAAGLRDAAGNDPAGIPALFRDVVGARTVRARP 4302

Qy       3786 ------TTRTT--TTGGADNGAQLHA-----RLAGQTHEQQHTTLLALVRSHIATVLGHT 3832

Db       4303 SAASASTTAGTAGTPGTADGAAETAAVTLADRAATVDGPARQRLLLEFVVGEVAEVLGHA 4362

Qy       3833 TPDTIPPDRAFRDLGFDSLTAVELRNRLSRTTGLRLPTTLAFDHPNPTTLTHHLHTQL-- 3890

Db       4363 RGHRIDAERGFLDLGFDSLTAVELRNRLNSAGGLALPATLVFDHPSPAALASHLDAELPR 4422

Qy       3891 -QPQPDNA----------VAPVLAELDKLESALSALDKTDS-ASERVTLRLK 3930

Db       4423 GASDQDGAGNRNGNENGTTASRSTAETDALLAQLTRLEGALVLTGLSDAPGSEEVLEHLR 4482

Qy       3931 SLMLR----------WNAPQHPTAESADDD--EKFTSATEAEIFK 3963

Db       4483 SLRSMVTGETGTGTASGAPDGAGSGAEDRPWAAGDGAGGGSEDGAGVPDFMNASAEELFG 4542

Qy       3964 FIDND 3968

Db       4543 LLDQD 4547
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RESULT 2
US-09-105-537-31
; Sequence 31, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 31
; LENGTH: 4613
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-105-537-31

Query Match 39.1%; Score 8148; DB 4; Length 4613;
Best Local Similarity 44.8%; Pred. No. 0;
Matches 1909; Conservative 463; Mismatches 1307; Indels 586; Gaps 94;

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Qy        15 GEVLGVADEADGGVVFVFPGQGPQWPGMGRELLDASDVFRESVRACEAAFAPYVDWSVEQ  74
Db       620 GLVRGVASGV-GRVAFVFPGQGTQWAGMGAELLDSSAVFAAAMAECEAALSPYVDWSLEA  678

Qy        75 VLRDSPDAPGLDRVDVVQPTLFAVMISLAALWRSQGVEPCAVLGHSLGEIAAAHVSGGLS  134
Db       679 VVRQAPGAPTLERVDVVQPVTFAVMVSLARVWQHHGVTPQAVVGHSQGEIAAAYVAGALS  738

Qy       135 LADAARVVTLWSQA-QTTLAGTGALVSVAATPDELLPRIAPWTEDNPARLAVAAVNGPRS  193
Db       739 LDDAARVVTLRSKSIAAHLAGKGGMLSLALSEDAVLERLAGFD-----GLSVAAVNGPTA  793

Qy       194 TVVSGAREAVADLVADLTAAQVRTRMIPVDVPAHSPLMYAIEERVVSGLLPITPRPSRIP  253
Db       794 TVVSGDPVQIEELARACEADGVRARVIPVDYASHSRQVEIIESELAEVLAGLSPQAPRVP  853

Qy       254 FHSSVTGGRLDTRELDAAYWYRNMSSTVRFEPAAR-LLLQQGPKTFVEMSPHPVLTMGLQ  312
Db       854 FFSTLEGAWITEPVLDGGYWYRNLRHRVGFAPAVETLATDEGFTHFVEVSAHPVLTMALP  913

Qy       313 ELAPDLGDTTGTADTVIMGTLRRGQGTLDHFLTSLAQ---------------LRGHGET  356
Db       914 ------GTVTGLA------TLRRDNGGQDRLVASLAEAWANGLAVDWSPLLPSATGHHSD  961

Qy       357 SATTVLS------ARLTALSPT----------------------QQQSLLLDLVRAHTM  387
Db       962 LPTYAFQTERHWLGEIEALAPAGEPAVQPAVLRTEAAEPAELDRDEQLRVILDKVRAQTA 1021

Qy       388 AVLNDDGNERTASDAGPSASFAHLGFDSVMGVELRNRLSKATGLRLPVTLIFDHTTPAAV  447
Db      1022 QVL----GYATGGQIEVDRTFREAGCTSLTGVDLRNRINAAFGVRMAPSMIFDFPTPEAL 1077

Qy       448 AARLRTAALGHLDEDTAPVPDSPSGHGGTAAADDPIAIIGMACRFPGGVRSPKDLWELAA  507
Db      1078 AEQLLLVVHGEAAANPAGAEPAPVAAAG--AVDEPVAIVGMACRLPGGVASPEDLWRLVA 1135

Qy       508 SGGDAIGPFPTDRGWPTEQRHAQDPTQPGTFYPQGGGFLHDAAHFDAGFFGISPREALAM  567
Db      1136 GGGDAISEFPQDRGWDVEGLYHPDPEHPGTSYVRQGGFIENVAGFDAAFFGISPREALAM 1195

Qy       568 DPQQRLLLETSWEAFERAGIDPLSVRGSRTGVFAGALSFDYGPRMDTASSEGAADVEGHI  627
Db      1196 DPQQRLLLETSWEAVEDAGIDPTSLRGRQVGVFTGAMTHEYGPSL----RDGGEGLDGYL 1251

Qy       628 LTGTTGSVLSGRIAYSFGLEGPAITVDTGCSASLVTLHLACQSLRSGECTLALAGGVSVM  687
Db      1252 LTGNTASVMSGRVSYTLGLEGPALTVDTACSSSLVALHLAVQALRKGEVDMALAGGVAVM 1311

Qy       688 STLGMFIEFSRQRGLSVDGRCKAYSAAADGTGWGEGVGMLLVERLSDAVRLGHRVLAVVR  747
Db      1312 PTPGMFVEFSRQRGLAGDGRSKAFAASADGTSWSEGVGVLLVERLSDARRNGHQVLAVVR 1371

Qy       748 GSAVNQDGASNGLTAPNGPAQERVIRQALANAGLSVADVDVVEGHGTGTTLGDPIEAQAL  807
Db      1372 GSALNQDGASNGLTAPNGPSQQRVIRRALADARLTTSDVDVVEAHGTGTRLGDPIEAQAL 1431

Qy       808 LATYGQ-RAGDRPLWLGSLKSNIGHTMAAAGVGGVIKMVMALREGVLPRTLHVDKPSPQV  866
Db      1432 IATYGQGRDDEQPLRLGSLKSNIGHTQAAAGVSGVIKMVQAMRHGLLPKTLHVDEPSDQI 1491

Qy       867 DWSAGAVRLLTEAVPWPGDAAGRLRRAGVSSFGIGGTNAHVILEEAPAAGGCVAGGGVLE  926
Db      1492 DWSAGAVELLTEAVDWPEKQDGGLRRAAVSSFGISGTNAHVVLEEAPV---------VVE 1542

Qy       927 GAPGLAISVAESVAAPVAVSAPVAESVPVPVPVPVPVPVSARSEAGLRAQAEALRQYVAV  986
Db      1543 GA-----SVVEPSVGGSAVGGGV----------TPWVVSAKSAAALDAQIERLAAF-AS 1585

Qy       987 RPDVSLADVGA--------GLACGRAVLEHRAVVLAADREELVQGLGALAAGEPDRRVTT 1038
Db      1586 RDRTDDADAGAVDAGAVAHVLADGRAQFEHRAVALGAGADDLVQAL-----ADPDGLI-R 1639

Qy      1039 GHAPGGDRGGVVFVFPGQGGQWAGMGVRLLASSPVFARRMQACEEALAPWVDWSVVDILR 1098
Db      1640 GTASG--VGRVAFVFPGQGTQWAGMGAELLDSSAVFAAAMAECEAALSPYVDWSLEAVVR 1697

Qy      1099 RDAGDAVWERADVVQPVLFSVMVSLAALWRSYGIEPDAVLGHSQGEIAAAHVCGALSLKD 1158
Db      1698 QAPGAPTLERVDVVQPVTFAVMVSLARVWQHHGVTPQAVVGHSQGEIAAAYVAGALPLDD 1757

Qy      1159 AAKTVALRSRALAA-VRGRGGMASVPLPAQEVEQLIGERWAGRLWVAAVNGPRSTAVSGD 1217
Db      1758 AARVVTLRSKSIAAHLAGKGGMLSLALNEDAVLERLSD--FDGLSVAAVNGPTATVVSGD 1815

Qy      1218 AEAVDEVLAYCAGTGVRARRIPVDYASHCPHVQPLREELLELLGDISPQPSGVPFFSTVE 1277
Db      1816 PVQIEELAQACKADGFRARIIPVDYASHSRQVEIIESELAQVLAGLSPQAPRVPFFSTLE 1875

Qy      1278 GTWLDTTTLDAAYWYRNLHQPVRFSDAVQALA-DDGHRVFVEVSPHPTLVPAIEDTTEDT 1336
Db      1876 GTWITEPVLDGTYWYRNLRHRVGFAPAIETLAVDEGFTHFVEVSAHPVLTMTLPET---- 1931

Qy      1337 AEDVTAIGSLRRGDNDTRRFLTALAHTHTTGIGTPTTWHHHYTHHHTHPHPHTHLDLPTY 1396
Db      1932 ---VTGLGTLRREQGGQERLVTSLAEAWVNGL--PVAWTSLLPATASRP------GLPTY 1980

Qy      1397 PFQHQHYWLESSQPGAGSGSGAGAGSGAGSGRAGTAGGTAEVESRFWDAVARQDLETVAT 1456
Db      1981 AFQAERYWLENTPAALATG---------------------------------------- 1999

Qy      1457 TLAVPPSAGLDTVVPALSAWHRHQHDQARINTWTYQETWKPLTLPTTHQPHQT-----WL 1511
Db      2000 ------------------------------DDWRYRIDWK--RLPAAEGSERTGLSGRWL 2027

Qy      1512 IAIPETQTHHPHITNILTNLHHHGITPIPLTLNHTHTNPQHLHHTLHHTRQQAQNHTTG- 1570
Db      2028 AVTPE--DHSAQAAAVLTALVDAGAKVEVLTAG-ADDDREALAARLTAL-------TTGD 2077

Qy      1571 AITGLLSLLALDETPHPHHPHTPTGTLLNLTLTQTHTQTHPPTPLWYATTNATTTHPNDP 1630
Db      2078 GFTGVVSLL-------------DGLVPQVAWVQALGDAGIKAPLWSVTQGAVSVGRLDT 2123

Qy      1631 LTHPTQAQTWGLARTTLLEHPTHTAGIIDLPTTPTPHTLQHLTQTLTQPHHQTQLAIRTT 1690
Db      2124 PADPDRAMLWGLGRVVALEHPERWAGLVDLPAQPDAAALAHLVTALSGATGEDQIAIRTT 2183

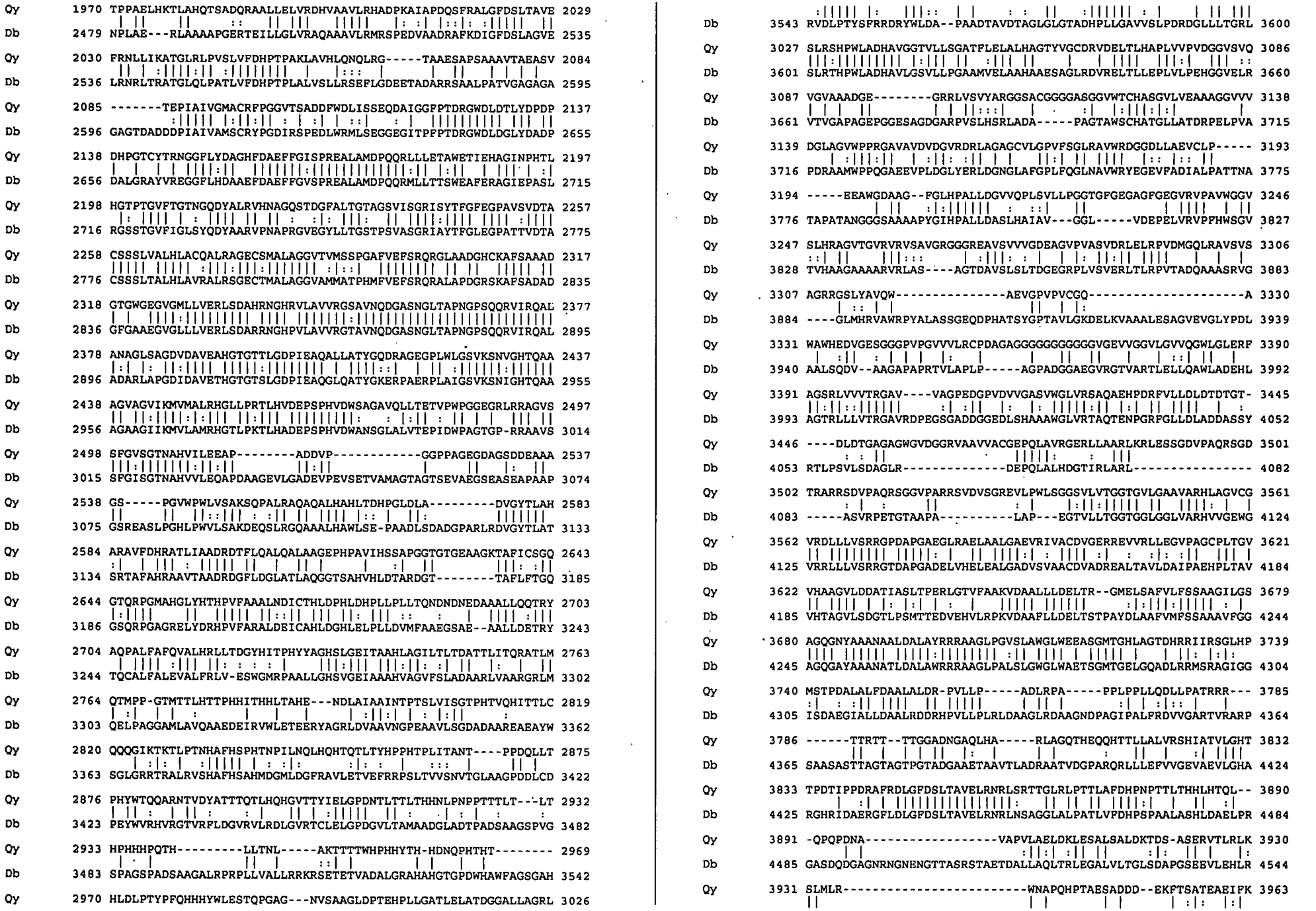
Qy      1691 GTHTRRLTPTTLTPTH-QPPTP--TPHGTTLITGGTGALATHLTHHLTTHQPTQHLLLTS 1747
Db      2184 GLHARRL---ARAPLHGRRPTRDWQPHGTVLITGGTGALGSHAARWM-AHHGAEHLLLVS 2239

Qy      1748 RTGPHTPHAQHLTTQLQQKGIHLTITTCDTSNPDQLQQLLNTIPPQHPLTTVIHTAGILD 1807
Db      2240 RSGEQAPGATQLTAELTASGARVTIAACDVADPHAMRTLLDAIPAETPLTAVVHTAGALD 2299

Qy      1808 DATLTNLTPTQLNNVLRAKAHSAHLLHQLTQHTPLTAFVLYSSAAATFGAPGQANYAAAN 1867
Db      2300 DGIVDTLTAEQVRRAHRAKAVGASVLDELTRDLDLDAFVLFSSVSSTLGIPGQGNYAPHN 2359

Qy      1868 AYLDALAHHRHTHHLPATSIAWGTWQGNGLADSDKARAYLDRRGFRPMSPELATAAVTQA 1927
Db      2360 AYLDALAARRRATGRSAVSVAWGPWDGGGMAAGDGVAERLRNHGVPGMDPELALAALESA 2419

Qy      1928 IADTERPYVVIADIDWSK-------------IEHTSQTSDLVSA-----ARE-REPAVQRP 1969
Db      2420 LGRDETA-ITVADIDWDRFYLAYSSGRPQPLVEELPEVRRIIDARDSATSGQGGSSAQGA 2478
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Db       4545 SLRSMVTGETGTGTASGAPDGAGSGAEDRPWAAGDGAGGGSEDGAGVPDFMNASAEELFG 4604

Qy       3964 FIDND 3968
                :| |
Db       4605 LLDQD 4609


RESULT 3
US-09-105-537-6
; Sequence 6, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
;  APPLICANT: Sherman, D.H.
;  APPLICANT: Liu, H.
;  APPLICANT: Xue, Y.
;  APPLICANT: Zhao, L.
;  TITLE OF INVENTION: DNA encoding methymycin and pikromycin
;  FILE REFERENCE: 600.438US1
;  CURRENT APPLICATION NUMBER: US/09/105,537A
;  CURRENT FILING DATE: 1998-06-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 11877
;   TYPE: PRT
;   ORGANISM: Streptomyces venezuelae
US-09-105-537-6

  Query Match             39.1%;  Score 8148;  DB 4;  Length 11877;
  Best Local Similarity   44.8%;  Pred. No. 0;
  Matches 1909;  Conservative  463;  Mismatches 1307;  Indels  586;  Gaps   94;

Qy         15 GEVLGVADEADGGVVFVFPGQGPQWPGMGRELLDASDVFRESVRACEAAFAPYVDWSVEQ  74
              | | |||    | | ||||||| || ||| ||||:| ||  ::  |||| :||||||:|
Db        956 GLVRGVASGV-GRVAFVFPGQGTQWAGMGAELLDSSAVFAAAMAECEAALSPYVDWSLEA 1014

Qy         75 VLRDSPDAPGLDRVDVVQPTLFAVMISLAALWRSQGVEPCAVLGHSLGEIAAAHVSGGLS  134
              |:| :| || |:|||||||  ||||:||| :|:  || | ||:||| ||||||:|:| ||
Db       1015 VVRQAPGAPTLERVDVVQPVTFAVMVSLARVWQHHGVTPQAVVGHSQGEIAAAYVAGALS 1074

Qy        135 LADAARVVTLWSQA-QTTLAGTGALVSVAATPDELLPRIAPWTEDNPARLAVAAVNGPRS  193
              | |||||||| |::    ||| | ::|:| : | :| |:| :      |:||||||| :
Db       1075 LDDAARVVTLRSKSIAAHLAGKGGMLSLALSEDAVLERLAGFD-----GLSVAAVNGPTA 1129

Qy        194 TVVSGAREAVADLVADLTAAQVRTRMIPVDVPAHSPLMYAIEERVVSGLLPITPRPSRIP  253
              |||||    : :|     |  || |:|||| :||  :  ||  :   |  ::|:  |:|
Db       1130 TVVSGDPVQIEELARACEADGVRARVIPVDYASHSRQVEIIESELAEVLAGLSPQAPRVP 1189

Qy        254 FHSSVTGGRLDTRELDAAYWYRNMSSTVRFEPAAR-LLLQQGPKTFVEMSPHPVLTMGLQ  312
              | |:: |  :    ||  |||||:   | | ||    |   :|   |||:| |||||| |
Db       1190 FFSTLEGAWITEPVLDGGYWYRNLRHRVGFAPAVETLATDEGFTHFVEVSAHPVLTMALP 1249

Qy        313 ELAPDLGDTTGTADTVIMGTLRRGQGTLDHFLTSLAQ---------------LRGHGET  356
                 | || |      ||||  |  |  : |||:                   ||
Db       1250 ------GTVTGLA------TLRRDNGGQDRLVASLAEAWANGLAVDWSPLLPSATGHHSD 1297

Qy        357 SATTVLS------ARLTALSPT----------------------QQQSLLLDLVRAHTM  387
                |          : ||:|                      :|  ::|| ||| |
Db       1298 LPTYAFQTERHWLGEIEALAPAGEPAVQPAVLRTEAAEPAELDRDEQLRVILDKVRAQTA 1357

Qy        388 AVLNDDGNERTASDAGPSASFAHLGFDSVMGVELRNRLSKATGLRLPVTLIFDHTTPAAV  447
               ||       |        :|   |  |: ||:||||:: | |:|:  ::|||  || |:
Db       1358 QVL----GYATGGQIEVDRTFREAGCTSLTGVDLRNRINAAFGVRMAPSMIFDFPTPEAL 1413

Qy        448 AARLRTAALGHLDEDTAPVPDSPSGHGGTAAADDPIAIIGMACRFPGGVRSPKDLWELAA  507
              | :|    |   : |   :|    |  | |:|:|||:||||| |||| ||:||| | |
Db       1414 AEQLLLVVHGEAAANPAGAEPAPVAAAG--AVDEPVAIVGMACRLPGGVASPEDLWRLVA 1471

Qy        508 SGGDAIGPFPTDRGWPTEQRHAQDPTQPGTFYPQGGGFLHDAAHFDAGFFGISPREALAM  567
              |||||  || |||| |  :  ||  ||| | : |||: : | ||| ||||||||||||
Db       1472 GGGDAISEFPQDRGWDVEGLYHPDPEHPGTSYVRQGGFIENVAGFDAAFFGISPREALAM 1531

Qy        568 DPQQRLLLETSWEAFERAGIDPLSVRGSRTGVFAGALSFDYGPRMDTASSEGAADVEGHI  627
```

```
                |||||||||||||| | ||||| |:|| : ||| ||:: :||| :     :|   ::|::
Db       1532 DPQQRLLLETSWEAVEDAGIDPTSLRGRQVGVFTGAMTHEYGPSL----RDGGEGLDGYL 1587

Qy        628 LTGTTGSVLSGRIAYSFGLEGPAITVDTGCSASLVTLHLACQSLRSGECTLALAGGVSVM  687
              ||| | ||:|||::|: |||||:|||| ||:||| |||| |:|| ||  :||||||:||
Db       1588 LTGNTASVMSGRVSYTLGLEGPALTVDTACSSSLVALHLAVQALRKGEVDMALAGGVAVM 1647

Qy        688 STLGMFIEFSRQRGLSVDGRCKAYSAAADGTGWGEGVGMLLVERLSDAVRLGHRVLAVVR  747
              | |||:||||||||: ||| ||::|:|||| | ||||:||||||||| | ||:||||||
Db       1648 PTPGMFVEFSRQRGLAGDGRSKAFAASADGTSWSEGVGVLLVERLSDARRNGHQVLAVVR 1707

Qy        748 GSAVNQDGASNGLTAPNGPAQERVIRQALANAGLSVADVDVVEGHGTGTTLGDPIEAQAL  807
              |||:|||||||||||||||:|:||||:|||:| |: :|||||| ||||| ||||||||||
Db       1708 GSALNQDGASNGLTAPNGPSQQRVIRRALADARLTTSDVDVVEAHGTGTRLGDPIEAQAL 1767

Qy        808 LATYGQ-RAGDRPLWLGSLKSNIGHTMAAAGVGGVIKMVMALREGVLPRTLHVDKPSPQV  866
              :||||| |  ::|| |||||||||||| ||||| |||||| |:| |:||:|||||:|| |:
Db       1768 IATYGQGRDDEQPLRLGSLKSNIGHTQAAAGVSGVIKMVQAMRHGLLPKTLHVDEPSDQI 1827

Qy        867 DWSAGAVRLLTEAVPWPGDAAGRLRRAGVSSFGIGGTNAHVILEEAPAAGGCVAGGGVLE  926
              ||||||| |||||| ||    | |||| |||||| ||||||:|||||          |:|
Db       1828 DWSAGAVELLTEAVDWPEKQDGGLRRAAVSSFGISGTNAHVVLEEAPV---------VVE 1878

Qy        927 GAPGLAISVAESVAAPVAVSAPVAESVPVPVPVPVPVPVSARSEAGLRAQAEALRQYVAV  986
              ||     || |      ||   |            | |||:| | | || | |  : |
Db       1879 GA-----SVVEPSVGGSAVGGGV----------TPWVVSAKSAAALDAQIERLAAF-AS 1921

Qy        987 RPDVSLADVGA--------GLACGRAVLEHRAVVLAADREELVQGLGALAAGEPDRRVTT 1038
              |      || ||       ||||  ||| ||||| | |  ::||| |      :||  :
Db       1922 RDRTDDADAGAVDAGAVAHVLADGRAQFEHRAVALGAGADDLVQAL-----ADPDGLI-R 1975

Qy       1039 GHAPGGDRGGVVFVFPGQGGQWAGMGVRLLASSPVFARRMQACEEALAPWVDWSVVDILR 1098
              | | |   | | ||||||| ||||||  || || |||  |  || ||:|:||||:  ::|
Db       1976 GTASG--VGRVAFVFPGQGTQWAGMGAELLDSSAVFAAAMAECEAALSPYVDWSLEAVVR 2033

Qy       1099 RDAGDAVWERADVVQPVLFSVMVSLAALWRSYGIEPDAVLGHSQGEIAAAHVCGALSLKD 1158
              :  |    || |||||| |:|||||| :|: :|: | ||:|||||||||:| ||| | |
Db       2034 QAPGAPTLERVDVVQPVTFAVMVSLARVWQHHGVTPQAVVGHSQGEIAAAYVAGALPLDD 2093

Qy       1159 AAKTVALRSRALAA-VRGRGGMASVPLPAQEVEQLIGERWAGRLWVAAVNGPRSTAVSGD 1217
              ||: | |||:::|| : |:||| |: |     | : : :     | |||||| :| ||||
Db       2094 AARVVTLRSKSIAAHLAGKGGMLSLALNEDAVLERLSD--FDGLSVAAVNGPTATVVSGD 2151

Qy       1218 AEAVDEVLAYCAGTGVRARRIPVDYASHCPHVQPLREELLELLGDISPQPSGVPFFSTVE 1277
                 ::|:   |   | ||| ||||||||    |: :  || ::|  :|||   ||||||:|
Db       2152 PVQIEELAQACKADGFRARIIPVDYASHSRQVEIIESELAQVLAGLSPQAPRVPFFSTLE 2211

Qy       1278 GTWLDTTTLDAAYWYRNLHQPVRFSDAVQALA-DDGHRVFVEVSPHPTLVPAIEDTTEDT 1336
              |||:    ||  ||||||   | |: |:: || |:|   ||||| || |   : :|
Db       2212 GTWITEPVLDGTYWYRNLRHRVGFAPAIETLAVDEGFTHFVEVSAHPVLTMTLPET---- 2267

Qy       1337 AEDVTAIGSLRRGDNDTRRFLTALAHTHTTGIGTPTTWHHHYTHHHTHPHPHTHLDLPTY 1396
                 || :|:|||       | :|:||     |:  | |         :|      ||||
Db       2268 ---VTGLGTLRREQGGQERLVTSLAEAWVNGL--PVAWTSLLPATASRP------GLPTY 2316

Qy       1397 PFQHQHYWLESSQPGAGSGSGAGAGSGAGSGRAGTAGGTAEVESRFWDAVARQDLETVAT 1456
              || : ||||::      :|
Db       2317 AFQAERYWLENTPAALATG---------------------------------------- 2335

Qy       1457 TLAVPPSAGLDTVVPALSAWHRHQHDQARINTWTYQETWKPLTLPTTHQPHQT-----WL 1511
                                          : | |:  ||   ||      :|      ||
Db       2336 -----------------------------DDWRYRIDWK--RLPAAEGSERTGLSGRWL 2363

Qy       1512 IAIPETQTHHPHITNILTNLHHHGITPIPLTLNHTHTNPQHLHHTLHHTRQQAQNHTTG- 1570
                 ||    |      :|| | |      ||      : : | .  |          |||
Db       2364 AVTPE--DHSAQAAAVLTALVDAGAKVEVLTAG-ADDDREALAARLTAL-------TTGD 2413

Qy       1571 AITGLLSLLALDETPHPHHPHTPTGTLLNLTLTQTHTQTHPPTPLWYATTNATTTHPNDP 1630
                 ||::|||                | :  :   |          |||  |  | :    |
Db       2414 GFTGVVSLL--------------DGLVPQVAWVQALGDAGIKAPLWSVTQGAVSVGRLDT 2459

Qy       1631 LTHPTQAQTWGLARTTLLEHPTHTAGIIDLPTTPTPHTLQHLTQTLTQPHHQTQLAIRTT 1690
                 | :|  |||  |   ||||   ||::|||  |    | ||   |:    : |:|||||
```



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Qy       3680 AGQGNYAAANAALDALAYRRRAAGLPGVSLAWGLWEEASGMTGHLAGTDHRRIIRSGLHP 3739
Db       4581 AGQGAYAAANATLDALAWRRRAAGLPALSLGWGLWAETSGMTGELGQADLRRMSRAGIGG 4640

Qy       3740 MSTPDALALFDAALALDR-PVLLP-----ADLRPA-----PPLPPLLQDLLPATRRR--- 3785
Db       4641 ISDAEGIALLDAALRDDRHPVLLPLRLDAAGLRDAAGNDPAGIPALFRDVVGARTVRARP 4700

Qy       3786 ------TTRTT--TTGGADNGAQLHA-----RLAGQTHEQQHTTLLALVRSHIATVLGHT 3832
Db       4701 SAASASTTAGTAGTPGTADGAAETAAVTLADRAATVDGPARQRLLLEFVVGEVAEVLGHA 4760

Qy       3833 TPDTIPPDRAFRDLGFDSLTAVELRNRLSRTTGLRLPTTLAFDHPNPTTLTHHLHTQL-- 3890
Db       4761 RGHRIDAERGFLDLGFDSLTAVELRNRLNSAGGLALPATLVFDHPSPAALASHLDAELPR 4820

Qy       3891 -QPQPDNA------------------VAPVLAELDKLESALSALDKTDS-ASERVTLRLK 3930
Db       4821 GASDQDGAGNRNGNENGTTASRSTAETDALLAQLTRLEGALVLTGLSDAPGSEEVLEHLR 4880

Qy       3931 SLMLR------------------------WNAPQHPTAESADDD--EKFTSATEAEIFK 3963
Db       4881 SLRSMVTGETGTGTASGAPDGAGSGAEDRPWAAGDGAGGGSEDGAGVPDFMNASAEELFG 4940

Qy       3964 FIDND 3968
Db       4941 LLDQD 4945
```

RESULT 4
US-08-804-227C-2
; Sequence 2, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
; APPLICANT: DeHoff, Bradley S.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rosteck, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS G. PLANT 1501
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCI(DOS) Text only
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,227C
; FILING DATE: February 21, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Plant, Thomas, G.
; REGISTRATION NUMBER: 35,784
; REFERENCE/DOCKET NUMBER: X-8231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-2459
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4472 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-804-227C-2

Query Match 37.0%; Score 7705.5; DB 2; Length 4472;
Best Local Similarity 44.3%; Pred. No. 0;
Matches 1849; Conservative 453; Mismatches 1380; Indels 495; Gaps 97;

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Qy         13 AAGEVLGVADEADGGVVFVFPGQGPQWPGMGRELLDASDVFRESVRACEAAFAPYVDWSV 72
Db        571 AAGGAGAAGGAGGGGVVLVFPGQGTQWVGMGAGLLGSSEVFAASMRECARALSVHVGWDL 630

Qy         73 EQVLRDSPDAPGLDRVDVVQPTLFAVMISLAALWRSQGVEPCAVLGHSLGEIAAAHVSGG 132
Db        631 LEVV---SGGAGLERVDVVQPVTWAVMVSLARYWQAMGVDVAAVVGHSQGEIAAATVAGA 687

Qy        133 LSLADAARVVTLWS-QAQTTLAGTGALVSVAATPDELLPRIAPWTEDNPARLAVAAVNGP 191
Db        688 LSLEDAAAVVALRAGLIGRYLAGRGAMAAVPLPAGEVEAGLAKW-----PGVEVAAVNGP 742

Qy        192 RSTVVSGAREAVADLVADLTAAQVRTRMIPVDVPAHSPLMYAIE---ERVVSGLLPITPR 248
Db        743 ASTVVSGDRRAVAGYVAVCQAEGVQARLIPVDYASHSRHVEDLKGELERVLSG---IRPR 799

Qy        249 PSRIPFHSSVTGGRLDTRELDAAYWYRNMSSTVRFEPAARLLLQQGPKTFVEMSPHPVLT 308
Db        800 SPRVPVCSTVAGEQPGEPVFDAGYWFRNLRNRVEFSAVVGGLLEEGHRRFIEVSAHPVLV 859

Qy        309 MGLQELAPDLGDTTGTADTVI--MGTLRRGQGTLDHFLTSLAQLRGHGET---------- 356
Db        860 HAIEQ-------TAEAADRSVHATGTLRRQDDSPHRLLTSTAEAWAHGATLTWDPALPPG 912

Qy        357 SATTV-----------------------------LSARLTALSPTQQQ-SLLLDLVRA 384
Db        913 HLTTLPTYPFNHHHYWLDTIDGGGGDDATQEKESGPLTRELRGLPSSQKQLGFLLDLVCR 972

Qy        385 HTMAVLNDDGNERTASDAGPSASFAHLGFDSVMGVELRNRLSKATGLRLPVTLIFDHTTP 444
Db        973 HTAVVLGLD----TAAEVDPDLSFKKQGIQSMTGVELRNRLLTETGLALPTTLVYDRPTP 1028

Qy        445 AAVAARLRTAALGHLDEDTAPVPDSPSGHGGTAA-----ADDPIAIIGMACRFPGGVRSP 499
Db       1029 RALAQFLHTELL----------DGSPSGSVLAPAQKSFEAQEPIAVVGMGCRFPGGVGSP 1078

Qy        500 KDLWELAASGGDAIGPFPTDRGWPTEQRHAQDPTQPGTFYPQGGGFLHDAAHFDAGFFGI 559
Db       1079 EALWRLVVEGVDAVSPFPGDRGWDVEGLYDPEPGVAGKSYVREGGFLHDAAEFDAEFFGI 1138

Qy        560 SPREALAMDPQQRLLLETSWEAFERAGIDPLSVRGSRTGVFAGALSFDYGPRMDTASSEG 619
Db       1139 SPREAVAMDPQQRLLLETSWEAIERAGIDPHSLHGSRTGVYAGVMPQEYGPRL----AEG 1194

Qy        620 AADVEGHILTGTTGSVLSGRIAYSFGLEGPAITVDTGCSASLVTLHLACQSLRSGECTLA 679
Db       1195 AEGSDGYLLTGTSGSVVSGRVAYTLGLEGPAVTVDTACSSSLVALHLAVQALRGGECDMA 1254

Qy        680 LAGGVSVMSTLGMFIEFSRQRGLSVDGRCKAYSAAADGTGWGEGVGMLLVERLSDAVRLG 739
Db       1255 LAGGVTVMAGPGMFVEFSRQRGLAADGRCKAFADGADGTAWAEGAGVVLVERLSDARRLG 1314

Qy        740 HRVLAVVRGSAVNQDGASNGLTAPNGPAQERVIRQALANAGLSVADVDVVEGHGTGTTLG 799
Db       1315 HPVLAVVCGSAVNQDGASNGLTAPSGPSQERVIRQALGNARLTVADVDVVEAHGTGTRLG 1374

Qy        800 DPIEAQALLATYGQ-RAGDRPLWLGSLKSNIGHTMAAAGVGGVIKMVMALREGVLPRTLH 858
Db       1375 DPIEAQALLGTYGRDRDGGRPVWLGSLKSNIGHAQAAAGVAGVIKMVLAMRYGWLPRTLH 1434

Qy        859 VDKPSPQVDWSAGAVRLLTEAVPWPGDAAGRLRRAGVSSFGIGGTNAHVILEEAPAAGGC 918
Db       1435 VDEPSRHVDWSAGGVWLLTEAREWPG--VDRPRRAAVSAFGVSGTNAHLILE-------- 1484

Qy        919 VAGGGVLEGAPGLAISVAESVAAPVAVSAPVAESVPV--PVPVPVPVPVSARSEAGLRAQ 976
Db       1485 ------------APDTAEAESATTPVRSEVSESAAVLDARSGVVPVVVSGRSRVVVREA 1531

Qy        977 AEALRQYVAVRPDVSLADVGAGLACGRAVLEHRAVVLAADREELVQGLGALAAGEPDRRV 1036
Db       1532 AGRLAEVVEA-GGVGLADVAVTMA-GRSRFGYRAVVLARGEAELAGRLRALAGGDPDAGV 1589
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Db       3608 RVAIHSAPEAAVHSAAEGGDSAGVWTRHGEGTLVPDPEPTPPDADWARAWPPAGE-RVEP 3666

Qy       3156 DGVRDRLAGAGCVLGPVFSGLRAVWRDGGDLLAEVCLPEEAWGDAAGFGLHPALLDGVVQ 3215
               : :|    |   |  |:|:|||||    ||||| ||: |   |  ||:||||||  :|
Db       3667 AELYERFGALGYEYGEAFAGVRAVWRQPDALLAEVLLPDRASTGAGRFGVHPALLDAALQ 3726

Qy       3216 PLSVLLPGG-TGFGEGAGFGEGVRVPAVWGGVSLHRAGVTGVRVRVSAVGRGGGREAVSV 3274
              |    : ||     | |     | :|  | ||||:  |   :|||::  | |    |||:
Db       3727 P---WIAGGLLEVPEDA-----VLLPFAWQGVSLYATGAGALRVRLTKAGDG----AVSL 3774

Qy       3275 VVGDEAGVPVASVDRLELRPVDMGQLRA-VSVSAGRRGSLYAVQ------------WAE 3320
                | :|  | |:  | :||:   :|   :   || | ||| |:             ||
Db       3775 QAADTSGAAVLSLGALVMRPLARRKLDVLLGTDAGER-SLYRVEWQPRLLPAGPPRSWAV 3833

Qy       3321 VGP-------VPVCGQAWAWHEDVGESGGGPV---PGVVVLRCPDAGAGG---------- 3360
              :||       |  |          :  |||    | |  ||   | | |
Db       3834 LGPDADRLAGTPGLGD---------QPDGGPTALYPEVRALR--KALAAGAPRPEAVVLP 3882

Qy       3361 --GGGGGGGGGVGEVVGGVLGVVQGWLGLERFAGSRLVVVTRGAVVAGPEDGPVDVVGAS 3418
                | |      | :     | :| ||   |    : |:|:||||| | | :   |:  |
Db       3883 VLSGAGATPESVRQTTERCLTALQDWLDAEELVDTPLIVLTRGAVAAVPGEEIGDLACAG 3942

Qy       3419 VWGLVRSAQAEHPDRFVLLDLDTDTGTDLDTGAGAGWGVDGGRVAAVVACGEPQLAVRGE 3478
              ||||||||::||| || |:| |                |    | |          ||:|
Db       3943 VWGLVRSARSEHPGRFALVDTD--------------GHPDDRTAL-------PLALRAV 3980

Qy       3479 RLLAARLKRLESSGDVPAQRSGDTRA---RRSDVPAQRSGGVPARRSVDVSGREVLPWLS 3535
                      |: :| : : |:|  |     |:  | :: |  ||            :
Db       3981 ---------LDGAGQL-SLRAGTARTPVLLRAGTPEEQRG--PA------------FDP 4015

Qy       3536 GGSVLVTGGTGVLGAAVARHLAGVCGVRDLLLVSRRGPDAPGAEGLRAELAALGAEVRIV 3595
              |:||||| || ||  :|||||   ||| |||:|| |  | ||: | |||| | ||
Db       4016 AGTVLVTGATGTLGRLLARHLAAEHGVRHLLLLSRGGRAAEGADELAAELAGLEAEPCFA 4075

Qy       3596 ACDVGERREVVRLLEGVPAGCPLTGVVHAAGVLDDATIASLTPERLGTVFAAKVDAALLL 3655
              |||  :|  : |:|  |||  |||||:|||||||| |: :|||||:|||   | |||| |
Db       4076 ACDAADREALARVLAEVPADRPLTGVIHAAGVLDDGTLDALTPERIGTVMRPKADAALNL 4135

Qy       3656 DELTRGMELSAFVLFSSAAGILGSAGQGNYAAANAALDALAYRRRAAGLPGVSLAWGLWE 3715
              ||||   || | :|| ||||||  || ||||||  |||||  ||| ||| ||||||||
Db       4136 HELTRTSPLSVFAVFSGAAGILGRPGQANYAAANTFLDALAQHRRAHGLPAVSLAWGLWG 4195

Qy       3716 EASGMTGHLAGTDHRRIIRSGLHPMSTPDALALFDAALA--LDRPVLLPADLRPA----- 3768
              |:||||||:||| ||: ||| ||:    ||||| |||   : |:|:|  |  |
Db       4196 GATGMTGHLSGTDLRRMRRSGIAPMTHDQGLALFDRALAASAEDPLLVPMRLDLAALVRE 4255

Qy       3769 ------PPLPPLLQDLLPATRR-RTTRTTTTGGAD---NGAQLHARLAGQTHEQQHTTLL 3818
                    :|  |  ||||    |       |||      |     ||||   | :   |:
Db       4256 RAEHGPDAVPGPLLGLLPARAAVRQAAAPVRGGAPAPAGGEGTAERLAGLGEEARLRELV 4315

Qy       3819 ALVRSHIATVLGHTTPDTIPPDRAFRDLGFDSLTAVELRNRLSRTTGLRLPTTLAFDHPN 3878
              |||: :: |||:: || : | | |:|||||||||||||||   ||||||| | || |
Db       4316 RLVRAEVSGVLGYSGPDAVEPGRPFKDLGFDSLTAVELRNRLGAATGLRLPTALVFDRPT 4375

Qy       3879 PTTLTHHLHTQLQPQPD--NAVAPVLAELDKLESALSALDKTDSASE----RVTLRLKSL 3932
                :|  :|    |  :  |      |: | :|: || : |   :    |:|    :|
Db       4376 SQAVAEYLAAELAGPRDGGDTAAAAFEGLEALAAAVGALAEDDLRRDVLRRRLTELAAAL 4435

Qy       3933 MLRWNAPQHPTAESADDDEKFTSATEAEIFKFIDNDL 3969
                :  |  |   :| ||:  || : ::| ||:  |
Db       4436 TPQGRNPSAPAPAPSDLDERLDSANDDDLFAFIEEQL 4472


RESULT 5
US-09-036-987A-6
; Sequence 6, Application US/09036987A
; Patent No. 6143526
;  GENERAL INFORMATION:
;    APPLICANT:  Baltz, Richard H.
;    APPLICANT:  Broughton, Mary C.
;    APPLICANT:  Crawford, Kathryn P.
;    APPLICANT:  Madduri, Krishnamurthy
;,   APPLICANT:  Merlo, Donald J.
;    APPLICANT:  Treadway, Patti J.
;    APPLICANT:  Turner, Jan R.
;    APPLICANT:  Waldron, Clive
;    TITLE OF INVENTION:  Biosynthetic Genes For Spinosyn Insecticide
;    TITLE OF INVENTION:  Production
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dow AgroSciences LLC Patent Department
;      STREET:  9330 Zionsville Road
;      CITY:  Indianapolis
;      STATE:  Indiana
;      COUNTRY:  USA
;      ZIP:  46268
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/036,987A
;      FILING DATE:  09-MAR-1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stuart, Donald R
;      REGISTRATION NUMBER:  28,479
;      REFERENCE/DOCKET NUMBER:  50,608
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317)337-4816
;      TELEFAX:  (317)337-4847
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5588 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-036-987A-6

  Query Match             35.0%;  Score 7281.5;  DB 4;  Length 5588;
  Best Local Similarity   36.1%;  Pred. No. 0;
  Matches 1821;  Conservative  490;  Mismatches 1349;  Indels 1389;  Gaps   86;

Qy         12 PAAGEVLGVADEADGGVVFVFPGQGPQWPGMGRELLDASDVFRESVRACEAAFAPYVDWS 71
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Db        546 PAANVVQGAAD-CKGKVAFVFPGQGSHWQGMARELSESSPVFRRKLAECAAATAPYVDWS 604

Qy         72 VEQVLRDSPDAPGLDRVDVVQPTLFAVMISLAALWRSQGVEPCAVLGHSLGEIAAAHVSG 131
              :  |||  |||| ||| ||:|  |||:|:||| |||| |||| ||:||| |||||||:|
Db        605 LLGVLRGDPDAPALDRDDVIQLALFAMMVSLAELWRSCGVEPAAVVGHSQGEIAAAHVAG 664

Qy        132 GLSLADAARVVTLWSQAQTTLAGTGALVSVAATPDELLPRIAPWTEDNPARLAVAAVNGP 191
              |||  || |::     | : | | | ::::|     :: |||   |     | |||||||
Db        665 ALSLTDAVRIIAARCDAVSALTGKGGMLAIALPESAVVKRIAGLPE-----LTVAAVNGP 719

Qy        192 RSTVVSGAREAVADLVADLTAAQVRTRMIPVDVPAHSPLMYAIEERVVSGLLPITPRPSR 251
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Db        720 GSTVVSGEPSALERLQTELTAENVQTRRVGIDYASHSPQIAQVQGRLLDRLGEVGSEPAE 779

Qy        252 IPFHSSVTGGRLDTRELDAAYWYRNMSSTVRFEPAARLLLQQGPKTFVEMSPHPVLTMGL 311
              | |:|:||| | ||  ||| |||:|:   |||:     :  || : |||:||||:|| |:
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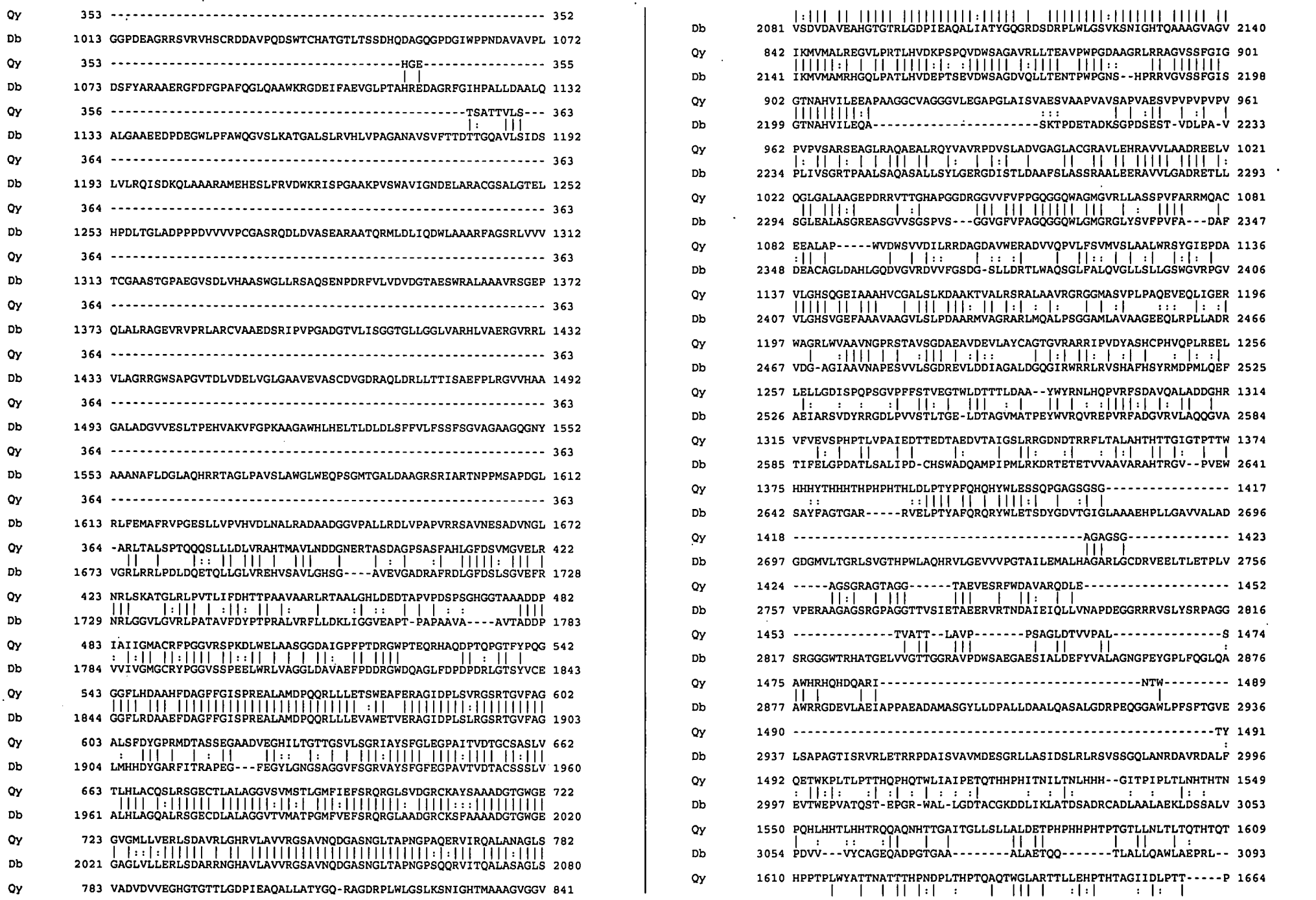
Qy        312 QELAPDLGDTTGTADT--VIMGTLRRGQGTLDHFLTSLA--QLRG--------------- 352
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Db        840 QE-------TLEAADAGGVVVGSLRRGEGGSRRWLTSLAECQVRGLPVNWEQVFLNTGAR 892

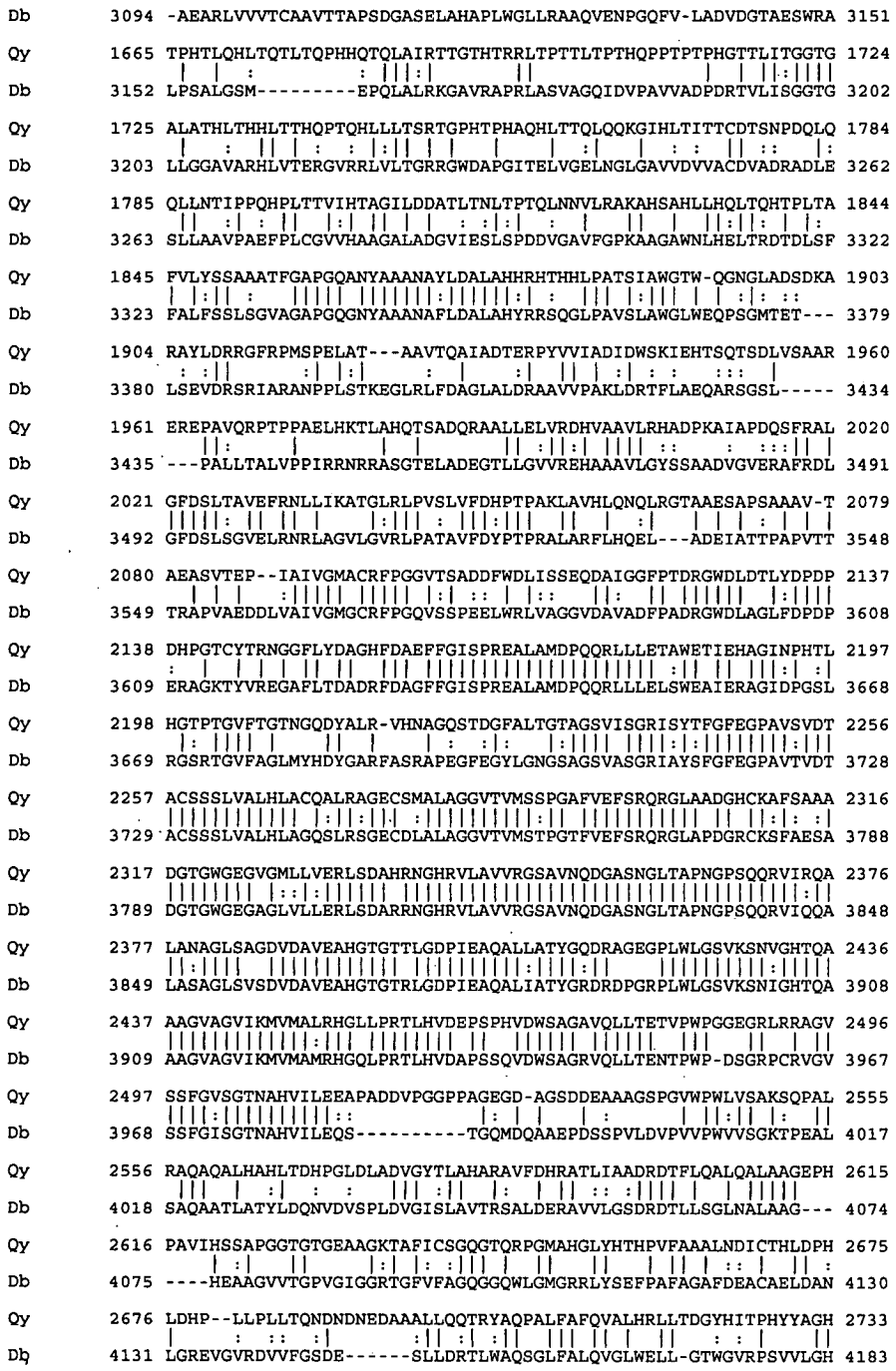
Qy        353 ------------------------------------------------------------ 352

Db        893 RVPLPTYPFQRQRYWLESAEYDAGDLGSVGLLSAEHPLLGAAVTLADAGGFLLTGKLSVK 952

Qy        353 ------------------------------------------------------------ 352

Db        953 TQPWLADHVVGGAILLPGTAFVEMLIRAADQVGCDLIEELSLTTPLVLPATGAVQVQIAV 1012
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Db 3094 -AEARLVVVTCAAVTTAPSDGASELAHAPLWGLLRAAQVENPGQFV-LADVDGTAESWRA 3151
Qy 1665 TPHTLQHLTQTLTQPHHQTQLAIRTTGTHTRRLTPTTLTPTHQPPTPTPHGTTLITGGTG 1724
Db 3152 LPSALGSM---------EPQLALRKGAVRAPRLASVAGQIDVPAVVADPDRTVLISGGTG 3202
Qy 1725 ALATHLTHHLTTHQPTQHLLLTSRTGPHTPHAQHLTTQLQQKGIHLTITTCDTSNPDQLQ 1784
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Qy 1785 QLLNTIPPQHPLTTVIHTAGILDDATLTNLTPTQLNNVLRAKAHSAHLLHQLTQHTPLTA 1844
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Qy 3639 ERLGTVFAAKVDAALLLDELTRGMELSAFVLFSSAAGILGSAGQGNYAAANAALDALAYR 3698
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Qy       3869 PTTLAFDHPNPTTLTHHLHTQL----QPQP-----DNAVAPVLAELDKLESALSALDKTD 3919
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Db       5329 LVKVAAQLR 5337
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RESULT 6
US-09-370-700-6
; Sequence 6, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/370,700
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/36987
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 5588
; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-6

Query Match 35.0%; Score 7281.5; DB 4; Length 5588;
Best Local Similarity 36.1%; Pred. No. 0;
Matches 1821; Conservative 490; Mismatches 1349; Indels 1389; Gaps 86;

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Qy        252 IPFHSSVTGGRLDTRELDAAYWYRNMSSTVRFEPAARLLLQQGPKTFVEMSPHPVLTMGL 311
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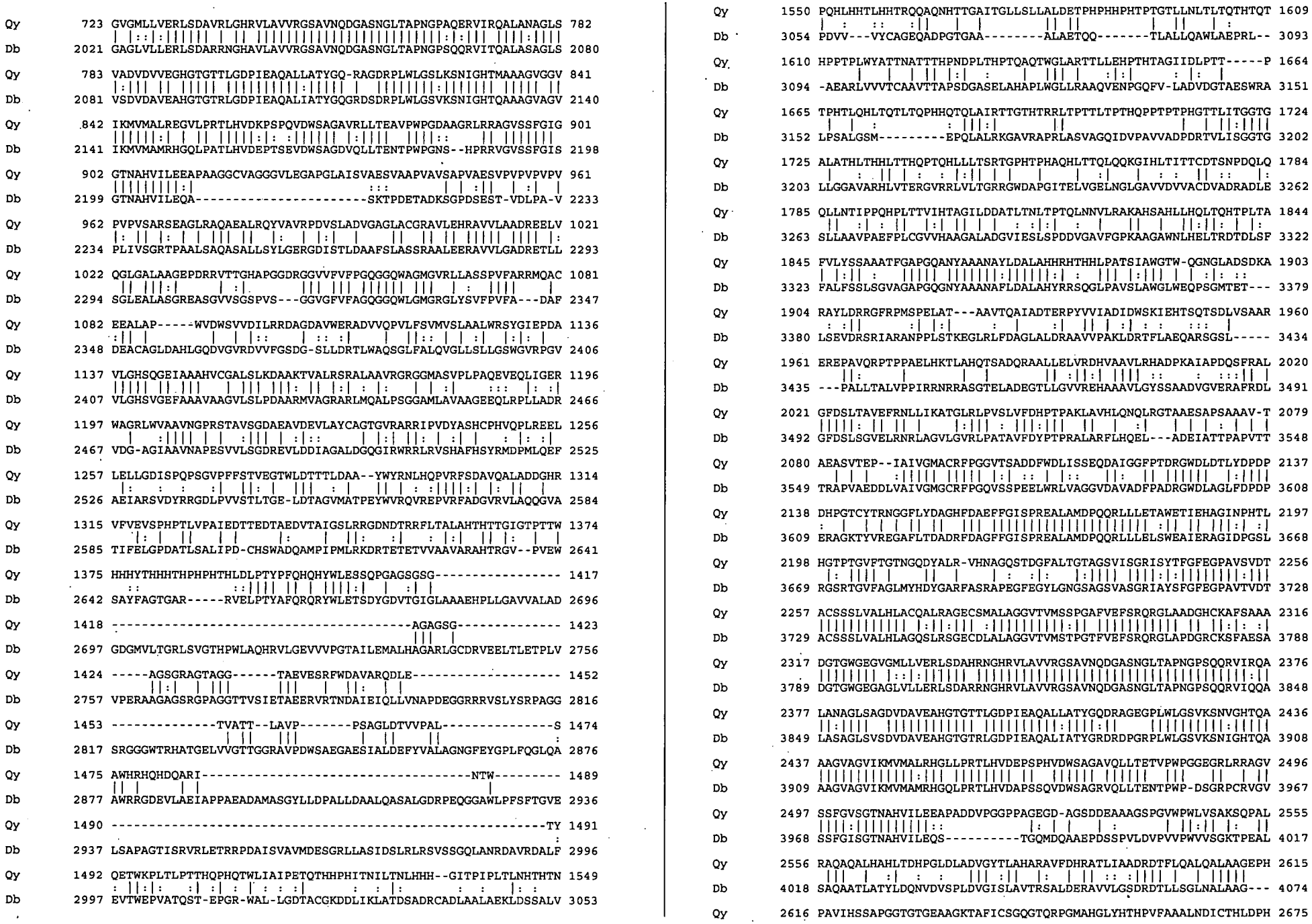
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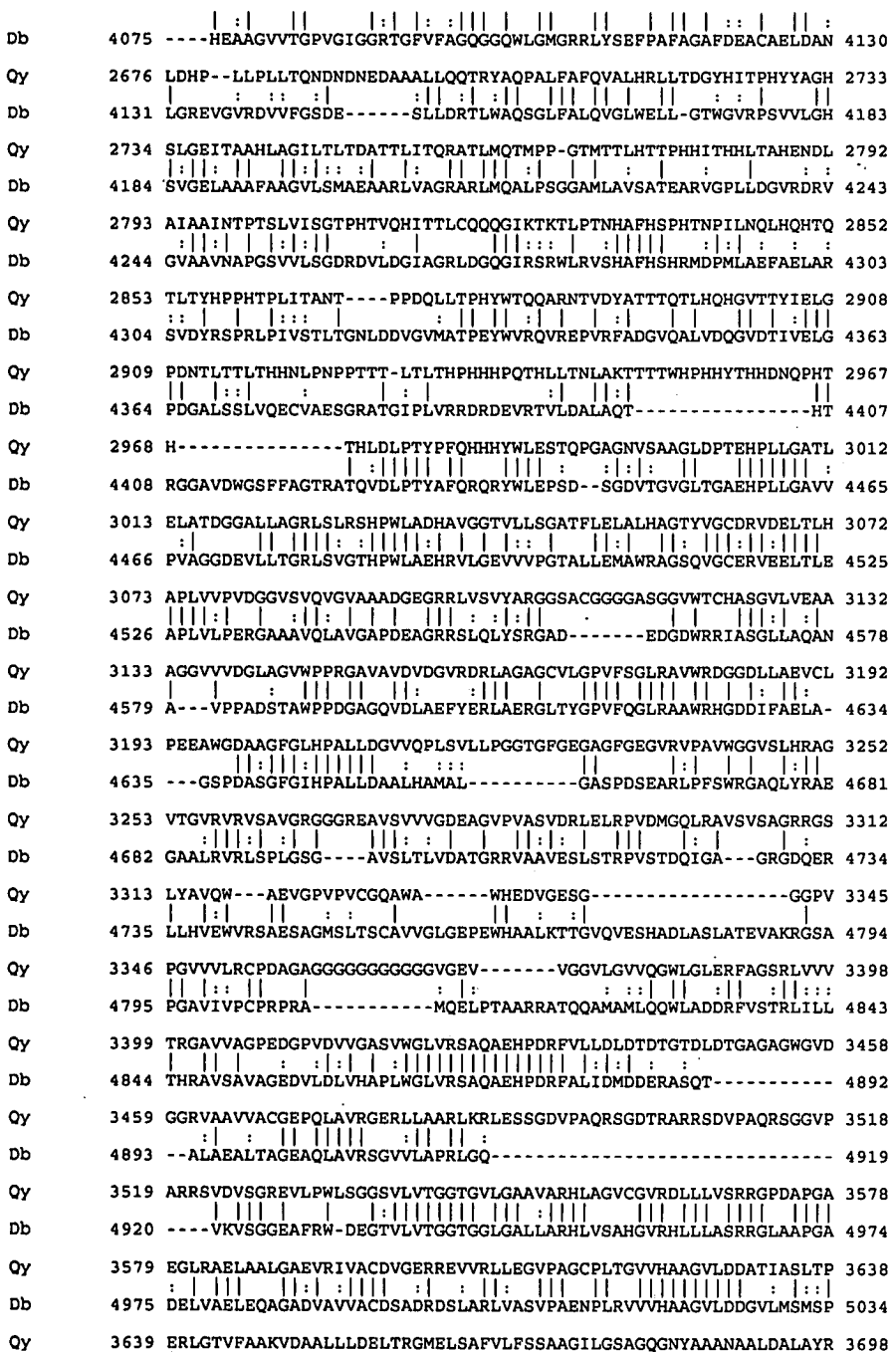
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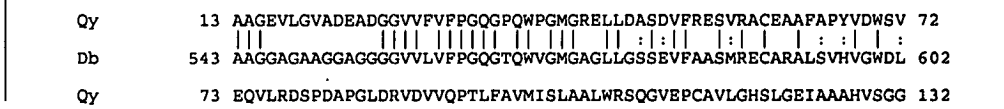
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RESULT 7
US-08-804-227C-14
; Sequence 14, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
; APPLICANT: DeHoff, Bradley S.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rosteck, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS G. PLANT 1501
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCI(DOS) Text only
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,227C
; FILING DATE: February 21, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Plant, Thomas, G.
; REGISTRATION NUMBER: 35,784
; REFERENCE/DOCKET NUMBER: X-8231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-2459
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4545 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-804-227C-14

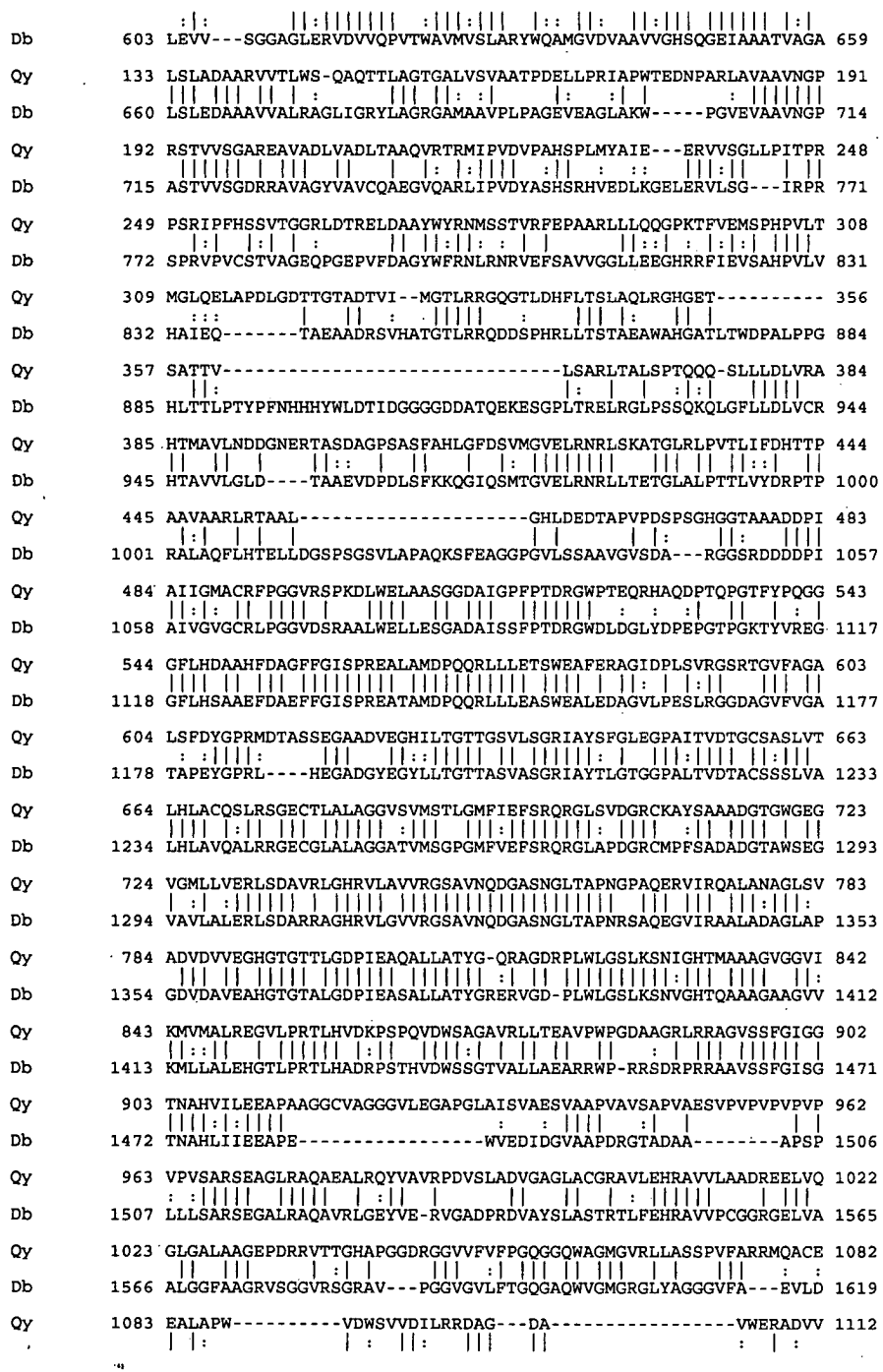
Query Match 34.8%; Score 7255; DB 2; Length 4545;
Best Local Similarity 41.8%; Pred. No. 0;
Matches 1792; Conservative 452; Mismatches 1428; Indels 616; Gaps 96;

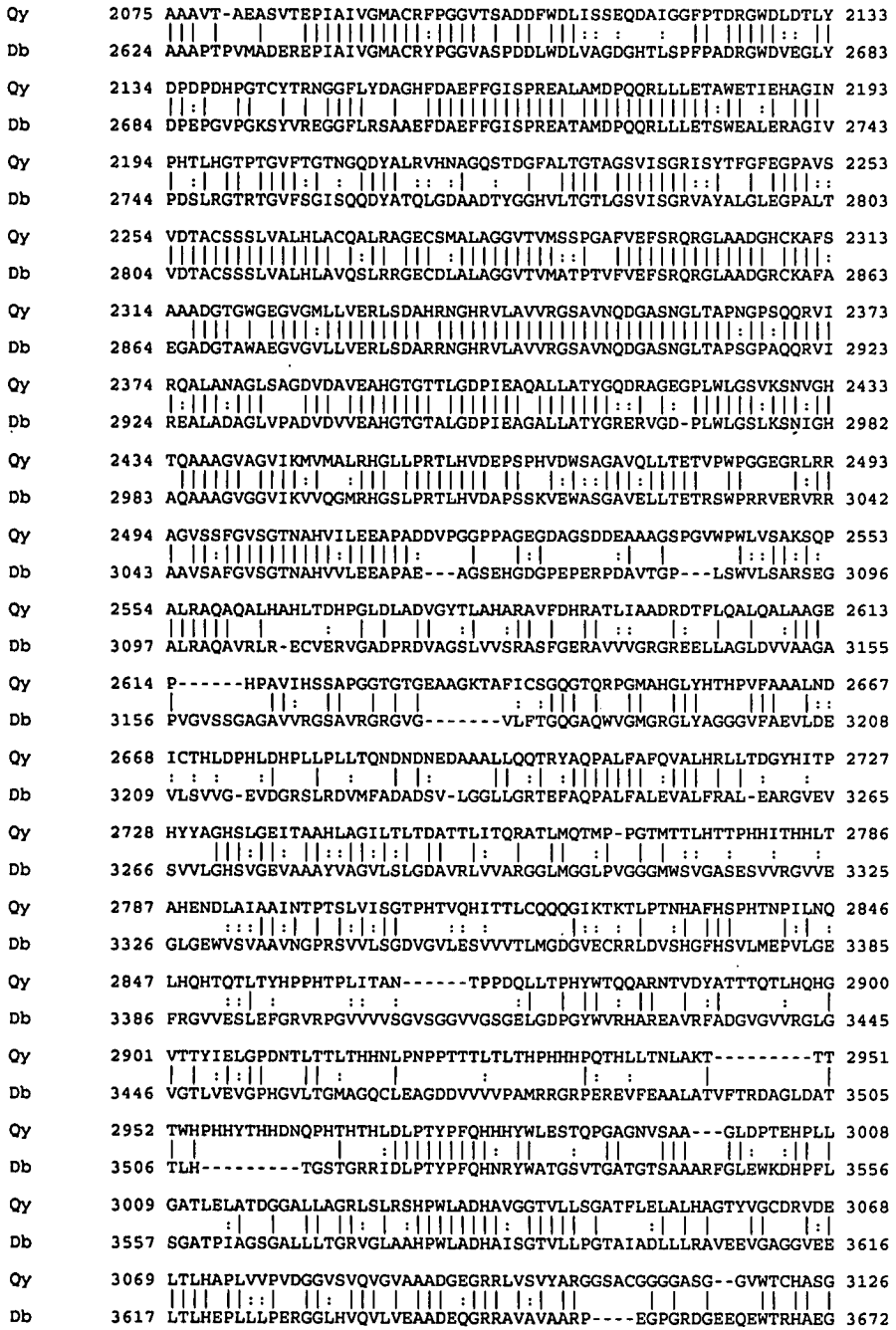


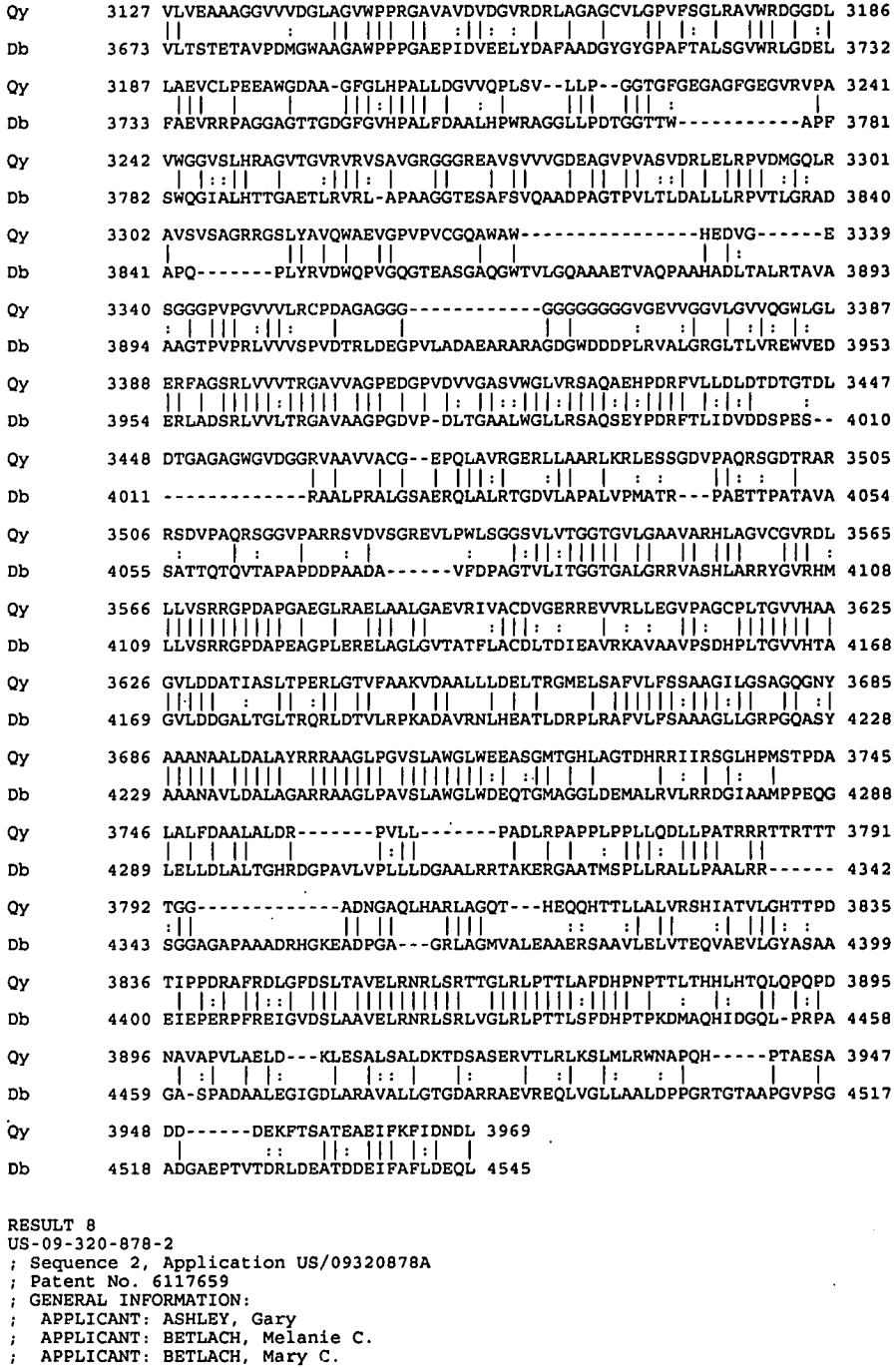
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Qy         13 AAGEVLGVADEADGGVVFVFPGQGPQWPGMGRELLDASDVFRESVRACEAAFAPYVDWSV 72

Db        543 AAGGAGAAGGAGGGGVVLVFPGQGTQWVGMGAGLLGSSEVFAASMRECARALSVHVGWDL 602

Qy         73 EQVLRDSPDAPGLDRVDVVQPTLFAVMISLAALWRSQGVEPCAVLGHSLGEIAAAHVSGG 132
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Db 603 LEVV---SGGAGLERVDVVQPVTWAVMVSLARYWQAMGVDVAAVVGHSQGEIAAATVAGA 659
Qy 133 LSLADAARVVTLWS-QAQTTLAGTGALVSVAATPDELLPRIAPWTEDNPARLAVAAVNGP 191
Db 660 LSLEDAAAVVALRAGLIGRYLAGRGAMAAVPLPAGEVEAGLAKW-----PGVEVAAVNGP 714
Qy 192 RSTVVSGAREAVADLVADLTAAQVRTRMIPVDVPAHSPLMYAIE---ERVVSGLLPITPR 248
Db 715 ASTVVSGDRRAVAGYVAVCQAEGVQARLIPVDYASHSRHVEDLKGELERVLSG---IRPR 771
Qy 249 PSRIPPHSSVTGGRLDTRELDAAYWYRNMSSTVRPEPAARLLLQQGPKTFVEMSPHPVLT 308
Db 772 SPRVPVCSTVAGEQPGEPVFDAGYWFRNLRNRVEFSAVVGGLLEEGHRRFIEVSAHPVLV 831
Qy 309 MGLQELAPDLGDTTGTADTVI--MGTLRRGQGTLDHFLTSLAQLRGHGET---------- 356
Db 832 HAIEQ-------TAEAADRSVHATGTLRRQDDSPHRLLTSTAEAWAHGATLTWDPALPPG 884
Qy 357 SATTV-------------------------------LSARLTALSPTQQQ-SLLLDLVRA 384
Db 885 HLTTLPTYPFNHHHYWLDTIDGGGGDDATQEKESGPLTRELRGLPSSQKQLGFLLDLVCR 944
Qy 385 HTMAVLNDDGNERTASDAGPSASFAHLGFDSVMGVELRNRLSKATGLRLPVTLIFDHTTP 444
Db 945 HTAVVLGLD----TAAEVDPDLSFKKQGIQSMTGVELRNRLLTETGLALPTTLVYDRPTP 1000
Qy 445 AAVAARLRTAAL--------------------GHLDEDTAPVPDSPSGHGGTAAADDPI 483
Db 1001 RALAQFLHTELLDGSPSGSVLAPAQKSFEAGGPGVLSSAAVGVSDA---RGGSRDDDDPI 1057
Qy 484 AIIGMACRFPGGVRSPKDLWELAASGGDAIGPFPTDRGWPTEQRHAQDPTQPGTFYPQGG 543
Db 1058 AIVGVGCRLPGGVDSRAALWELLESGADAISSFPTDRGWDLDGLYDPEPGTPGKTYVREG 1117
Qy 544 GFLHDAAHFDAGFFGISPREALAMDPQQRLLLETSWEAFERAGIDPLSVRGSRTGVFAGA 603
Db 1118 GFLHSAAEFDAEFFGISPREATAMDPQQRLLLEASWEALEDAGVLPESLRGGDAGVFVGA 1177
Qy 604 LSFDYGPRMDTASSEGAADVEGHILTGTTGSVLSGRIAYSFGLEGPAITVDTGCSASLVT 663
Db 1178 TAPEYGPRL----HEGADGYEGYLLTGTTASVASGRIAYTLGTGGPALTVDTACSSSLVA 1233
Qy 664 LHLACQSLRSGECTLALAGGVSVMSTLGMFIEFSRQRGLSVDGRCKAYSAAADGTGWGEG 723
Db 1234 LHLAVQALRRGECGLALAGGATVMSGPGMFVEFSRQRGLAPDGRCMPFSADADGTAWSEG 1293
Qy 724 VGMLLVERLSDAVRLGHRVLAVVRGSAVNQDGASNGLTAPNGPAQERVIRQALANAGLSV 783
Db 1294 VAVLALERLSDARRAGHRVLGVVRGSAVNQDGASNGLTAPNRSAQEGVIRAALADAGLAP 1353
Qy 784 ADVDVVEGHGTGTTLGDPIEAQALLATYG-QRAGDRPLWLGSLKSNIGHTMAAAGVGGVI 842
Db 1354 GDVDAVEAHGTGTALGDPIEASALLATYGRERVGD-PLWLGSLKSNVGHTQAAAGAAGVV 1412
Qy 843 KMVMALREGVLPRTLHVDKPSPQVDWSAGAVRLLTEAVPWPGDAAGRLRRAGVSSFGIGG 902
Db 1413 KMLLALEHGTLPRTLHADRPSTHVDWSSGTVALLAEARRWP-RRSDRPRRAAVSSFGISG 1471
Qy 903 TNAHVILEEAPAAGGCVAGGGVLEGAPGLAISVAESVAAPVAVSAPVAESVPVPVPVPVP 962
Db 1472 TNAHLIIEEAPE----------------WVEIDGVAAPDRGTADAA--------APSP 1506
Qy 963 VPVSARSEAGLRAQAEALRQYVAVRPDVSLADVGAGLACGRAVLEHRAVVLAADREELVQ 1022
Db 1507 LLLSARSEGALRAQAVRLGEYVE-RVGADPRDVAYSLASTRTLFEHRAVVPCGGRGELVA 1565
Qy 1023 GLGALAAGEPDRRVTTGHAPGGDRGGVVFVFPGQGGQWAGMGVRLLASSPVFARRMQACE 1082
Db 1566 ALGGFAAGRVSGGVRSGRAV---PGGVGVLFTGQGAQWVGMGRGLYAGGGVFA---EVLD 1619
Qy 1083 EALAPW----------VDWSVVDILRRDAG---DA----------------VWERADVV 1112
Db 1620 EVLSMVGEVDGRSLRDVMFGDVDV---DAGAGADAGAGAGAGVGSGSGSVGGLLGRTEFA 1676
Qy 1113 QPVLFSVMVSLAALWRSYGIEPDAVLGHSQGEIAAAHVCGALSLKDAAKTVALRSRALAA 1172
Db 1677 QPALPALEVALFRALEARGVEVSVVLGHSVGEVAAAYVAGVLSLGDAVRLVVARGGLMGG 1736
Qy 1173 VRGRGGMASVPLPAQEVEQLI---GERWAGRLWVAAVNGPRSTAVSGDAEAVDEVLAYCA 1229
Db 1737 LPVGGGMWSVGASESVVRGVVEGLGE-WVS---VAAVNGPRSVVLSGDVGVLESVVASLM 1792
Qy 1230 GTGVRARRIPVDYASHCPHVQPLREE---LLELL--GDISPQPSGVPFFSTVEGTWLDTT 1284
Db 1793 GDGVECRRLDVSHGFHSVLMEPVLGEFRGVVESLEFGRVRP---GVVVVSGVSGGVVGSG 1849
Qy 1285 TL-DAAYWYRNLHQPVRFSDAVQALADDGHRVFVEVSPHPTLVPAIEDTTEDTAEDVTAI 1343
Db 1850 ELGDPGYWVRHAREAVRFADGVGVVRGLGVGTLVEVGPHGVLT-GMAGECLGAGDDVVVV 1908
Qy 1344 GSLRRGDNDTRRFLTALAHTHTTGIGTPTTWHHHYTHHHTHPHPHTHLDLPTYPFQHQHY 1403
Db 1909 PAMRRGRAEREVFEAALATVFTRDAGLDATALHTGS-------TGRRIDLPTYPFQRDRY 1961
Qy 1404 WLESSQPGAGSGSGAGAGSGAGS---GRAGTAGGTAEVESRFWDAVARQDLETVATTLAV 1460
Db 1962 WLDPVRTAVTGVEPAGSPADARATERGRSTTAG--------------------------- 1994
Qy 1461 PPSAGLDTVVPALSAWHRHQHDQARINTWTYQETWKPLTL------PTTHQPHQTWLIAI 1514
Db 1995 ----------------------------IRYRVAWQPAVVDRGNPGPAGHV-----LLLA 2021
Qy 1515 PETQTHHPHITNILTNLHHHGITPIPLTLNHTHTNPQHLHHTLHHTRQQAQNHTTGAITG 1574
Db 2022 PDEDT---ADSG 2030
Qy 1575 LLSLLALDETPHPHHPHT---PTGT-------LLN------------------------ 1599
Db 2031 LAPAIARELAVRGAEVHTVAVPVGTGREAAGDLLRAAGDGAARSTRVLWLAPAEPDAADA 2090
Qy 1600 LTLTQTHTQTHPPTPLWYATTNATTTHPNDPLTHPTQAQTWGLARTTLLEHPTHTAGIID 1659
Db 2091 VALVQALGEAVPEAPLWITTREAAAVRP-DETPSVGGAQLWGLGQVAALELGRRWGGLAD 2149
Qy 1660 LPTTPTPHTLQHLTQTLTQPHHQTQLAIRTTGTHTRRLTPTTL-------TPTHQPPTPT 1712
Db 2150 LPGSASPAVLRTFVGALL-AGGENQFAVRPSGVHVRRVVPAPVPVPASARTVTTAPATAV 2208
Qy 1713 ------------------PHGTTLITGGTGALATHLTHHLTTHQPTQHLLLTSRTGPHTP 1754
Db 2209 GEDARNDTSDVVVPDDRWSSGTVLITGGTGALGAQVARRL-ARSGAARLLLVGRRGAAGP 2267
Qy 1755 HAQHLTTQLQQKGIHLTITTCDTSNPDQLQQLLNTIPPQHPLTTVIHTAGILDDATLTNL 1814
Db 2268 GVGELVEELTALGSEVAVEACDVADRDALAALLAGLPEERPLVAVLHAAGVLDDGVLDSL 2327
Qy 1815 TPTQLNNVLRAKAHSAHLLHQLTQHTPLTAFVLYSSAAATFGAPGQANYAAANAYLDALA 1874
Db 2328 TSDRVDAVLRDKVTAARHLDELTADLPLDAFVLFSSIVGVWGNGGQAVYAAANAALDALA 2387
Qy 1875 HHRHTHHLPATSIAWGTWQGNGLADSDKARAYLDRRGFRPMSPELA----------T 1921
Db 2388 QRRRARGARAASIAWGPWAGAGMASGTAAKSF-ERDGVTALDPERALDVLDDVVGAGGTS 2446
Qy 1922 AAVTQAIADTERPYVVIADIDW------SKIEHTSQTSDLVSAAR--------EREPAVQ 1967
Db 2447 AAGTHAAGESS---LLVADVDWETFVGRSVTRRTWSLFDGVSAARSARAGHAADDRAALT 2503
Qy 1968 RPTPPAELHKTLAHQ----------TSADQRAALLELVRDHVAAVLRHADPKAIAPD 2014
Db 2504 PGTRPGDGAPGGSGQDGGEGRPWLSVGPSPAERRRALLTLVRSEAAGILRHASADAVDPE 2563
Qy 2015 QSFRALGFDSLTAVEFRNLLIKATGLRLPVSLVFDHPTPAKLAVHLQNQLRGTAAESAPS 2074
Db 2564 LAFRSAGFDSLTVLELRNRLTAATGLNLPNTLLFDHPTPLSLASHLHDELFGPDSEAEPA 2623





RESULT 8
US-09-320-878-2
; Sequence 2, Application US/09320878A
; Patent No. 6117659
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.

```
;  APPLICANT: McDANIEL, Robert
;  APPLICANT: TANG, Li
;  TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
;  FILE REFERENCE: 300622002120
;  CURRENT APPLICATION NUMBER: US/09/320,878A
;  CURRENT FILING DATE: 1999-05-27
;  EARLIER APPLICATION NUMBER: CIP OF 09/141,908
;  EARLIER FILING DATE: 1998-08-28
;  EARLIER APPLICATION NUMBER: CIP OF 09/073,538
;  EARLIER FILING DATE: 1998-05-06
;  EARLIER APPLICATION NUMBER: CIP OF 08/846,247
;  EARLIER FILING DATE: 1997-04-30
;  EARLIER APPLICATION NUMBER: 60/119,139
;  EARLIER FILING DATE: 1999-02-08
;  EARLIER APPLICATION NUMBER: 60/100,880
;  EARLIER FILING DATE: 1998-09-22
;  EARLIER APPLICATION NUMBER: 60/087,080
;  EARLIER FILING DATE: 1998-05-28
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 3739
;   TYPE: PRT
;   ORGANISM: Streptomyces venezuelae
US-09-320-878-2

  Query Match             34.0%;  Score 7079;  DB 3;  Length 3739;
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Db         32 AKAGEPVAIVGMACRLPGGVASPEDLWRLVAGGEDAISEFPQDRGWDVEGLYDPNPEATG 91

Qy        537 TFYPQGGGFLHDAAHFDAGFFGISPREALAMDPQQRLLLETSWEAFERAGIDPLSVRGSR 596
               | :  |||::|  ||| ||||||||||||||||||||| |||||| |||   : ||:
Db         92 KSYAREAGFLYEAGEFDADFFGISPREALAMDPQQRLLLEASWEAFEHAGIPAATARGTS 151

Qy        597 TGVFAGALSFDYGPRMDTASSEGAADVEGHILTGTTGSVLSGRIAYSFGLEGPAITVDTG 656
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Db        152 VGVFTGVMYHDYATRL-TDVPEG---IEGYLGTGNSGSVASGRVAYTLGLEGPAVTVDTA 207

Qy        657 CSASLVTLHLACQSLRSGECTLALAGGVSVMSTLGMFIEFSRQRGLSVDGRCKAYSAAAD 716
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Db        208 CSSSLVALHLAVQALRKGEVDMALAGGVTVMSTPSTFVEFSRQRGLAPDGRSKSFSSTAD 267

Qy        717 GTGWGEGVGMLLVERLSDAVRLGHRVLAVVRGSAVNQDGASNGLTAPNGPAQERVIRQAL 776
              || | ||||:|||||||| | |||:||||||:||||||||:||||||||:|:||||:||
Db        268 GTSWSEGVGVLLVERLSDARRKGHRILAVVRGTAVNQDGASSGLTAPNGPSQQRVIRRAL 327

Qy        777 ANAGLSVADVDVVEGHGTGTTLGDPIEAQALLATYGQ-RAGDRPLWLGSLKSNIGHTMAA 835
              |:| |: :|||||| ||||| |||||||||::||||| | |::|| |||||||||| ||
Db        328 ADARLTTSDVDVVEAHGTGTRLGDPIEAQAVIATYGQGRDGEQPLRLGSLKSNIGHTQAA 387

Qy        836 AGVGGVIKMVMALREGVLPRTLHVDKPSPQVDWSAGAVRLLTEAVPWPGDAAGRLRRAGV 895
              ||| |||||| |:| |||||:||||:||: |||||||| ||||| ||      | |||| |
Db        388 AGVSGVIKMVQAMRHGVLPKTLHVEKPTDQVDWSAGAVELLTEAMDWPDKGDGGLRRAAV 447

Qy        896 SSFGIGGTNAHVILEEAPAAGGCVAGGGVLEGAPGLAISVAESVAAPVAVSAPVAESVPV 955
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Db        448 SSFGVSGTNAHVVLEEAPA----------------------------AEETPASEATPA 478

Qy        956 PVPVP----VPVPVSARSEAGLRAQAEALRQYVAVRPDVSLADVGA---GLACGRAVLEH 1008
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Db        479 VEPSVGAGLVPWLVSAKTPAALDAQIGRLAAF-ASQGRTDAADPGAVARVLAGGRAEFEH 537

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Db        538 RAVVLGTGQDDFAQALTAPEGLIRGTP----------SDVGRVAFVFPGQGTQWAGMGA 586

Qy       1066 RLLASSPVFARRMQACEEALAPWVDWSVVDILRRDAGDAVWERADVVQPVLFSVMVSLAA 1125
               ||  |  ||  |  || ||: :||||:  ::|:  |     || |||||| |:||||||
Db        587 ELLDVSKEFAAAMAECESALSRYVDWSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLAK 646

Qy       1126 LWRSYGIEPDAVLGHSQGEIAAAHVCGALSLKDAAKTVALRSRALAA-VRGRGGMASVPL 1184
              :|: :|: | ||:|||||||||:| |||:| |||: | |||::||  : |:||| |: |
Db        647 VWQHHGVTPQAVVGHSQGEIAAAYVAGALTLDDAARVVTLRSKSIAAHLAGKGGMISLAL 706

Qy       1185 ----PAQEVEQLIGERWAGRLWVAAVNGPRSTAVSGDAEAVDEVLAYCAGTGVRARRIPV 1240
                  | :| | |      | :|||||| :| ||||   : |:   |  ||||| |||
Db        707 SEEATRQRIENLHG------LSIAAVNGPTATVVSGDPTQIQELAQACEADGVRARIIPV 760

Qy       1241 DYASHCPHVQPLREELLELLGDISPQPSGVPFFSTVEGTWLDTTTLDAAYWYRNLHQPVR 1300
              ||||| ||: :  || |:|  :||:   ||||||:|| |:    ||  ||||||   |
Db        761 DYASHSAHVETIESELAEVLAGLSPRTPEVPFFSTLEGAWITEPVLDGTYWYRNLRHRVG 820

Qy       1301 FSDAVQALA-DDGHRVFVEVSPHPTLVPAIEDTTEDTAEDVTAIGSLRRGDNDTRRFLTA 1359
              |: ||: || |:|   |:||| || |   : :|       || :|:|||       | :|:
Db        821 FAPAVETLATDEGFTHFIEVSAHPVLTMTLPET-------VTGLGTLRREQGGQERLVTS 873

Qy       1360 LAHTHTTGIG------TPTTWHHHYTHHHTHPHPHTHLDLPTYPFQHQHYWLESSQPGAG 1413
              ||   | |:        ||   |             | :|||| || :|||| |    |
Db        874 LAEAWTNGLTIDWAPVLPTATGH------------HPELPTYAFQRRHYWLHDSPAVQG 920

Qy       1414 SGSGAGAGSGAGSGRAGTAGGTAEVESRFWDAVARQDLETVATTLAVPPSAGLDTVVPAL 1473
              |
Db        921 SVQ---------------------------------------------------------- 923

Qy       1474 SAWHRHQHDQARINTWTYQETWKPLTLPTTHQP---HQTWLIAIPETQTHHPHITNILTN 1530
                        ::| |:  || | :    :        ||: :|| ::       :|
Db        924 ------------DSWRYRIDWKRLAVADASERAGLSGRWLVVVPEDRS--AEAAPVLAA 968

Qy       1531 LHHHGITPIPLTLNHTHTNPQHLHHTLHHTRQQAQNHTTGAITGLLSLLALDETPHPHHP 1590
              |   |  |: | :     :|      |  | :|     ||: |:||||| ||: || ||
Db        969 LSGAGADPVQLDV-----SPLGDRQRLAATLGEALAAAGGAVDGVLSLLAWDESAHPGHP 1023

Qy       1591 HTPT-GTLLNLTLTQTHTQTHPPTPLWYATTNATTTHPNDPLTHPTQAQTWGLARTTLLE 1649
                | ||  ||| | |          ||| |  | :    | :| | ||  ||: |   ||
Db       1024 APFTRGTGATLTLVQALEDAGVAAPLWCVTHGAVSVGRADHVTSPAQAMVWGMGRVAALE 1083

Qy       1650 HPTHTAGIIDLPTTPTPHTLQHLTQTLTQPHHQTQLAIRTTGTHTRRLTPTTLTPTHQPP 1709
              ||    |:||||:       | :|  |      : |:|:| :|   |||   :| | |
Db       1084 HPERWGGLIDLPSDADRAALDRMTTVLAGGTGEDQVAVRASGLLARRLVRASL-PAHGTA 1142

Qy       1710 TP--TPHGTTLITGGTGALATHLTHHLTTHQPTQHLLLTSRTGPH----TPHAQH----- 1758
              :|     || |:||     |       |       || |: :|     | |
Db       1143 SPWWQADGTVLVTGAEEPAAAEAARRLARDGAGHLLLHTTPSGSEGAEGTSGAAEDSGLA 1202

Qy       1759 -LTTQLQQKGIHLTITTCDTSNPDQLQQLLNTIPPQHPLTTVIHTAGILDDATLTNLTPT 1817
                | :|   |   |: ||| :: :  :||  :   |||: |:|   :|   |
Db       1203 GLVAELADLGATATVVTCDLTDAEAAARLLAGVSDAHPLSAVLHLPPTVDSEPLAATDAD 1262

Qy       1818 QLNNVLRAKAHSAHLLHQLTQHTPLT-----AFVLYSSAAATFGAPGQANYAAANAYLDA 1872
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Db       1263 ALARVVTAKATAALHLDRLLREAAAAGGRPPVLVLFSSVAAIWGGAGQGAYAAGTAFLDA 1322

Qy       1873 LAHHRHTHHLPATSIAWGTWQGNGLADSDKARAYLDRRGFRPMSPELATAAVTQAI--AD 1930
              ||          ||:||  |:|: : :       | | | ||::|  |  |:  |:   |
Db       1323 LAGQHRADGPTVTSVAWSPWEGSRVTEGATGER-LRRLGLRPLAPATALTALDTALGHGD 1381

Qy       1931 TERPYVVIADIDWSKIE---HTSQTSDLVSAARAREPAV--QRPTPPAE---LHKTLAHQ 1982
              |    | |||:|||       |::   |::    |   |:  |: | |  |:   | : |
Db       1382 TA---VTIADVDWSSFAPGFTTARPGTLLADLPEARRALDEQQSTTAADDTVLSRELGAL 1438

Qy       1983 TSADQRAALLELVRDHVAAVLRHADPKAIAPDQSFRALGFDSLTAVEFRNLLIKATGLRL 2042
              | |:|:  : ||||:|:| || |  |:|:   ::|| |||||||||| || |  |||| |
Db       1439 TGAEQQRRMQELVREHLAVVLNHPSPEAVDTGRAFRDLGFDSLTAVELRNRLKNATGLAL 1498

Qy       2043 PVSLVFDHPTPAKLAVHLQNQLRGTAAESAPSAAAVTAEASV-TEPIAIVGMACRFPGGV 2101
              | :||||:|||  ||  |  :: |   | | :   :  :  |  ||:|||||||| ||||
Db       1499 PATLVFDYPTPRTLAEFLLAEILG---EQAGAGEQLPVDGGVDDEPVAIVGMACRLPGGV 1555

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                | :| | |::  :||| ||| |||||:: |||||||  |  | | |||| :|| |||:|
Db       1556 ASPEDLWRLVAGGEDAISGFPQDRGWDVEGLYDPDPDASGRTYCRAGGFLDEAGEFDADF 1615
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Db       3688 APAAGGRPELAARLRALAA-------ALGDDGDDATDLDEASDDDLFSFIDKELG 3735


RESULT 9
US-09-428-517-3
; Sequence 3, Application US/09428517
; Patent No. 6251636
; GENERAL INFORMATION:
;  APPLICANT: Betlach, Mary C.
;  APPLICANT: Shah, Sanjay Krishnakant
;  APPLICANT: McDaniel, Robert
;  APPLICANT: Tang, Li
;  TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
;  FILE REFERENCE: 30062-20029.00
;  CURRENT APPLICATION NUMBER: US/09/428,517
;  CURRENT FILING DATE: 1999-10-28
;  EARLIER APPLICATION NUMBER: 60/120,254
;  EARLIER FILING DATE: 1999-02-16
;  EARLIER APPLICATION NUMBER: 60/106,100
;  EARLIER FILING DATE: 1998-10-29
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 3816
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Recombinant
;   OTHER INFORMATION: Oleandolide PKS
US-09-428-517-3

  Query Match             33.8%;  Score 7041.5;  DB 4;  Length 3816;
  Best Local Similarity   41.7%;  Pred. No. 0;
  Matches 1654;  Conservative  450;  Mismatches 1206;  Indels  655;  Gaps   82;

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              |:||||  ||| ||||: ||: |||| ::||: :  || ||||  :: :  ||   || |
Db         30 DEPIAITSMACHFPGGIESPEQLWELLSAGGEVLSEFPDDRGWDLDEIYHPDPEHSGTSY 89

Qy        540 PQGGGFLHDAAHFDAGFFGISPREALAMDPQQRLLLETSWEAFERAGIDPLSVRGSRTGV 599
               : ||||  |  ||  ||||||||||||||||||||||||: |||||:|| :::||||||
Db         90 VRHGGFLDHATQFDTDFFGISPREALAMDPQQRLLLETSWQLFERAGVDPHTLKGSRTGV 149

Qy        600 FAGALSFDYGPRMDTASSEGAADVEGHILTGTTGSVLSGRIAYSFGLEGPAITVDTGCSA 659
              | ||    |  |:||      |: ||::|||   :|:||||:|:|||||||:|||| ||:
Db        150 FVGAAHMGYADRVDTP----PAEAEGYLLTGNASAVVSGRISYTFGLEGPAVTVDTACSS 205

Qy        660 SLVTLHLACQSLRSGECTLALAGGVSVMSTLGMFIEFSRQRGLSVDGRCKAYSAAADGTG 719
              ||| |||| |:|| |||:||: |||:|||   :|:||||||||: ||| ||::|:||| |
Db        206 SLVALHLAVQALRRGECSLAVVGGVAVMSDPKVFVEFSRQRGLARDGRSKAFAASADGFG 265

Qy        720 WGEGVGMLLVERLSDAVRLGHRVLAVVRGSAVNQDGASNGLTAPNGPAQERVIRQALANA 779
              : ||| :||:|||||| |||||||||||||||||||||||| |||||:|:|||| |||:|
Db        266 FAEGVSLLLLERLSDARRLGHRVLAVVRGSAVNQDGASNGLAAPNGPSQQRVIRAALADA 325

Qy        780 GLSVADVDVVEGHGTGTTLGDPIEAQALLATYGQ-RAGDRPLWLGSLKSNIGHTMAAAGV 838
              ||: ||||||| ||||| |||||||||||||||  |   ||:||||:|||||| ||||
Db        326 GLAPADVDVVEAHGTGTRLGDPIEAQALLATYGQGRTSGRPVWLGSVKSNIGHTQAAAGV 385

Qy        839 GGVIKMVMALREGVLPRTLHVDKPSPQVDWSAGAVRLLTEAVPWPGDAAGRLRRAGVSSF 898
               ||:|||:||  ||:|:|||||:||| |||| ||| ||||  ||  :|  ||||||:|:|
Db        386 AGVMKMVLALERGVVPKTLHVDEPSPHVDWSTGAVELLTEERPWEPEAE-RLRRAGISAF 444

Qy        899 GIGGTNAHVILEEAPAAGGCVAGGGVLEGAPGLAISVAESVAAPVAVSAPVAESVPVPVP 958
              |: |||||||:|||||                                  | | |
Db        445 GVSGTNAHVIVEEAPAE------------------------------------PEPEP 466

Qy        959 VP-----------VPVPVSARSEAGLRAQAEALRQYVAVRPDVSLADVGAGLACGRAVLE 1007
              |           ||  || |    ||||| | :|:      : |||  |   |:| |
Db        467 EPGTRVVAAGDLVVPWVVSGRDAGALRAQAARLAAHVS-STGAGVVDVGWSLVATRSVFE 525

Qy       1008 HRAVVLAADREELVQGLGALAAGEPDRRVTTGHAPGGDRGGVVFVFPGQGGQWAGMGVRL 1067
              ||||::  | : :   |  |||     | :| ||   |  |||||||| || ||  |
```

```
Db        526 HRAVMVGTDLDSMAGSLAGFAAGGVVPGVVSGVAPAEGR-RVVFVFPGQGSQWVGMAAGL 584

Qy       1068 LASSPVFARRMQACEEALAPWVDWSVVDILRRDAGDAVWERADVVQPVLFSVMVSLAALW 1127
              | : ||||  :  |   | |   ||:|::||   |:||  | ||||| |::||||||  |
Db        585 LDACPVFAEAVAECAAVLDPLTGWSLVEVLR--GGEAVLGRVDVVQPALWAVMVSLARTW 642

Qy       1128 RSYGIEPDAVLGHSQGEIAAAHVCGALSLKDAAKTVALRSRALAAVRGRGGMASVPLPAQ 1187
              | ||:|| ||:|||||||||| | | ||| | |: | |||||:| : | ||| || |||
Db        643 RYYGVEPAAVVGHSQGEIAAACVAGGLSLADGARVVVLRSRAIARIAGGGGMVSVSLPAG 702

Qy       1188 EVEQLIGERWAGRLWVAAVNGPRSTAVSGDAEAVDEVLAYCAGTGVRARRIPVDYASHCP 1247
              |  :: : : ||| |||||| || |||||:|:||:|| |   ||||||:|||||||
Db        703 RVRTML-DTYGGRLSVAAVNGPSSTVVSGDAQALDELLAGCEREGVRARRVPVDYASHSA 761

Qy       1248 HVQPLREELLELLGDISPQPSGVPFFSTVEGTWLDTTTLDAAYWYRNLHQPVRFSDAVQA 1307
               :  ||:|||| | ||:|| | |||||||   ||||| ||| ||: || : ||| :||:
Db        762 QMDQLRDELLEALADITPQHSSVPFFSTVTADWLDTTALDAGYWFTNLRETVRFQEAVEG 821

Qy       1308 LADDGHRVFVEVSPHPTLVPAIEDTTEDTAEDVTAIGSLRRGDNDTRRFLTALAHTHTTG 1367
              |   |   ||| |||| ||| || | :    |  |:||||| :    ||||:||     |
Db        822 LVAQGMGAFVECSPHPVLVPGIEQTLDTVEADAVALGSLRRDEGGLGRFLTSLAEAFVQG 881

Qy       1368 IGTPTTWHHHYTHHHTHPHPHTHLDLPTYPFQHQHYWLESSQPGAGSGSGAGAGSGAGSG 1427
              :  |  |  :          | | :|||||||| | :|||                 ||
Db        882 V--PVDWSRTF----EGASPRT-VDLPTYPFQRQRFWLE-----------------GSP 916

Qy       1428 RAGTAGGTAEVESRFWDAVARQDLETVATTLAVPPSAGLDTVVPALSAWHRHQHDQARIN 1487
               : |   | :  ||||| |:|   ||  | :   | |   :||||:| | :  : ::
Db        917 ALSSNGVEGEADVAFWDAVEREDSAVVAEELGIDAKA-LHMTLPALSSWRRRERQRRKVQ 975

Qy       1488 TWTYQETWKPLTLPTTHQPHQ-TWLIAIPETQTHHPHITNILTNLHHHGITPIPLTLNHT 1546
              | |:  || |      :  |  ||: :|: :     :|  :  :    | ::
Db        976 RWRYRVEWKRLPNSRAQESLQGGWLLVVPQGRAGDVRVTQSVAEVAAKGGEATVLEVDAL 1035

Qy       1547 HTNPQHLHHTLHHTRQQAQNHTTGAITGLLSLLALDETPHPHHPHTPTGTLLNLTLTQTH 1606
              | |    :  ||          : |::| || :|    ||    |  :| | |
Db       1036 H--PDRAAYAEALTRWP-------GVRGVVSFLAWEEQALAEHPVLSAGLAASLALAQAL 1086

Qy       1607 TQT----HPPTPLWYATTNATTTHPND--PLTHPTQAQTWGLARTTLLEHPTHTAGIIDL 1660
                    ||  |  |      |   :  |  || ||  |   ||||    |:|||
Db       1087 IDVGGSGESAPRLWLVTEAAVVIGAADTGAVIDPVHAQLWGFGRVLALEHPELWGGLIDL 1146

Qy       1661 PTTP------TPHTLQHLTQTL------TQPHHQTQLAIRTTGTHTRRLTPTTLTPTHQP 1708
              |          | |    |  :          : |:|:|||||:  ||  :  :
Db       1147 PAVAGEPGSITDHAHADLLATVLATMVQAAARGEDQVAVRTTGTYVPRLVRSGGSAHSGA 1206

Qy       1709 PTPTPHGTTLITGGTGALATHLTHHLTTHQPTQHLLLTSRTGPHTPHAQHLTTQLQQKGI 1768
                 |  | |:||| | |  |:  |  :  | :||  :       |: |  :
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Qy       1769 HLTITTCDTSNPDQLQQLLNTIPPQHPLTTVIHTAGILDDATLTNLTPTQLNNVLRAKAH 1828
               : :   || : | |: ||:    :|||  |||   ::: |::      :   : :|
Db       1265 KIELADVDTEDSDALRSLLDRTTGEHPLRAVIHAPTVVEFASVAESDLVRFARTISSKIA 1324

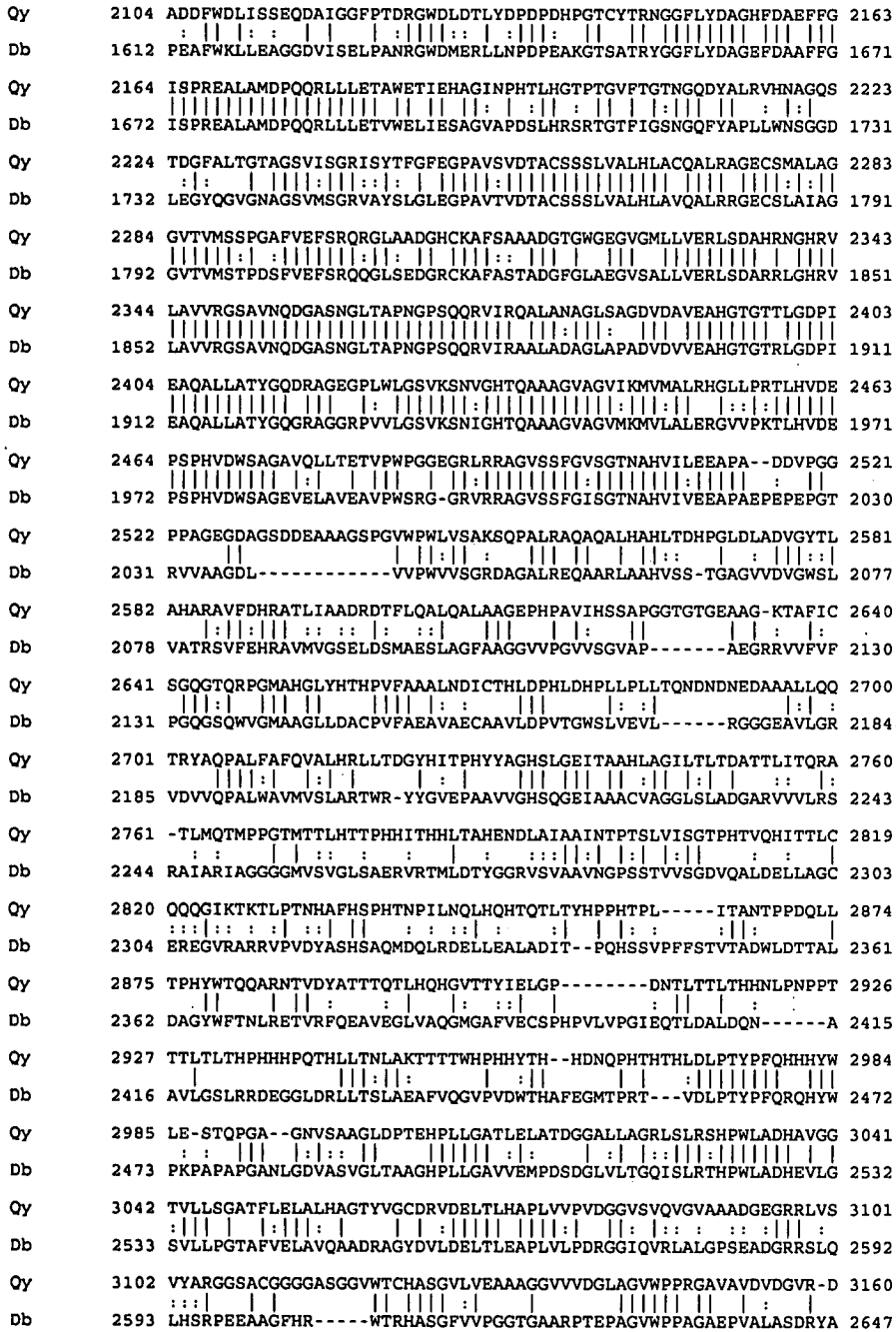
Qy       1829 SAHLLHQL-----TQHTPLTAFVLYSSAAATFGAPGQANYAAANAYLDALAHHRHTHHLP 1883
                 | ::     | |      | :|| |  :|: ||: ||| ||:|||:| ||    ||
Db       1325 GVEQLDEVLSGIDTAHD----VVFFSSVAGVWGSAGQSAYAAGNAFLDAVAQHRRLRGLP 1380

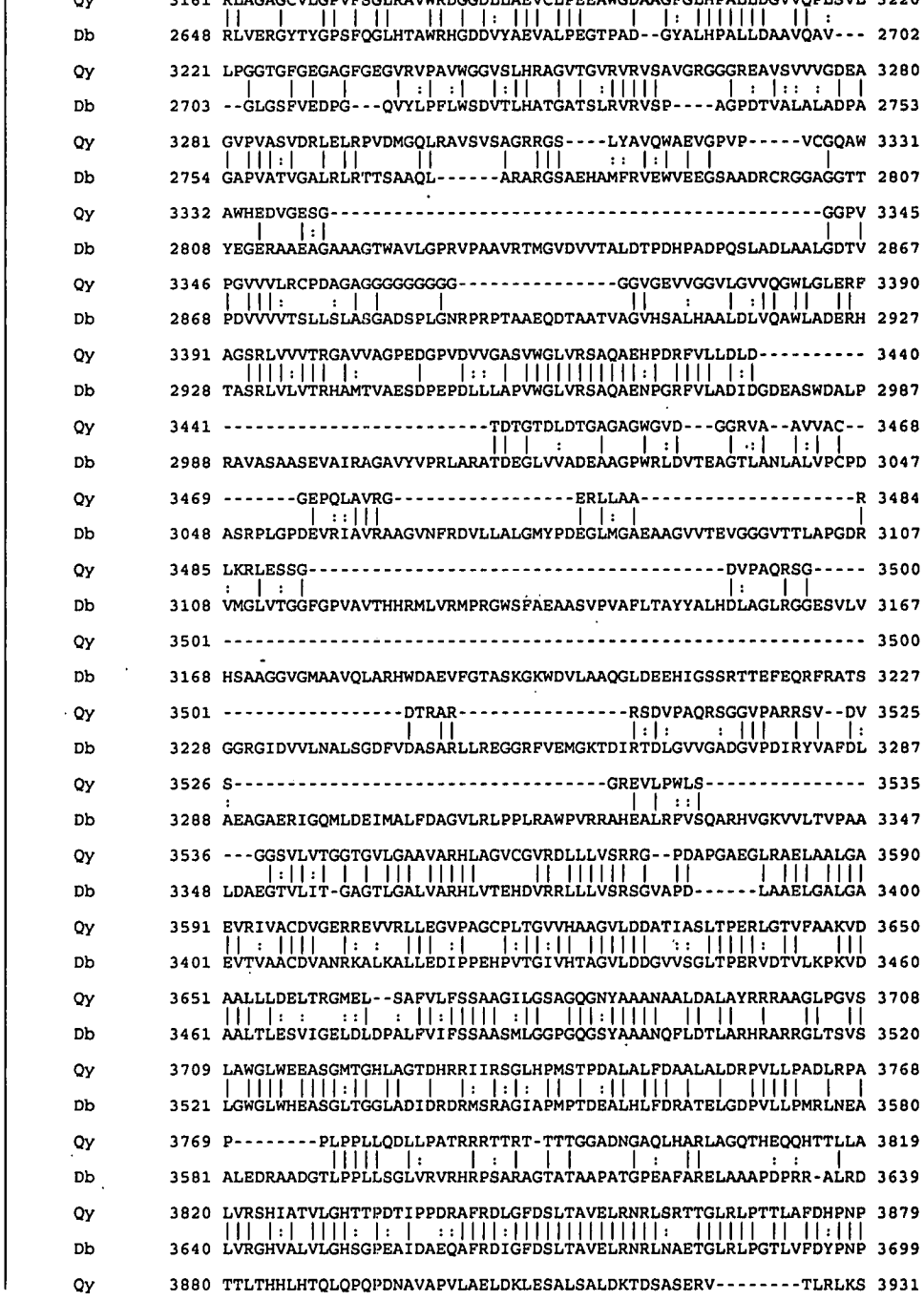
Qy       1884 ATSIAWGTWQGNGLADSDKARA-----YLDRRGFRPMSPELATAAVTQAIADTERPYVVI 1938
              ||:|| |     | |:: |      |||||| | :|   | |:: | : | :  : |:
Db       1381 GTSVAWTPW------DDDRSLASLGDSYLDRRGLRALSIPGALASL-QEVLDQDEVHAVV 1433

Qy       1939 ADIDW-------SKIEHTSQTSDL-------VSAARAREPAVQRPTPPAELHKTLAHQTS 1984
              ||:||       | :  ||   |:       :| |   :   :      || : |   |
Db       1434 ADVDWERFYAGFSAVRRTSFFDDVHDAHRPALSTAATNDGQARDEDGGTELVRRLRPLTE 1493

Qy       1985 ADQRAALLELVRDHVAAVLRHADPKAIAPDQSFRALGFDSLTAVEFRNLLIKATGLRLPV 2044
               :|:  |: ||:  ||||| |:   |: | ::|| :||||||: ||  |   ||:|||
Db       1494 TEQQRELVSLVQSEVAAVLGHSSTDAVQPQRAFREIGFDSLTAVQLRNRLTATTGMRLPT 1553

Qy       2045 SLVFDHPTPAKLAVHLQNQLRGTAAESAPSAAAVTAEA-SVTEPIAIVGMACRFPGGVTS 2103
              :||||:||   || :|:::| | :   ||:  :|   |    :|: ||||||||||: :
Db       1554 TLVFDYPTTNGLAEYLRSELFGVS--GAPADLSVVRNADEEDDPVVIVGMACRFPGGIDT 1611
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Db       3700 SALADHLLELLAPATQPTAAPLLAELERVEQLLSAAASPGGPASAVDEETRTLIATRLAT 3759

Qy       3932 LMLRW---------NAP-----------------QHPTAESADDDEKFTSATEAEIFKF 3964
Db       3760 LASQWTHLPVGSPGNADNRSGPGESGQAQESGATGEHTAAWTSDDD----------LFAF 3809

Qy       3965 IDNDL 3969
Db       3810 LDKRL 3814


RESULT 10
US-09-105-537-33
; Sequence 33, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
;  APPLICANT: Sherman, D.H.
;  APPLICANT: Liu, H.
;  APPLICANT: Xue, Y.
;  APPLICANT: Zhao, L.
;  TITLE OF INVENTION: DNA encoding methymycin and pikromycin
;  FILE REFERENCE: 600.438US1
;  CURRENT APPLICATION NUMBER: US/09/105,537A
;  CURRENT FILING DATE: 1998-06-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
;   LENGTH: 3739
;   TYPE: PRT
;   ORGANISM: Streptomyces venezuelae
US-09-105-537-33

  Query Match           33.7%;  Score 7017;  DB 4;  Length 3739;
  Best Local Similarity  42.4%;  Pred. No. 0;
  Matches 1676;  Conservative  390;  Mismatches 1177;  Indels  712;  Gaps   82;

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Qy        537 TFYPQGGGFLHDAAHFDAGFFGISPREALAMDPQQRLLLETSWEAFERAGIDPLSVRGSR 596
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Qy        597 TGVFAGALSFDYGPRMDTASSEGAADVEGHILTGTTGSVLSGRIAYSFGLEGPAITVDTG 656
Db        152 VGVFTGVMYHDYATRL-TDVPEG---IEGYLGTGNSGSVASGRVAYTLGLEGPAVTVDTA 207

Qy        657 CSASLVTLHLACQSLRSGECTLALAGGVSVMSTLGMFIEFSRQRGLSVDGRCKAYSAAAD 716
Db        208 CSSSLVALHLAVQALRKGEVDMALAGGVTVMSTPSTFVEFSRQRGLAPDGRSKSFSSTAD 267

Qy        717 GTGWGEGVGMLLVERLSDAVRLGHRVLAVVRGSAVNQDGASNGLTAPNGPAQERVIRQAL 776
Db        268 GTSWSEGVGVLLVERLSDARRKGHRILAVVRGTAVNQDGASSGLTAPNGPSQQRVIRRAL 327

Qy        777 ANAGLSVADVDVVEGHGTGTTLGDPIEAQALLATYGQ-RAGDRPLWLGSLKSNIGHTMAA 835
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Qy        836 AGVGGVIKMVMALREGVLPRTLHVDKPSPQVDWSAGAVRLLTEAVPWPGDAAGRLRRAGV 895
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Qy        896 SSFGIGGTNAHVILEEAPAAGGCVAGGGVLEGAPGLAISVAESVAAPVAVSAPVAESVPV 955
Db        448 SSFGVSGTNAHVVLEEAPA----------------------------AEETPASEATPA 478

Qy        956 PVPVP----VPVPVSARSEAGLRAQAEALRQYVAVRPDVSLADVGA---GLACGRAVLEH 1008
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Qy       1009 RAVVLAADREELVQGLGA---LAAGEPDRRVTTGHAPGGDRGGVVFVFPGQGGQWAGMGV 1065
Db        538 RAVVLGTGQDDFAQALTAPEGLIRGTP----------SDVGRVAFVFPGQGTQWAGMGA 586

Qy       1066 RLLASSPVFARRMQACEEALAPWVDWSVVDILRRDAGDAVWERADVVQPVLFSVMVSLAA 1125
Db        587 ELLDVSKEFAAAMAECESALSRYVDWSLEAVVRQAPGAPTLERVDVVQPVTFAVMVSLAK 646

Qy       1126 LWRSYGIEPDAVLGHSQGEIAAAHVCGALSLKDAAKTVALRSRALAA-VRGRGGMASVPL 1184
Db        647 VWQHHGVTPQAVVGHSQGEIAAAYVAGALTLDDAARVVTLRSKSIAAHLAGKGGMISLAL 706

Qy       1185 ----PAQEVEQLIGERWAGRLWVAAVNGPRSTAVSGDAEAVDEVLAYCAGTGVRARRIPV 1240
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Qy       1241 DYASHCPHVQPLREELLELLGDISPQPSGVPFFSTVEGTWLDTTTLDAAYWYRNLHQPVR 1300
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Qy       1301 FSDAVQALA-DDGHRVFVEVSPHPTLVPAIEDTTEDTAEDVTAIGSLRRGDNDTRRFLTA 1359
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Qy       1360 LAHTHTTGIG------TPTTWHHHYTHHHTHPHPHTHLDLPTYPFQHQHYWLESSQPGAG 1413
Db        874 LAEAWTNGLTIDWAPVLPTATGH------------HPELPTYAFQRRHYWLHDSPAVQG 920

Qy       1414 SGSGAGAGSGAGSGRAGTAGGTAEVESRFWDAVARQDLETVATTLAVPPSAGLDTVVPAL 1473
Db        921 SVQ---------------------------------------------------------- 923

Qy       1474 SAWHRHQHDQARINTWTYQETWKPLTLPTTHQP---HQTWLIAIPETQTHHPHITNILTN 1530
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Qy       1531 LHHHGITPIPLTLNHTHTNPQHLHHTLHHTRQQAQNHTTGAITGLLSLLALDETPHPHHP 1590
Db        969 LSGAGADPVQLDV-----SPLGDRQRLAATLGEALAAAGGAVDGVLSLLAWDESAHPGHP 1023

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Db       1024 APFTRGTGATLTLVQALEDAGVAAPLWCVTHGAVSVGRADHVTSPAQAMVWGMGRVAALE 1083

Qy       1650 HPTHTAGIIDLPTTPTPHTLQHLTQTLTQPHHQTQLAIRTTGTHTRRLTPTTLTPTHQPP 1709
Db       1084 HPERWGGLIDLPSDADRAALDRMTTVLAGGTGEDQVAVRASGLLARRLVRASL-PAHGTA 1142

Qy       1710 TP--TPHGTTLITGGTGALATHLTHHLTTHQPTQHLLLTSRTGPH----TPHAQH----- 1758
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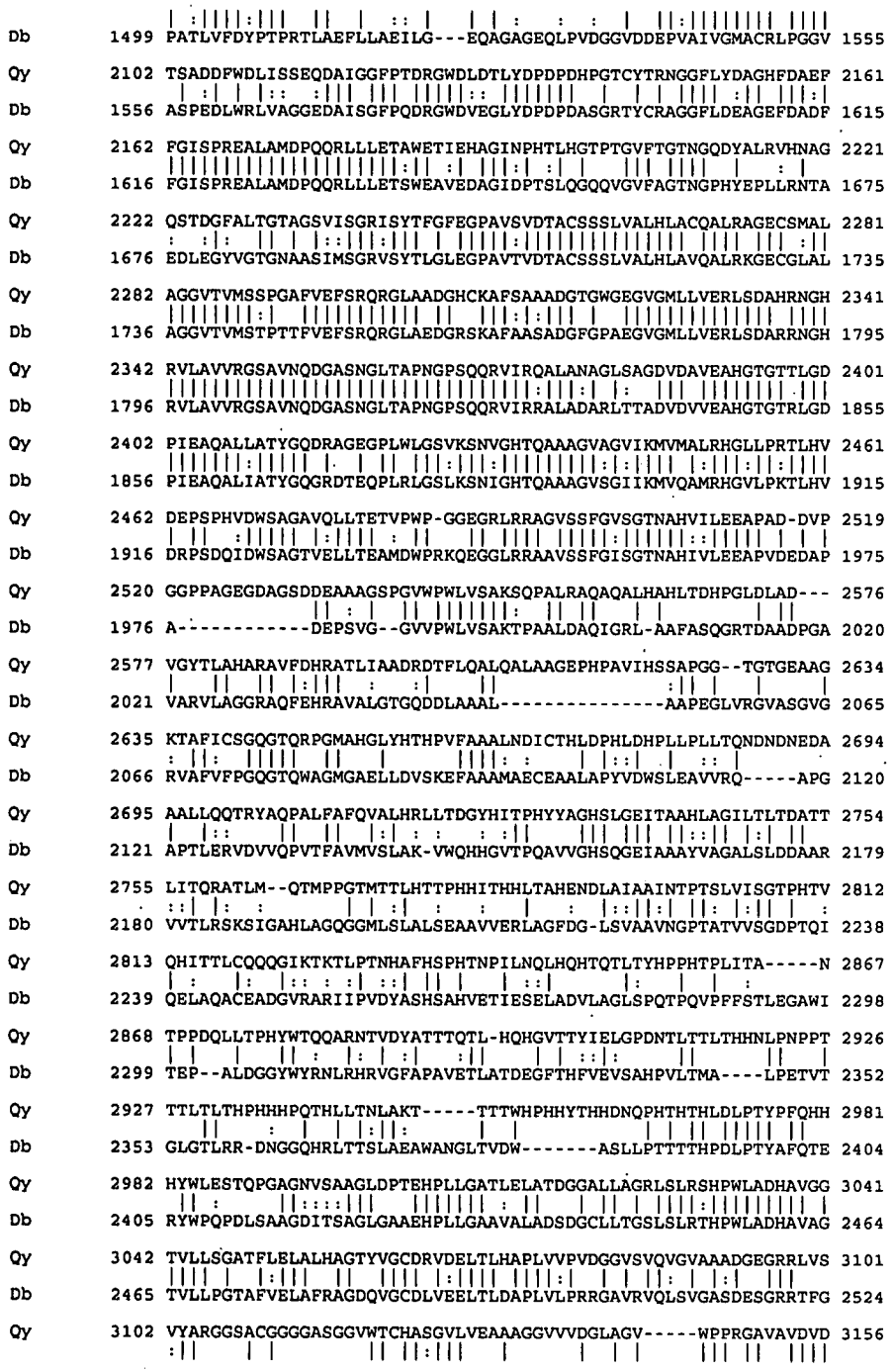
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Qy       1873 LAHHRHTHHLPATSIAWGTWQGNGLADSDKARAYLDRRGFRPMSPELATAAVTQAI--AD 1930
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Qy       1931 TERPYVVIADIDWSKIE---HTSQTSDLVSAARAREPAV--QRPTPPAE---LHKTLAHQ 1982
Db       1382 TA---VTIADVDWSSFAPGFTTARPGTLLADLPEARRALDEQQSTTAADDTVLSRELGAL 1438

Qy       1983 TSADQRAALLELVRDHVAAVLRHADPKAIAPDQSFRALGFDSLTAVEFRNLLIKATGLRL 2042
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Qy       2043 PVSLVFDHPTPAKLAVHLQNQLRGTAAESAPSAAAVTAEASV-TEPIAIVGMACRFPGGV 2101
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Db 1556 ASPEDLWRLVAGGEDAISGFPQDRGWDVEGLYDPDPDASGRTYCRAGGFLDEAGEFDADF 1615
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Db 1616 FGISPREALAMDPQQRLLLETSWEAVEDAGIDPTSLQGQQVGVFAGTNGPHYEPLLRNTA 1675
Qy 2222 QSTDGFALTGTAGSVISGRISYTFGFEGPAVSVDTACSSSLVALHLACQALRAGECSMAL 2281
Db 1676 EDLEGYVGTGNAASIMSGRVSYTLGLEGPAVTVDTACSSSLVALHLAVQALRKGECGLAL 1735
Qy 2282 AGGVTVMSSPGAFVEFSRQRGLAADGHCKAFSAAADGTGWGEGVGMLLVERLSDAHRNGH 2341
Db 1736 AGGVTVMSTPTTFVEFSRQRGLAEDGRSKAFAASADGFGPAEGVGMLLVERLSDARRNGH 1795
Qy 2342 RVLAVVRGSAVNQDGASNGLTAPNGPSQQRVIRQALANAGLSAGDVDAVEAHGTGTTLGD 2401
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Qy 2402 PIEAQALLATYGQDRAGEGPLWLGSVKSNVGHTQAAAGVAGVIKMVMALRHGLLPRTLHV 2461
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Db 2066 RVAFVFPGQGTQWAGMGAELLDVSKEFAAAMAECEAALAPYVDWSLEAVVRQ-----APG 2120
Qy 2695 AALLQQTRYAQPALFAFQVALHRLLTDGYHITPHYYAGHSLGEITAAHLAGILTLTDATT 2754
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Qy 2927 TTLTLTHPHHHPQTHLLTNLAKT-----TTTWHPHHYTHHDNQPHTHTHLDLPTYPFQHH 2981
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Db 2525 LYAHPEDAPG-----EAEWTRHATGVLAARA------DRTAPVADPEAWPPPGAEPVDVD 2573
Qy 3157 GVRDRLAGAGCVLGPVFSGLRAVWRDGGDLLAEVCLPEEAWG-DAAGFGLHPALLDGVVQ 3215
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Qy 3216 PLSVLLPGGTGFGEGAGFGEGVRVPAVWGGVSLHRAGVTGVRVRVSAVGRGGGREAVSVV 3275
Db 2634 ------AAGAGRGVRRGHAAAVRLER----DLLYAVGATALRVRLAP----AGPDTVSVS 2679
Qy 3276 VGDEAGVPVASVDRLELRPVDMGQLRAVSVSAGRRGSLYAVQW--------AEVGPVPVC 3327
Db 2680 AADSSGQPVFAADSLTVLPVDPAQLAAFSDPT--LDALHLLEWTAWDGAAQALPGAVVLG 2737
Qy 3328 GQA----------------WAWHEDVGES---GGGPVPGVVVLRCPDAGAGGGGGGGGGG 3368
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Qy 3429 EHPDRFVLLDL--------DTDTGTDLDTGAGAGWGVD-----GGRVAAVVACGEPQLAV 3475
Db 2852 ESPGRFVLLDLAGEARTAGDATAGDGLTTGDATVGGTSGDAALGSALATALGSGEPQLAL 2911
Qy 3476 RGERLLAARLKR--LES----SGD- 3493
Db 2912 RDGALLVPRLARAAAPAAADGLAAADGLAALPLPAAPALWRLEPGTDGSLESLTAAPGDA 2971
Qy 3494 --VP 3495
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Qy 3496 AQR------------------------SGDTRARRSDVPA---------------------- 3511
Db 3032 GDRVMGLLSGAYAPVVVADARTVARMPEGWTFAQGASVPVVFLTAVYALRDLADVKPGER 3091
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Db 3092 LLVHSAAGGVGMAAVQLARHWGVEVHGTASHGKWDALRALGLDDAHIASSRTLDFESAFR 3151
Qy 3519 ---------------ARRSVDVS-- 3526
Db 3152 AASGGAGMDVVLNSLAREFVDASLRLLGPGGRFVEMGKTDVRDAERVAADHPGVGYRAFD 3211
Qy 3527 --GREVLPWLS 3535
Db 3212 LGEAGPERIGEMLAEVIALFEDGVLRHLPVTTWDVRRARDAFRHVSQARHTGKVVLTMPS 3271
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Qy 3592 VRIVACDVGERREVVRLLEGVPAGCPLTGVVHAAGVLDDATIASLTPERLGTVFAAKVDA 3651
Db 3332 VSVAACDVADREALTAVLDSIPAEHPLTAVVHTAGVLSDGTLPSMTAEDVEHVLRPKVDA 3391
Qy 3652 ALLLDELTR--GMELSAFVLFSSAAGILGSAGQGNYAAANAALDALAYRRRAAGLPGVSL 3709
Db 3392 AFLLDELTSTPGYDLAAFVMFSSAAAVFGGAGQGAYAAANATLDALAWRRRTAGLPALSL 3451
Qy 3710 AWGLWEEASGMTGHLAGTDHRRIIRSGLHPMSTPDALALFDAALALDRPVLLPADLRPAP 3769
Db 3452 GWGLWAETSGMTGGLSDTDRSRLARSGATPMDSELTLSLLDAAMRRDDPALVPIALDVAA 3511
Qy 3770 --------PLPPLLQDL--------LPATRRRTTRTTTTGGA-DNGAQLHARLAGQTHEQ 3812
Db 3512 LRAQQRDGMLAPLLSGLTRGSRVGGAPVNQRR----AAAGGAGEADTDLGGRLAAMTPDD 3567
Qy 3813 QHTTLLALVRSHIATVLGHTTPDTIPPDRAFRDLGFDSLTAVELRNRLSRTTGLRLPTTL 3872
Db 3568 RVAHLRDLVRTHVATVLGHGTPSRVDLERAFRDTGFDSLTAVELRNRLNAATGLRLPATL 3627

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Qy       3873 AFDHPNPTTLTHHLHTQL-----------------QPQPDNAVAPVLAELDKLESALSAL 3915
Db       3628 VFDHPTPGELAGHLLDELATAAGGSWAEGTGSGDTASATDRQTTAALAELDRLEGVLASL 3687

Qy       3916 DKTDSASERVTLRLKSLMLRWNAPQHPTAESADDDEKFTSATEAEIFKFIDNDLG 3970
Db       3688 APAAGGRPELAARLRALAA-------ALGDDGDDATDLDEASDDDLFSFIDKELG 3735


RESULT 11
US-08-804-227C-8
; Sequence 8, Application US/08804227C
; Patent No. 5876991
;  GENERAL INFORMATION:
;    APPLICANT:  DeHoff, Bradley S.
;    APPLICANT:  Kuhstoss, Stuart A.
;    APPLICANT:  Rosteck, Paul R., Jr.
;    APPLICANT:  Sutton, Kimberly L.
;    TITLE OF INVENTION:  POLYKETIDE SYNTHASE GENES
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  THOMAS G. PLANT  1501
;      STREET:  LILLY CORPORATE CENTER
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  ASCI(DOS) Text only
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/804,227C
;      FILING DATE:  February 21, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plant, Thomas, G.
;      REGISTRATION NUMBER:  35,784
;      REFERENCE/DOCKET NUMBER:  X-8231
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-2459
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4550 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-804-227C-8

  Query Match           33.3%;  Score 6941.5;  DB 2;  Length 4550;
  Best Local Similarity   41.0%;  Pred. No. 0;
  Matches 1760;  Conservative  450;  Mismatches 1496;  Indels  591;  Gaps  101;

Qy         13 AAGEVLG---VADEADGGVVFVFPGQGPQWPGMGRELLDASDVFRESVRACEAAFAPYVD 69
Db        505 AAGRVSGGVRSGRAVPGGVGVLFTGQGAQWVGMGRGLYAGGGVFAEVLDEVLSMVGEVDG 564

Qy         70 WSVEQVLRDSPDAPG----------------------LDRVDVVQPTLFAVMISLAAL 105
Db        565 RSLRDVMFGDVDVDAGAGADAGAGAGAGVGSGSGSVGGLLGRTEFAQPALFALEVALFRA 624

Qy        106 WRSQGVEPCAVLGHSLGEIAAAHVSGGLSLADAARVVTLWSQAQTTLAGTGALVSVAATP 165
Db        625 LEARGVEVSVVLGHSVGEVAAAYVAGVLSLGDAVRLVVARGGLMGGLPVGGGMWSVGASE 684

Qy        166 D---ELLPRIAPWTEDNPARLAVAAVNGPRSTVVSGAREAVADLVADLTAAQVRTRMIPV 222
Db        685 SVVRGVVEGLGEW-------VSVAAVNGPRSVVLSGDVGVLESVVASLMGDGVECRRLDV 737

Qy        223 DVPAHSPLMYAI--EER-VVSGLLPITPRPSRIPFHSSVTGGRLDTREL-DAAYWYRNMS 278
Db        738 SHGFHSVLMEPVLGEFRGVVESLEFGRVRPG-VVVVSGVSGGVVGSGELGDPGYWVRHAR 796

Qy        279 STVRFEPAARLLLQQGPKTFVEMSPHPVLTMGLQELAPDLGDTTGTADTVIMGTLRRGQG 338
Db        797 EAVRFADGVGVVRGLGVGTLVEVGPHGVLT-GMAGECLGAGD-----DVVVVPAMRRGRA 850

Qy        339 TLDHFLTSLAQL--RGHG------ETSAT-------TVLSARLTALSPTQQQSLLLD--- 380
Db        851 EREVFEAALATVFTRDAGLDATALHTGSTGRRIDLPTYPFQRRTHWSPALSRPVTADAGA 910

Qy        381 ---------------------------------------------LVRAHTMAVLNDDG 394
Db        911 GVTATDAVGHSVSPDPESTEGTSHRDTDDEADSASPEPMSPEDAVRLVRESTAAVLGHDD 970

Qy        395 NERTASDAGPSASFAHLGFDSVMGVELRNRLSKATGLRLPVTLIFDHTTPAAVAARLRTA 454
Db        971 PGEVALD----RTFTSQGMDSVTAVELCDLLKGASGLPLAATLVYDLPTPRAVAEHIVEA 1026

Qy        455 ALGHLDE--------DTAPVPDSPSGHGGTAAADDPIAIIGMACRFPGGVRSPKDLWELA 506
Db       1027 AGGPKDSVAGGPGVLSSAAVGVS-DARGGSRDDDDPIAIVGVGCRLPGGVDSRAALWELL 1085

Qy        507 ASGGDAIGPFPTDRGWPTEQRHAQDPTQPGTFYPQGGGFLHDAAHFDAGFFGISPREALA 566
Db       1086 ESGADAISSFPTDRGWDLDGLYDPEPGTPGKTYVREGGFLHSAAEFDAEFFGISPREATA 1145

Qy        567 MDPQQRLLLETSWEAFERAGIDPLSVRGSRTGVFAGALSFDYGPRMDTASSEGAADVEGH 626
Db       1146 MDPQQRLLLEASWEALEDAGVLPESLRGGDAGVFVGATAPEYGPRL----HEGADGYEGY 1201

Qy        627 ILTGTTGSVLSGRIAYSFGLEGPAITVDTGCSASLVTLHLACQSLRSGECTLALAGGVSV 686
Db       1202 LLTGTTASVASGRIAYTLGTGGPALTVDTACSSSLVALHLAVQALRRGECGLALAGGATV 1261

Qy        687 MSTLGMFIEFSRQRGLSVDGRCKAYSAAADGTGWGEGVGMLLVERLSDAVRLGHRVLAVV 746
Db       1262 MSGPGMFVEFSRQRGLAPDGRCMPFSADADGTAWSEGVAVLALERLSDARRAGHRVLGVV 1321

Qy        747 RGSAVNQDGASNGLTAPNGPAQERVIRQALANAGLSVADVDVVEGHGTGTTLGDPIEAQA 806
Db       1322 RGSAVNQDGASNGLTAPNRSAQEGVIRAALADAGLAPGDVDAVEAHGTGTALGDPIEASA 1381

Qy        807 LLATYG-QRAGDRPLWLGSLKSNIGHTMAAAGVGGVIKMVMALREGVLPRTLHVDKPSPQ 865
Db       1382 LLATYGRERVGD-PLWLGSLKSNVGHTQAAAGAAGVVKMLLALEHGTLPRTLHADRPSTH 1440

Qy        866 VDWSAGAVRLLTEAVPWPGDAAGRLRRAGVSSFGIGGTNAHVILEEAPAAGGCVAGGGVL 925
Db       1441 VDWSSGTVALLAEARRWP-RRSDRPRRAAVSSFGISGTNAHLIIEEAPE---------- 1488

Qy        926 EGAPGLAISVAESVAAPVAVSAPVAESVPVPVPVPVPVPVSARSEAGLRAQAEALRQYVA 985
Db       1489 ------WVEDIDGVAAPDRGTADAA--------APSPLLLSARSEGALRAQAVRLGEYVE 1534

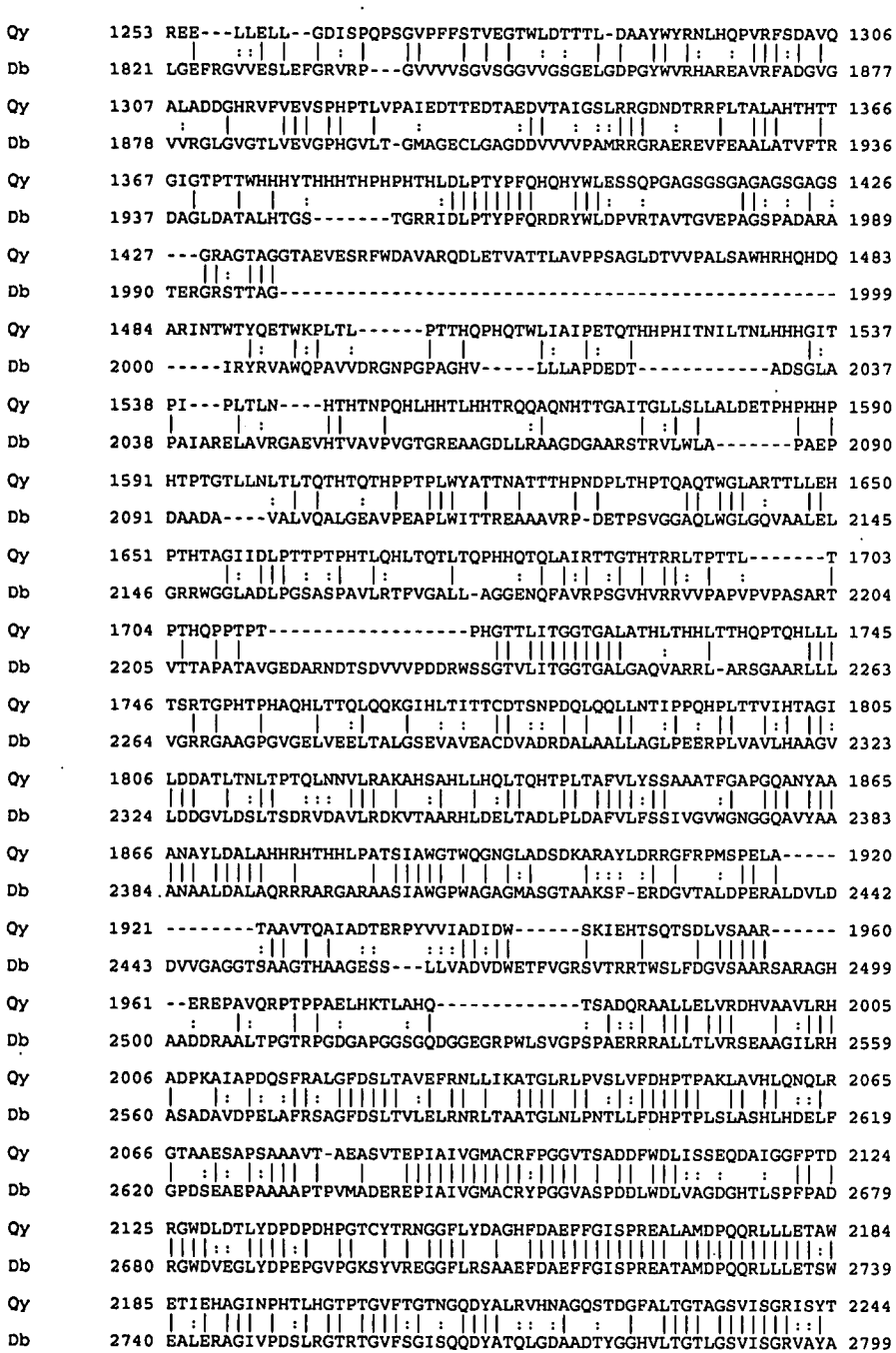
Qy        986 VRPDVSLADVGAGLACGRAVLEHRAVVLAADREELVQGLGALAAGEPDRRVTTGHAPGGD 1045
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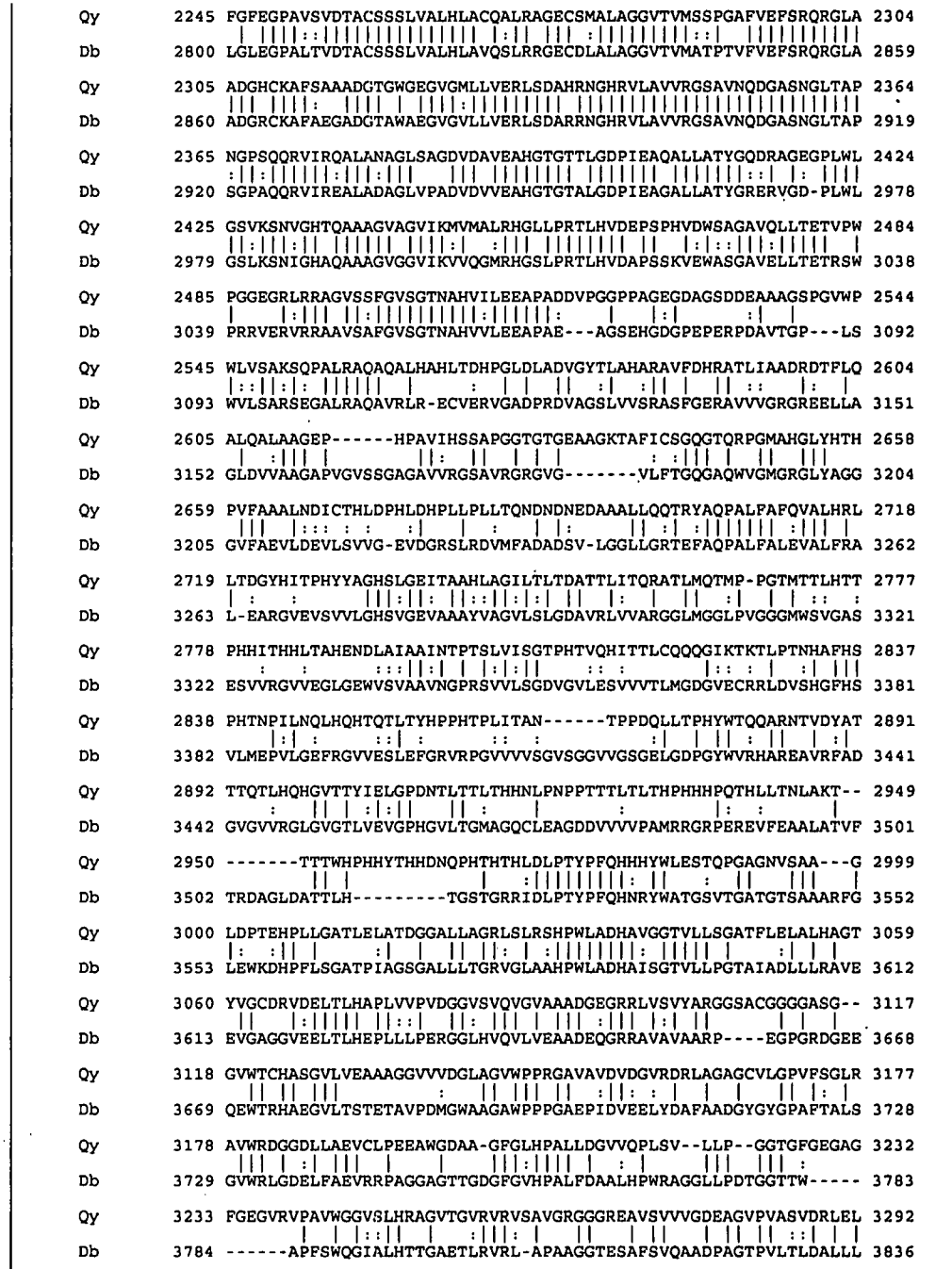
Qy       1046 RGGVVFVFPGQGGQWAGMGVRLLASSPVFARRMQACEEALAPW----------VDWSVVD 1095
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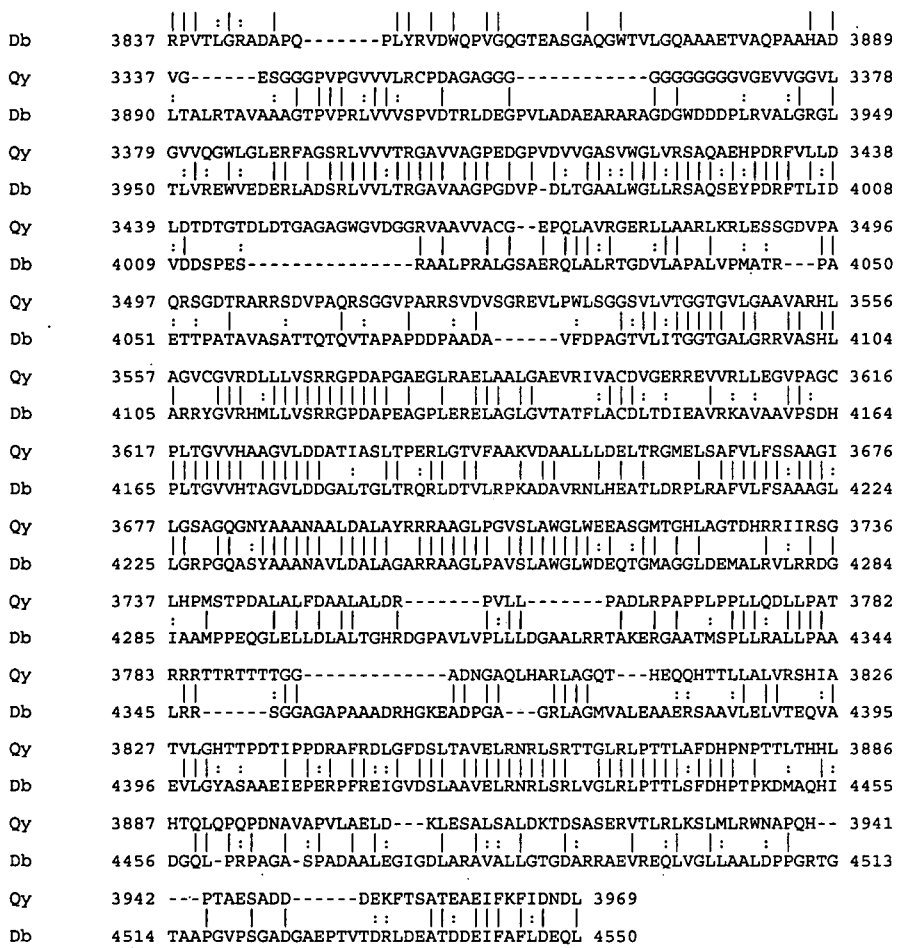
Qy       1096 ILRRDAG---DA----------------VWERADVVQPVLFSVMVSLAALWRSYGIEPD 1135
Db       1648 V---DAGAGADAGAGAGAGVGSGSGSVGGLLGRTEFAQPALFALEVALFRALEARGVEVS 1704

Qy       1136 AVLGHSQGEIAAAHVCGALSLKDAAKTVALRSRALAAVRGRGGMASVPLPAQEVEQLI-- 1193
Db       1705 VVLGHSVGEVAAAYVAGVLSLGDAVRLVVARGGLMGGLPVGGGMWSVGASESVVRGVVEG 1764

Qy       1194 -GERWAGRLWVAAVNGPRSTAVSGDAEAVDEVLAYCAGTGVRARRIPVDYASHCPHVQPL 1252
Db       1765 LGE-WVS---VAAVNGPRSVVLSGDVGVLESVVASLMGDGVECRRLDVSHGFHSVLMEPV 1820
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Db       3837 RPVTLGRADAPQ-------PLYRVDWQPVGQGTEASGAQGWTVLGQAAAETVAQPAAHAD 3889

Qy       3337 VG------ESGGGPVPGVVVLRCPDAGAGGG----------GGGGGGGGVGEVVGGVL 3378

Db       3890 LTALRTAVAAAGTPVPRLVVVSPVDTRLDEGPVLADAEARARAGDGWDDDPLRVALGRGL 3949

Qy       3379 GVVQGWLGLERFAGSRLVVVTRGAVVAGPEDGPVDVVGASVWGLVRSAQAEHPDRFVLLD 3438

Db       3950 TLVREWVEDERLADSRLVVLTRGAVAAGPGDVP-DLTGAALWGLLRSAQSEYPDRFTLID 4008

Qy       3439 LDTDTGTDLDTGAGAGWGVDGGRVAAVVACG--EPQLAVRGERLLAARLKRLESSGDVPA 3496

Db       4009 VDDSPES--------------RAALPRALGSAERQLALRTGDVLAPALVPMATR---PA 4050

Qy       3497 QRSGDTRARRSDVPAQRSGGVPARRSVDVSGREVLPWLSGGSVLVTGGTGVLGAAVARHL 3556

Db       4051 ETTPATAVASATTQTQVTAPAPDDPAADA------VFDPAGTVLITGGTGALGRRVASHL 4104

Qy       3557 AGVCGVRDLLLVSRRGPDAPGAEGLRAELAALGAEVRIVACDVGERREVVRLLEGVPAGC 3616

Db       4105 ARRYGVRHMLLVSRRGPDAPEAGPLERELAGLGVTATFLACDLTDIEAVRKAVAAVPSDH 4164

Qy       3617 PLTGVVHAAGVLDDATIASLTPERLGTVFAAKVDAALLLDELTRGMELSAFVLFSSAAGI 3676

Db       4165 PLTGVVHTAGVLDDGALTGLTRQRLDTVLRPKADAVRNLHEATLDRPLRAFVLFSAAAGL 4224

Qy       3677 LGSAGQGNYAAANAALDALAYRRRAAGLPGVSLAWGLWEEASGMTGHLAGTDHRRIIRSG 3736

Db       4225 LGRPGQASYAAANAVLDALAGARRAAGLPAVSLAWGLWDEQTGMAGGLDEMALRVLRRDG 4284

Qy       3737 LHPMSTPDALALFDAALALDR-------PVLL-------PADLRPAPPLPPLLQDLLPAT 3782

Db       4285 IAAMPPEQGLELLDLALTGHRDGPAVLVPLLLDGAALRRTAKERGAATMSPLLRALLPAA 4344

Qy       3783 RRRTTRTTTTGG-------------ADNGAQLHARLAGQT---HEQQHTTLLALVRSHIA 3826

Db       4345 LRR------SGGAGAPAAADRHGKEADPGA---GRLAGMVALEAAERSAAVLELVTEQVA 4395

Qy       3827 TVLGHTTPDTIPPDRAFRDLGFDSLTAVELRNRLSRTTGLRLPTTLAFDHPNPTTLTHHL 3886

Db       4396 EVLGYASAAEIEPERPPREIGVDSLAAVELRNRLSRLVGLRLPTTLSFDHPTPKDMAQHI 4455

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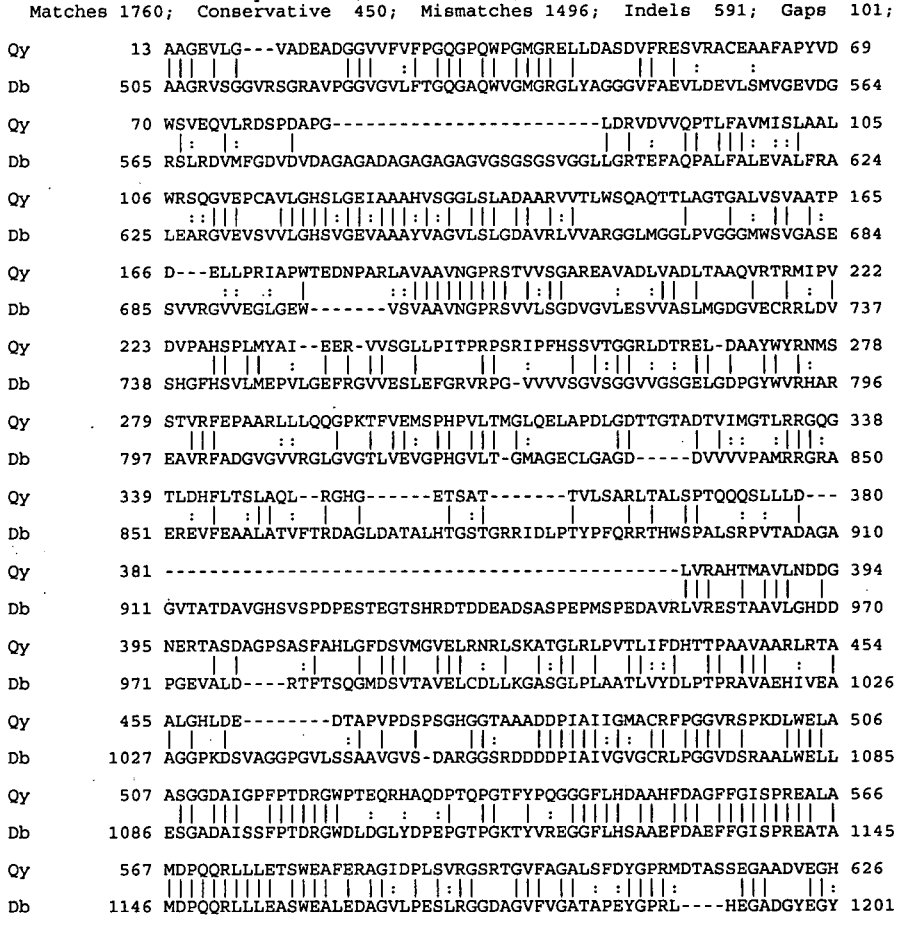
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RESULT 12
US-08-804-198-2
; Sequence 2, Application US/08804198
; Patent No. 5945320
;  GENERAL INFORMATION:
;    APPLICANT:  Burgett, Stanley G.
;    APPLICANT:  Kuhstoss, Stuart A.
;    APPLICANT:  Rao, Nagaraja R.
;    APPLICANT:  Richardson, Mark A.
;    APPLICANT:  Rosteck, Paul R., Jr.
;    TITLE OF INVENTION:  PLATENOLIDE SYNTHASE GENE
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PAUL R. CANTRELL  1138
;      STREET:  LILLY CORPORATE CENTER
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  Macintosh 7.0
;      SOFTWARE:  Microsoft Word 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/804,198
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CANTRELL, PAUL R.
;      REGISTRATION NUMBER:  36,470
;      REFERENCE/DOCKET NUMBER:  P9113
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-3885
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4550 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
US-08-804-198-2

  Query Match           33.3%;  Score 6941.5;  DB 2;  Length 4550;
  Best Local Similarity   41.0%;  Pred. No. 0;
  Matches 1760;  Conservative  450;  Mismatches 1496;  Indels  591;  Gaps  101;
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Qy         70 WSVEQVLRDSPDAPG-----------------------LDRVDVVQPTLFAVMISLAAL 105

Db        565 RSLRDVMFGDVDVDAGAGADAGAGAGAGVGSGSGSVGGLLGRTEFAQPALFALEVALFRA 624

Qy        106 WRSQGVEPCAVLGHSLGEIAAAHVSGGLSLADAARVVTLWSQAQTTLAGTGALVSVAATP 165

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Qy        166 D---ELLPRIAPWTEDNPARLAVAAVNGPRSTVVSGAREAVADLVADLTAAQVRTRMIPV 222

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Qy        223 DVPAHSPLMYAI--EER-VVSGLLPITPRPSRIPFHSSVTGGRLDTREL-DAAYWYRNMS 278

Db        738 SHGFHSVLMEPVLGEFRGVVESLEFGRVRPG-VVVVSGVSGGVVGSGELGDPGYWVRHAR 796

Qy        279 STVRFEPAARLLLQQGPKTFVEMSPHPVLTMGLQELAPDLGDTTGTADTVIMGTLRRGQG 338

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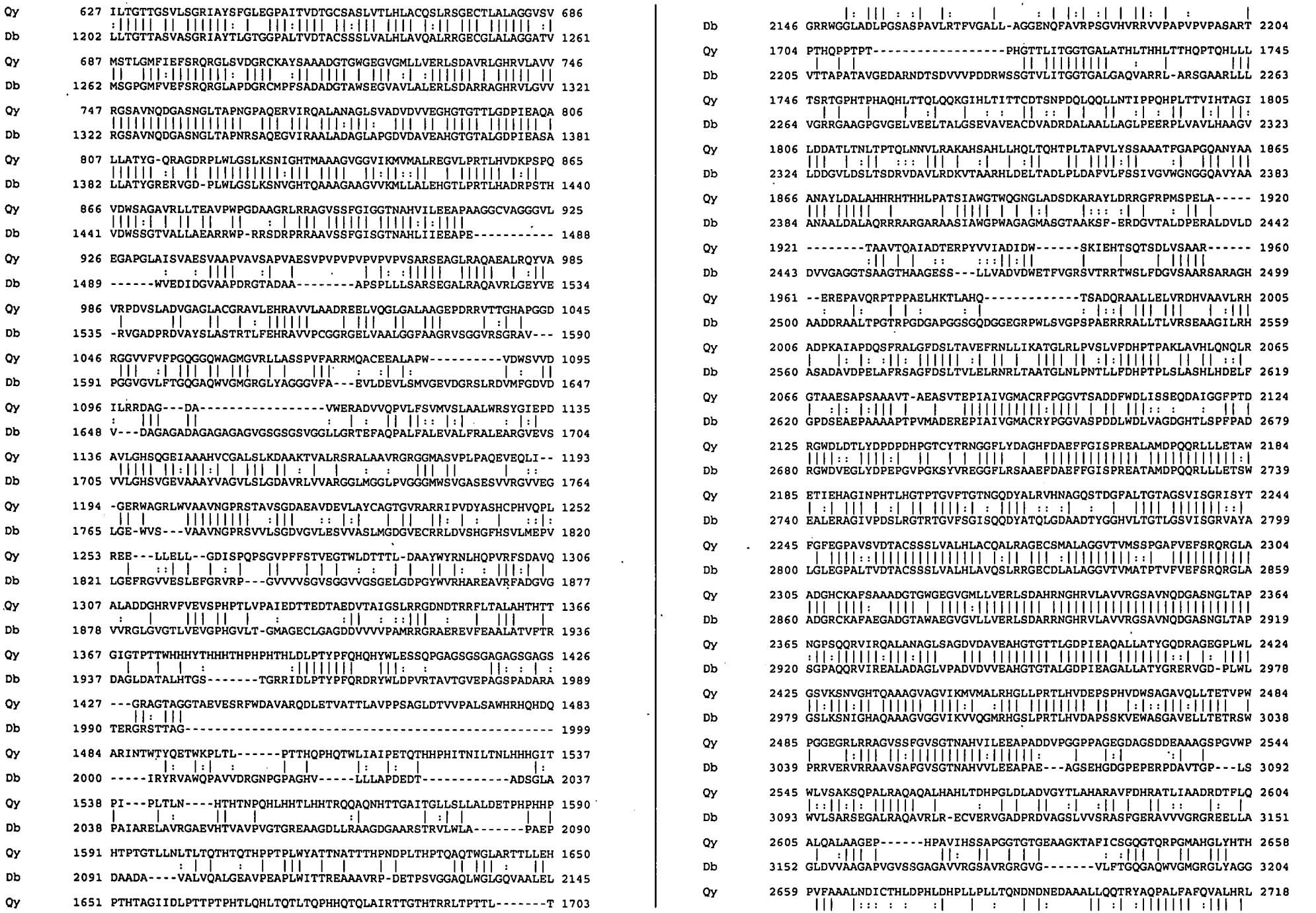
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Qy        567 MDPQQRLLLETSWEAFERAGIDPLSVRGSRTGVFAGALSFDYGPRMDTASSEGAADVEGH 626

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Db       3263 L-EARGVEVSVVLGHSVGEVAAAYVAGVLSLGDAVRLVVARGGLMGGLPVGGGMWSVGAS 3321

Qy       2778 PHHITHHLTAHENDLAIAAINTPTSLVISGTPHTVQHITTLCQQQGIKTKTLPTNHAFHS 2837

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Qy       2838 PHTNPILNQLHQHTQTLTYHPPHTPLITAN------TPPDQLLTPHYWTQQARNTVDYAT 2891

Db       3382 VLMEPVLGEFRGVVESLEFGRVRPGVVVVSGVSGGVVGSGELGDPGYWVRHAREAVRFAD 3441

Qy       2892 TTQTLHQHGVTTYIELGPDNTLTTLTHHNLPNPPTTTLTLTHPHHHPQTHLLTNLAKT-- 2949

Db       3442 GVGVVRGLGVGTLVEVGPHGVLTGMAGQCLEAGDDVVVVPAMRRGRPEREVFEAALATVF 3501

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Db       3502 TRDAGLDATTLH---------TGSTGRRIDLPTYPFQHNRYWATGSVTGATGTSAAARFG 3552

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Db       3784 ------APFSWQGIALHTTGAETLRVRL-APAAGGTESAFSVQAADPAGTPVLTLDALLL 3836

Qy       3293 RPVDMGQLRAVSVSAGRRGSLYAVQWAEVGPVPVCGQAWAW---------------HED 3336

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Qy       3337 VG------ESGGGPVPGVVVLRCPDAGAGGG------------GGGGGGGGVGEVVGGVL 3378

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Db       4051 ETTPATAVASATTQTQVTAPAPDDPAADA------VFDPAGTVLITGGTGALGRRVASHL 4104

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Db       4165 PLTGVVHTAGVLDDGALTGLTRQRLDTVLRPKADAVRNLHEATLDRPLRAFVLFSAAAGL 4224

Qy       3677 LGSAGQGNYAAANAALDALAYRRRAAGLPGVSLAWGLWEEASGMTGHLAGTDHRRIIRSG 3736

Db       4225 LGRPGQASYAAANAVLDALAGARRAAGLPAVSLAWGLWDEQTGMAGGLDEMALRVLRRDG 4284

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Db       4285 IAAMPPEQGLELLDLALTGHRDGPAVLVPLLLDGAALRRTAKERGAATMSPLLRALLPAA 4344

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Qy       3942 ---PTAESADD------DEKFTSATEAEIFKFIDNDL 3969

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RESULT 13
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; Sequence 2, Application US/09428517
; Patent No. 6251636
; GENERAL INFORMATION:
;  APPLICANT: Betlach, Mary C.
;  APPLICANT: Shah, Sanjay Krishnakant
;  APPLICANT: McDaniel, Robert
;  APPLICANT: Tang, Li
;  TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
;  FILE REFERENCE: 30062-20029.00
;  CURRENT APPLICATION NUMBER: US/09/428,517
;  CURRENT FILING DATE: 1999-10-28
;  EARLIER APPLICATION NUMBER: 60/120,254
;  EARLIER FILING DATE: 1999-02-16
;  EARLIER APPLICATION NUMBER: 60/106,100
;  EARLIER FILING DATE: 1998-10-29
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4150
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Recombinant
;   OTHER INFORMATION: Oleandolide PKS
US-09-428-517-2

  Query Match             33.2%;  Score 6912.5;  DB 4;  Length 4150;
  Best Local Similarity   40.9%;  Pred. No. 0;
  Matches 1685;  Conservative  447;  Mismatches 1328;  Indels  655;  Gaps   89;

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Qy         62 ---AAFAPYVDWSVEQVL---RDSPDAPGLDRVDVVQPTLFAVMISLAALWRSQGVEPCA 115

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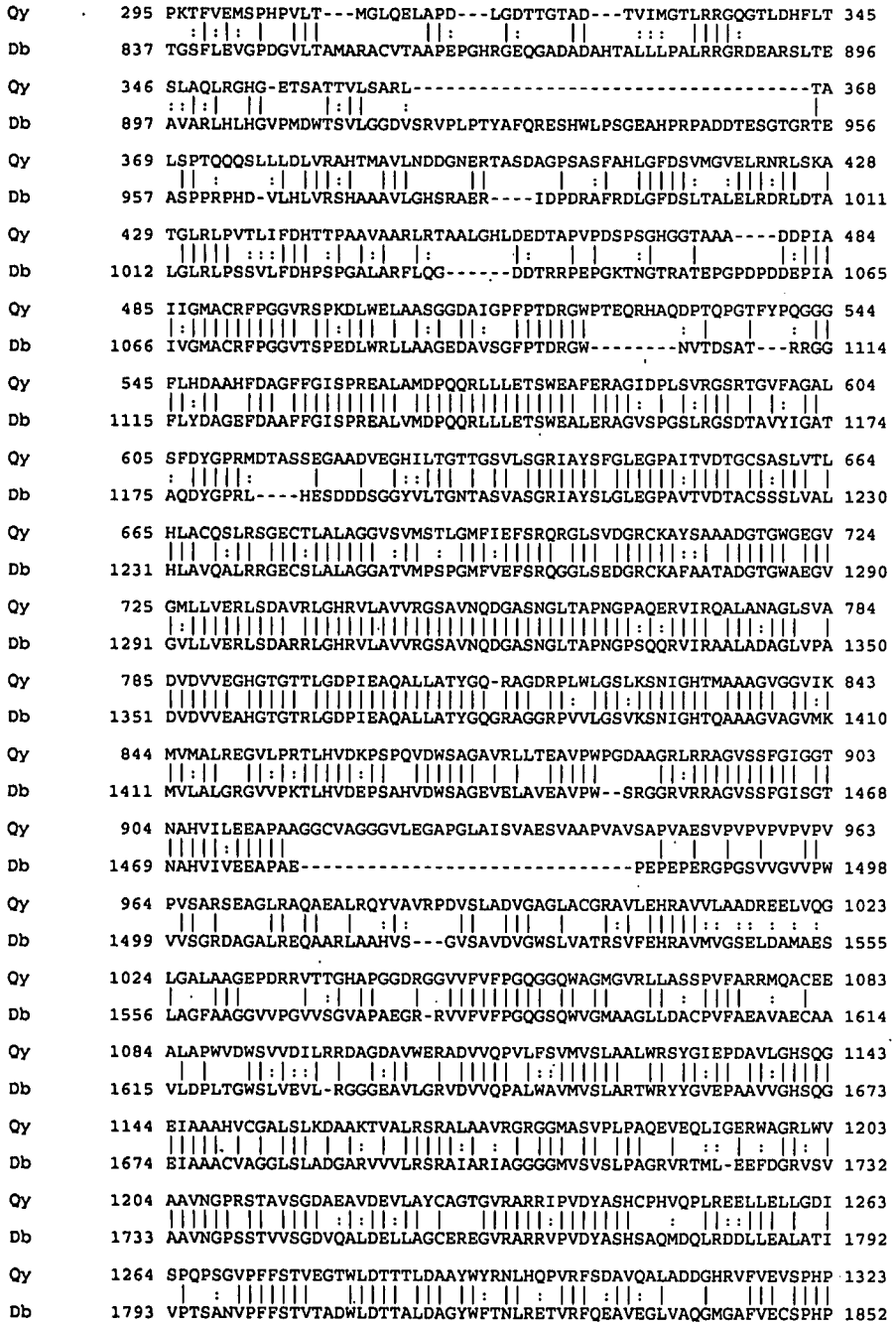
Db        661 LAGHSVGEIAAAHAAGILDLSDAAELVATRGALMRSLPGGGVMLSVQAPESE----VAPL 716

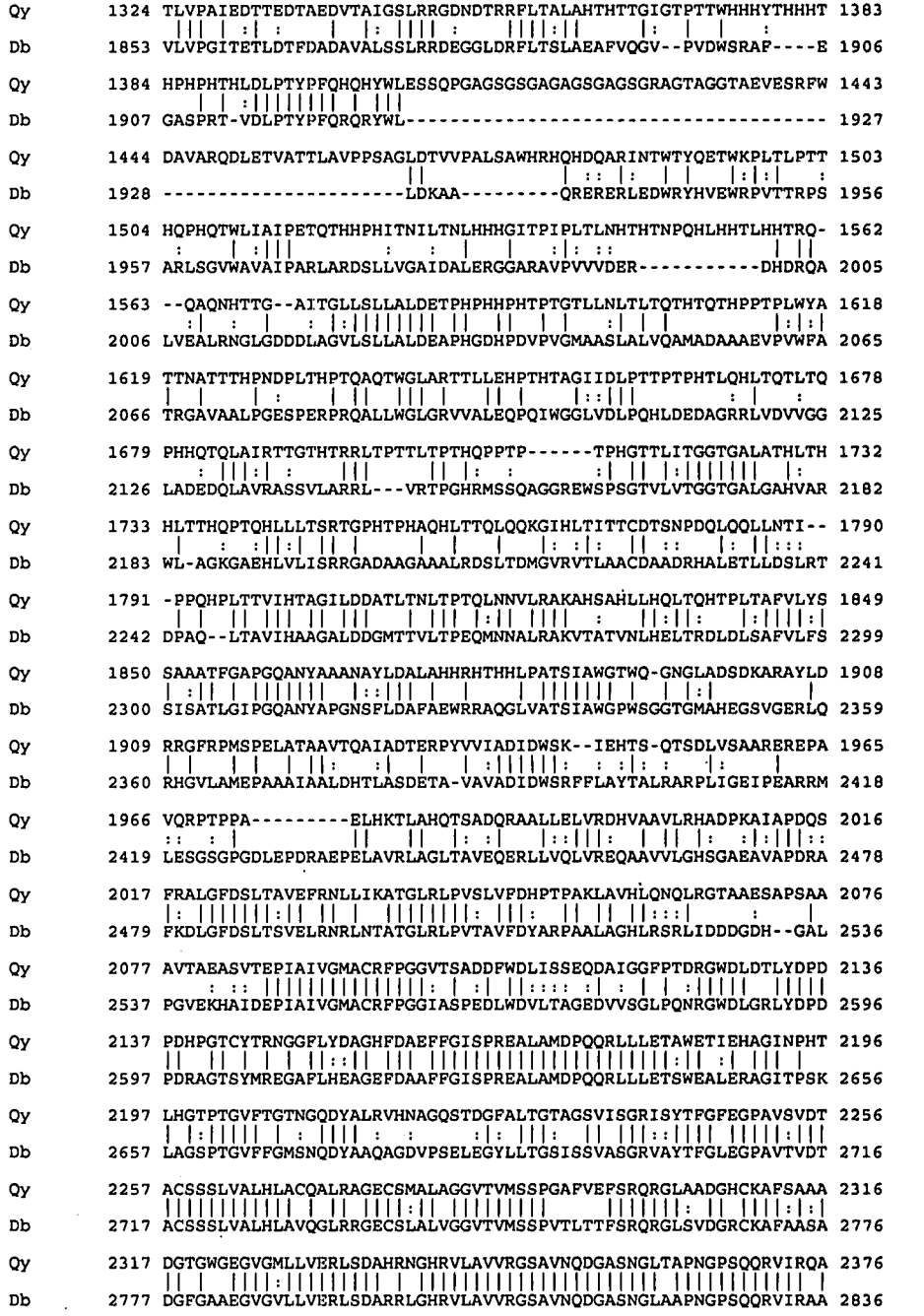
Qy        176 TEDNPARLAVAAVNGPRSTVVSGAREAVADLVADLTAAQVRTRMIPVDVPAHSPLMYAIE 235

Db        717 LLGREAHVGLAAVNGPDAVVVSGERGHVAAIEQILRDRGRKSRYLRVSHAFHSPLMEPVL 776

Qy        236 ERVVSGLLPITPRPSRIPFHSSVTGGRLDTREL-DAAYWYRNMSSTVRFEPAARLLLQQG 294

Db        777 EEFAEAVAGLTFRAPTTPLVSNLTGAPVDDRTMATPAYWVRHVREAVRFGDGIRALGKLG 836
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Db       2837 LADAGLAPADVDVVEAHGTGTRLGDPIEAQALLATYGQGRTSGRPVWLGSVKSNIGHTQA 2896

Qy       2437 AAGVAGVIKMVMALRHGLLPRTLHVDEPSPHVDWSAGAVQLLTETVPWPGGEGRLRRAGV 2496

Db       2897 AAGVAGVMKMVLALGRGVVPKTLHVDEPSPHVDWSAGEVELAVEAVPWSRG-GRVRRAGV 2955

Qy       2497 SSFGVSGTNAHVILEEAPADDVPGGPPAGEGDAGSDDEAAAGSPGVWPWLVSAKSQPALR 2556

Db       2956 SSFGISGTNAHVIVEEAPAEP------------SVEEGPGSVVGVVPWVVSGRDAGALR 3002

Qy       2557 AQAQALHAHLTDHPGLDLADVGYTLAHARAVFDHRATLIAADRDTFLQALQALAAGEPHP 2616

Db       3003 AQAARLAAHVSS-TGAGVVDVGWSLVATRSVFEHRAVMVGTDLDSMAGSLAGFAAGGVVP 3061

Qy       2617 AVIHSSAPGGTGTGEAAG-KTAFICSGQGTQRPGMAHGLYHTHPVFAAALNDICTHLDPH 2675

Db       3062 GVVSGVAP-------AEGRRVVFVFPGQGSQWVGMAAGLLDACPVFAEAVAECAAVLDRL 3114

Qy       2676 LDHPLLPLLTQNDNDNEDAAALLQQTRYAQPALFAFQVALHRLLTDGYHITPHYYAGHSL 2735

Db       3115 TGWSLVEVLRGGE-------AVLGRVDVVQPALWAVMVSLARTWR-YYGVEPAAVVGHSQ 3166

Qy       2736 GEITAAHLAGILTLTDATTLITQRA-TLMQTMPPGTMTTLHTTPHHITHHLTAHENDLAI 2794

Db       3167 GEIAAACVAGGLSLADGARVVVLRSRAIARIAGGGGMVSVGLSAERVRTMLDTYGGRVSV 3226

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Db       3406 --FVDLPTYAFQRQRYWLH---------------------------------------- 3422

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Qy       3088 GVAAADGEGRRLVSVYARGGSACGGGGASGGVWTCHASGVLVEAAAGGVVVDGLAGVWPP 3147

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Qy       3148 RGAVAVDVDGVRDRLAGAGCVLGPVFSGLRAVWR----DGGDLLAEVCLPEEAWGDAAGF 3203

Db       3446 ------DATAVSDLLSTDAEALHTVLPALSS-WRRRRVEHRRL--------QDWRYRVEW 3490

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Db       3491 KPFPAALDEV-------LGGGWLFVVPRGLADD---------------GVV-ARVVAAVT 3527

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Db       3528 ARGG---EVSVV---------------ELDPTRPDRRAYAEAVAGRGVSGVVSFLSWDDR 3569

Qy       3319 --AEVGPVP-------VCGQAWAWHEDVGESGGGPVPGVVVLRCPDAGAGGGGGGGGGGG 3369

Db       3570 RHSEHSVVPAGLAASLVLAQALV---DLGRVGEGP------------------------ 3601

Qy       3370 VGEVVGGVLGVVQGWLGLERFAGSRLVVVTRGAVVAGPEDGPV--DVVGASVWGLVRSAQ 3427

Db       3602 ----------------------RLWLVTRGAVVAGPSDAGVVIDPVQAQVWGFGRVLG 3637

Qy       3428 AEHPDRFVLLDLDTDTGTDLDTGAGAGWGVDGGRVAAVVACG-EPQLAVRGERLLAARLK 3486

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Db       3689 RAVVDGG-------------------GGG---------------WRPRGTVLVTGGLG 3712

Qy       3547 VLGAAVARHLAGVCGVRDLLLVSRRGPDAPGAEGLRAELAAL-GAEVRIVACDVGERREV 3605

Db       3713 GLGAHTARWLVG-GGADHVVLVSRRGGSAPGAGDLVRELEGLGGARVSVRACDVADRVAL 3771

Qy       3606 VRLLEGVPAGCPLTGVVHAAGVLDDATIASLTPERLGTVPAAKVDAALLLDELTRGMELS 3665

Db       3772 RALLSDL--GEPVTAVFHAAGVPQSTPLAEISVQEAADVMAAKVAGAVNLGELVDPCGLE 3829

Qy       3666 AFVLFSSAAGILGSAGQGNYAAANAALDALAYRRRAAGLPGVSLAWGLWEEASGMTGHLA 3725

Db       3830 AFVLFSSNAGVWGSGGQAVYAAANAFLDALAVRRRGVGLPATSVAWGMW-AGEGMAS--V 3886

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Db       3887 GGAARELSRRGVRAMDPERAVAVMADAVGRGEAFVAVADVDWERFVTGFASARPR----P 3942

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Qy       3938 APQHPTAESADDDEKFTSATEAEIFKFIDNDLGLS 3972

Db       4116 SRGREAGQDAGEHQDVEDATIDELFEVLDNELGNS 4150
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RESULT 14
US-09-036-987A-4
; Sequence 4, Application US/09036987A
; Patent No. 6143526
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Merlo, Donald J.
; APPLICANT: Treadway, Patti J.
; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; TITLE OF INVENTION: Production
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow AgroSciences LLC Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,987A
; FILING DATE: 09-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R

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;      REGISTRATION NUMBER:  28,479
;      REFERENCE/DOCKET NUMBER:  50,608
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (317)337-4816
;      TELEFAX:  (317)337-4847
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3170 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-036-987A-4

  Query Match            32.7%;  Score 6804.5;  DB 4;  Length 3170;
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  Matches 1581;  Conservative  380;  Mismatches 1115;  Indels  493;  Gaps   68;

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Qy       773 RQALANAGLSVADVDVVEGHGTGTTLGDPIEAQALLATYGQ-RAGDRPLWLGSLKSNIGH 831
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Qy       832 TMAAAGVGGVIKMVMALREGVLPRTLHVDKPSPQVDWSAGAVRLLTEAVPWPGDAAGRLR 891
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Qy       892 RAGVSSFGIGGTNAHVILEEAPAAGGCVAGGGVLEGAPGLAISVAESVAAPVAVSAPVAE 951
Db       439 RAGVSSFGVSGTNAHVILEHDP----------------LAVTENE------------E 468

Qy       952 SVPVPVPVPVPVPVSARSEAGLRAQAEALRQYVAVRPDVSLADVGAGLACGRAVLEHRAV 1011
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Qy      1132 IEPDAVLGHSQGEIAAAHVCGALSLKDAAKTVALRSRALAAVRGRGGMASVPLPAQEVEQ 1191
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Qy      1492 QETWKPLTLPTTHQPHQTWLIAIPETQTHHPHITNILTNLHHHGITPIPLTLNHTHTNPQ 1551
Db       979 RVDWVRVAPQPVRRTRETWLLVVPPGGIEEALVERLTDALNTRGISTLRLDVPPAATSGE 1038

Qy      1552 HLHHTLHHTRQQAQNHTTGAITGLLSLLALDETPHPHHPHTPTGTLLNLTLTQTHTQTHP 1611
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Qy      1612 PTPLWYATTNATTTHPNDPLTHPTQAQTWGLARTTLLEHPTHTAGIIDLPTTPTPHTLQH 1671
Db      1092 RIPLWTITRGAVKAGPADRLLRPMQAQAWGLGRVAALEHPERWGGLIDLPDSLDGDVLTR 1151

Qy      1672 LTQTLTQPHHQTQLAIRTTGTHTRRLTPTTLTPTHQPPTP--TPHGTTLITGGTGALATH 1729
Db      1152 LGEALTNGLAEDQLAIRQSGVLARRLVP---APANQPAGRKWRPRGSALITGGLGAVGAQ 1208

Qy      1730 LTHHLTTHQPTQHLLLTSRTGPHTPHAQHLTTQLQQKGIHLTITTCDTSNPDQLQQLLNT 1789
Db      1209 VARWL-AEIGAERIVLTSRRGNQAAGAAELEAELRALGAQVSIVACDVTDRAEMSALL-- 1265

Qy      1790 IPPQHPLTTVIHTAGILDDATLTNLTPTQLNNVLRAKAHSAHLLHQLTQHTPLTAFVLYS 1849
Db      1266 --AEFDVTAVFHAAGVGRLLPLAETDQNGLAEICAAKVRGAQVLDELCDSTDLDAFVLFS 1323

Qy      1850 SAAATFGAPGQANYAAANAYLDALAHHRHTHHLPATSIAWGTWQGNGLADSDKARAYLDR 1909
Db      1324 SGAGVWGGGGQGAYGAANAFLDTLAEQRRARGLPATSISWGSWAGGGMADG-AAGEHLRR 1382

Qy      1910 RGFRPMSPELATAAVTQAIADTERPYVVIADIDWSKIEHT------SQTSDLVSAARERE 1963
Db      1383 RGIRPM-PAASAILALQEVLDQDETCVSIADVDWDRFVPTFAATRATRLFDEVPAARKAM 1441

Qy      1964 PAVQRPTPP--AELHKTLAHQTSADQRAALLELVRDHVAAVLRHADPKAIAPDQSFRALG 2021
Db      1442 PA-NGPAEPGGSPFARNLAELPEAQRRHELVDLVCAQVATVLGHGSREEVQPERAFRALG 1500

Qy      2022 FDSLTAVEFRNLLIKATGLRLPVSLVFDHPTPAKLAVHLQNQLRGTAAESAPSAAAVTAE 2081
Db      1501 FDSLMAVDLRNRLTTATGLRLPTTTVFDYPNPAALAAHLLEELVGDVASAAVTAASAPAS 1560

Qy      2082 ASVTEPIAIVGMACRFPGGVTSADDFWDLISSEQDAIGGFPTDRGWDLDTLYDPDPDHPG 2141
Db      1561 ---DEPIAIVAMSCRFPGGAHSPEDLWRLVAAGTEVIGEFPSDRGWDAEGLYDPDASRPG 1617

Qy      2142 TCYTRNGGFLYDAGHFDAEFFGISPREALAMDPQQRLLLETAWETIEHAGINPHTLHGTP 2201
Db      1618 TTYARMAGFLYDAGEFDADLFGISPREALAMDPQQRLVLEIAWEALERAGIDPLSLKGSG 1677

Qy      2202 TGVFTGTNGQDYALRVHNAGQSTDGFALTGTAGSVISGRISYTFGFEGPAVSVDTACSSS 2261
Db      1678 VGTYIGAGSRGYATDVRQFPEEAEGYLLTGTSASVLSGRVAYSFGFEGPAVTVDTACSSS 1737

Qy      2262 LVALHLACQALRAGECSMALAGGVTVMSSPGAFVEFSRQRGLAADGHCKAFSAAADGTGW 2321
Db      1738 LVALHLACQSLRSGECDLALAGGVTVMSTPEMFVEFSRQRGLAPDGRCKSFAESADGTGW 1797

Qy      2322 GEGVGMLLVERLSDAHRNGHRVLAVVRGSAVNQDGASNGLTAPNGPSQQRVIRQALANAG 2381
Db      1798 GEGAGLLLLERLSDAHRNGHRVLAVVRGSAVNQDGASNGLAAPNGPSQQRVINQALANAA 1857

Qy      2382 LSAGDVDAVEAHGTGTTLGDPIEAQALLATYGQDRAGEGPLWLGSVKSNVGHTQAAAGVA 2441
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Db       1858 LSASDVDAVEAHGTGTRLGDPIEAQALIATYGQARERDRPLWLGSVKSNIGHTQAAAGVA 1917

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Db       1918 GVIKMVMAMRHGQLPASLHADEPTSEVDWSSGAVRLLAEQVPWPESD-RVRRVGVSSFGI 1976

Qy       2502 SGTNAHVILEEAPADDVPGGPPAGEGDAGSDDEAAAGSPGVWPWLVSAKSQPALRAQAQA 2561

Db       1977 SGTNAHVILEQAT------NAPDSTAETDKTESGSTVDIPVVPWLVSGKTTDSLRGQAER 2030

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Db       2031 VLSQVESRPEQRSLDVAYSLASGRAALDERAVVLGADRGELVAGLAALAAGQEASGVI-- 2088

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Db       2089 -----SGT-RASARFGFVFSGQGGQWLGMGRALYSKFPVFAAAFDEACAELEAHLGEDRR 2142

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Db       2143 VRDVVFGSD------AQLLDQTLWAQSGLFALQAGLLGLL-GSWGVRPDVVMGHSVGELA 2195

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Qy       2799 TPTSLVISGTPHTVQHITTLCQQQGIKTKTLPTNHAFHSPHTNPILNQLHQHTQTLTYHP 2858

Db       2256 APGSVVLSGDREVLASIVGRLTELRVRTRRLRVSHAFHSHRMDPMLGEFAQIAESAEFGK 2315

Qy       2859 PHTPLITANT----PPDQLLTPHYWTQQARNTVDYATTTQTLHQHGVTTYIELGPDNTLT 2914

Db       2316 PTTPLVSTLTGELDRAAEMSTPGYWVRQAREPVRFADGVQALAAQGIGTVVELGPDGTLA 2375

Qy       2915 TLTHHNLPNPP----TTTLTLTHPHHHPQTHLLTNLAKTTTTWHPHHYTHHDNQPHTHT- 2969

Db       2376 ALVRECATESDRVGRISSIPLMRRERDETRSVMTALA-----------------HLHTR 2417

Qy       2970 ----------------HLDLPTYPFQHHHYWLESTQPGA------GNVSA---AGLDPTE 3004

Db       2418 GGEVDWQAFFAGTGARQLELPTYAFQRQHYWIESSARPARDRADIGEVAEQFWTAVDQGD 2477

Qy       3005 HPLLGATLELATDGG----------ALLAGRLSLRSHPWLADHAVGGTVLLSGATFLELA 3054

Db       2478 LATLVAALDLGADDDTCASLSDVLPALSSWRSGLRNRS-----------LVDSCRYRIS 2525

Qy       3055 LHAGTYVGCDRVDELTLHAPLVVPVDGGVSVQVGVAAADGEGRRLVSVYARGGSACGGGG 3114

Db       2526 WHSSREVPAPKISGTWL---LVVP----------GAADDG----LVTALT---SSLVGGG 2565

Qy       3115 ASGGVWTCHASGVLVEAAAGGVVVDGLAGVWPPRGAVAVDVDGVRDRLAGAGCVLGPVFS 3174

Db       2566 AE------------------VVRIGLSEEDPHR-------EDVAQRLANALTDAGQL-- 2597

Qy       3175 GLRAVWRDGGDLLAEVCLPEEAWGDAAGFGLHPALLDGVVQPLSVLLPGGTGFGEGAGFG 3234

Db       2598 ---------GGVLSLLGLDE---SPAPGFSCLP-----------------TGF------- 2621

Qy       3235 EGVRVPAVWGGVSLHRAGVTGVRVRVSAVGRGGGREAVSVVVGDEAGVPVASVDRLELRP 3294

Db       2622 ------------------------------------ALTVQL------------------ 2627

Qy       3295 VDMGQLRAVSVSAGRRGSLYAVQWAEVGPVPVCGQAWAWHEDVGESGGGPVPGVVVLRCP 3354

Db       2628 -----LRAL-----RKADVEAPFWA---------------------------------- 2642

Qy       3355 DAGAGGGGGGGGGGVGEVVGGVLGVVQGWLGLERFAGSRLVVVTRGAVVAGPEDGPVDV 3414

Db       2643 ----------------------------------------VTRGGVAL--EDVRVSP 2657

Qy       3415 VGASVWGLVRSAQAEHPDRF-VLLDLDTDTGTDLDTGAGAGWGVDGGRVAAVVA-CGEPQ 3472
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Db       2658 EQALVWGLLRVAGLEHPEFWGGLIDLPSDWDDRL----------GARLAGVLADGGEDQ 2706

Qy       3473 LAVRGERLLAARLKRLESSGDVPAQRSGDTRARRSDVPAQRSGGVPARRSVDVSGREVLP 3532

Db       2707 VAIRRGGVFVRRLERAGASG--------------------AGSV--------------- 2730

Qy       3533 WLSGGSVLVTGGTGVLGAAVARHLAGVCGVRDLLLVSRRGPDAPGAEGLRAELAALGAEV 3592

Db       2731 WRPRGTVLVTGGTGGLGAHVARWLAG-AGAEHVVLTSRRGADAPGAGELRAELEALGARV 2789

Qy       3593 RIVACDVGERREVVRLLEGVPAGCPLTGVVHAAGVLDDATIASLTPERLGTVFAAKVDAA 3652

Db       2790 SIVPCDVADRDAVAGVLAGIGGECPLTAVVHAAGVGEAGDVVEMGLADFAAVLSAKVRGA 2849

Qy       3653 LLLDELTRGMELSAFVLFSSAAGILGSAGQGNYAAANAALDALAYRRRAAGLPGVSLAWG 3712

Db       2850 ANLDELLADSELDAFVMFSSVSGVWGAGGQGAYAAANAYLDALAEQRRARGLVGTAVAWG 2909

Qy       3713 LWEEASGMTGHLAGTDHRRIIRSGLHPMSTPDALALFDAALALDRPVLLPADL---RPAP 3769

Db       2910 PW-AGDGMA---AGETGAQLHRMGLASMEPSAALLALQGALDRDETSLVVADVDWARFAP 2965

Qy       3770 PLP-----PLLQDLLPATRRRTTRTTTTGGADNGAQLHARLAGQTHEQQHTTLLALVRSH 3824

Db       2966 AFTSARRRPLL-DTIDEARAALETTGEQAGTGKPVELTQRLAGLSRKERDDAVLDLVRAE 3024

Qy       3825 IATVLGHTTPDTIPPDRAFRDLGFDSLTAVELRNRLSRTTGLRLPTTLAFDHPNPTTLTH 3884

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Db       3085 HLCAELFP-TETTVDSALAELDRIEQQLSMLTGEARARDRIATRLRALHEKWNSAAEVPT 3143

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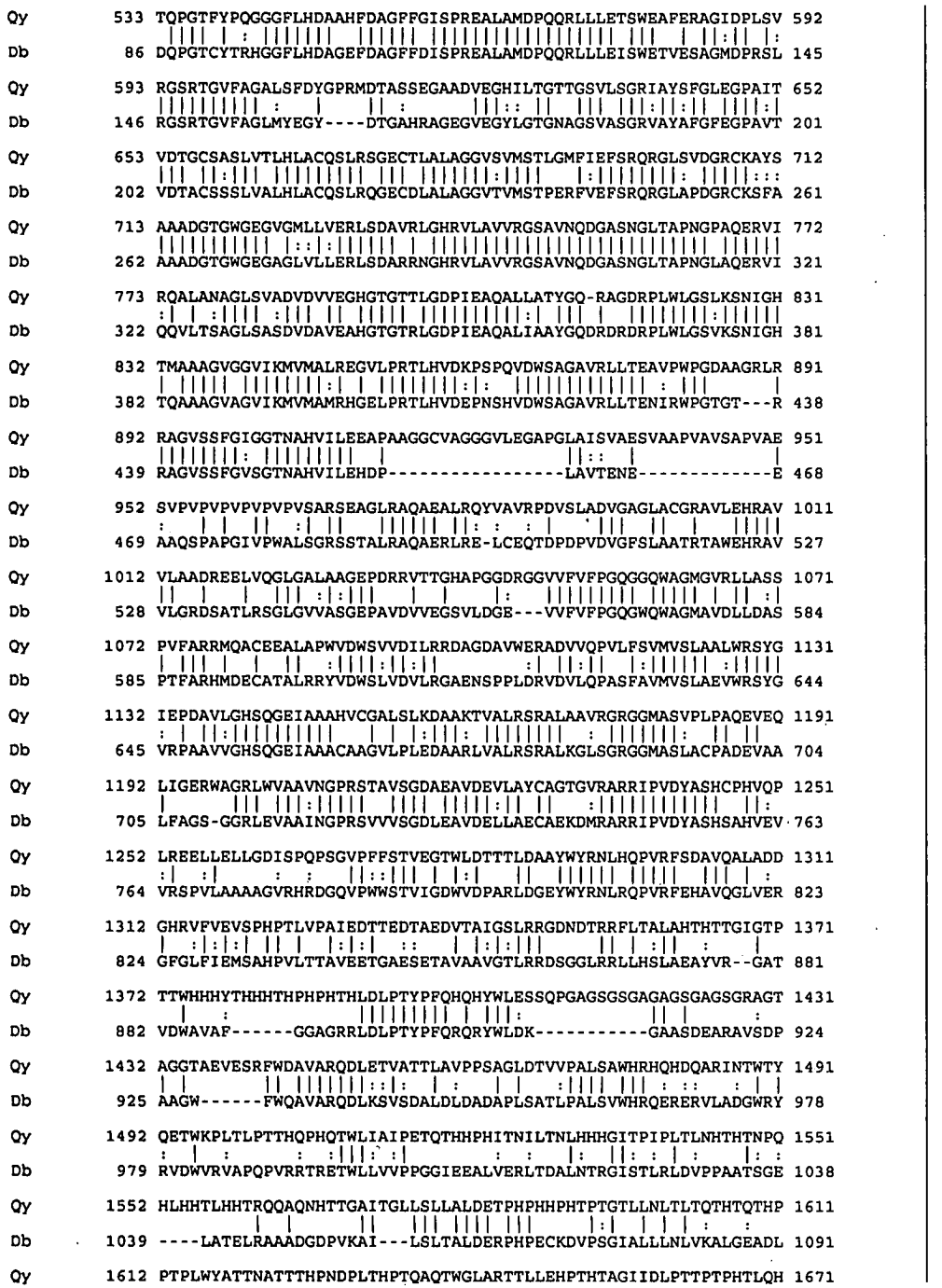
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RESULT 15
US-09-370-700-4
; Sequence 4, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/370,700
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/36987
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 3170
; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-4

 Query Match 32.7%; Score 6804.5; DB 4; Length 3170;
 Best Local Similarity 44.3%; Pred. No. 0;
 Matches 1581; Conservative 380; Mismatches 1115; Indels 493; Gaps 68;

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Qy       3415 VGASVWGLVRSAQAEHPDRF-VLLDLDTDTGTDLDTGAGAGWGVDGGRVAAVVA-CGEPQ 3472

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Db       3025 TAAVLGRDDATALAPSRPFQELGFDSLMAVELRNRLNTATGIQLPASTIFDYPNAESLSR 3084

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Search completed: June 17, 2003, 13:09:23
Job time : 173.193 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 17, 2003, 12:50:57 ; Search time 194.578 Seconds
(without alignments)
2720.102 Million cell updates/sec

Title: US-09-914-286-3
Perfect score: 20829
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20829	100.0	3972	21	AAB23749	S. avermitilis ave
2	20829	100.0	3972	22	AAG65264	Streptomyces averm
3	20817	99.9	3972	22	AAG65268	Streptomyces averm
4	12972	62.3	5532	21	AAB23752	S. avermitilis ave
5	12972	62.3	5532	22	AAG65267	Streptomyces averm
6	11330.5	54.4	6239	21	AAB23750	S. avermitilis ave
7	11330.5	54.4	6239	22	AAG65265	Streptomyces averm
8	8151	39.1	4551	21	AAB18637	Amino acid sequenc
9	8151	39.1	4551	21	AAY67201	Narbonolide syntha
10	8148	39.1	4613	21	AAY77192	S. venezuelae macr
11	8148	39.1	4613	21	AAY77200	S. venezuelae pik
12	8148	39.1	12199	21	AAY77180	S. venezuelae pik
13	7705.5	37.0	4472	18	AAW22601	Tylactone synthase
14	7281.5	35.0	5588	20	AAY39301	SpnE a polyketide
15	7281.5	35.0	5588	22	AAB70969	S. spinosa protein
16	7255	34.8	4545	18	AAW22611	Hybrid srmG/tylG O
17	7221.5	34.7	6797	22	AAB31558	Pimaricin biosynth
18	7190.5	34.5	4881	21	AAB23751	S. avermitilis ave
19	7190.5	34.5	4881	22	AAG65266	Streptomyces averm
20	7098	34.1	5069	19	AAW52846	A. mediterranei ri
21	7089.5	34.0	11096	22	AAE10129	Streptomyces nours
22	7079	34.0	3739	21	AAB18638	Amino acid sequenc
23	7079	34.0	3739	21	AAY67202	Narbonolide syntha
24	7041.5	33.8	3816	21	AAY92708	S. antibioticus 8,
25	7017	33.7	3739	21	AAY77193	S. venezuelae macr
26	7017	33.7	3739	21	AAY77201	S. venezuelae pik
27	6941.5	33.3	4550	18	AAW23716	Platenolide syntha
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31	6804.5	32.7	3170	20	AAY39299	SpnC a polyketide
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37	6555	31.5	3729	18	AAW22603	Tylactone synthase
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43	6344	30.5	4630	18	AAW19629	Streptomyces venez
44	6302.5	30.3	3546	22	AAB82212	Polyketide synthas
45	6299.5	30.2	5087	22	AAU10700	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAB23749
ID AAB23749 standard; Protein; 3972 AA.
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AC AAB23749;
XX
DT 10-JAN-2001 (first entry)
XX
DE S. avermitilis avermectin aglycon synthase protein SEQ ID NO:3.
XX
KW Streptomyces avermitilis; avermectin aglycon synthase; biosynthesis;
KW multifunctional enzyme; polyketide; avermectin; veterinary drug;
KW agrochemical.
XX
OS Streptomyces avermitilis.
XX
PN WO200050605-A1.
XX
PD 31-AUG-2000.
XX
PF 23-FEB-2000; 2000WO-JP01041.
XX
PR 24-FEB-1999; 99JP-0046961.
XX
PA (KITA) KITASATO INST.
XX
PI Omura S, Ikeda H;
XX
DR WPI; 2000-565458/52.
DR N-PSDB; AAA92301.
XX
PT Avermectin aglycone synthase DNA and proteins encoded by all or part of
PT it for the production of avermectin and its derivatives for drug and

PT agrochemical use -
XX
PS Claim 32; Page 203-223; 314pp; Japanese.
XX
CC The present sequence represents an avermectin aglycon synthase protein.
CC Also described are: (1) polypeptides encoded by all or part of the DNA;
CC (2) expression vectors containing the DNA; (3) host cells transformed by
CC the vectors; (4) preparation of the polypeptides by culture of the
CC transformants; (5) preparation of avermectin aglycon or its derivatives
CC by culture of transformed avermectin-producing microorganisms; and (6)
CC oligonucleotides of 5-60 bases in length containing sense or antisense
CC sequences from the avermectin aglycon synthase DNA. The enzymes are
CC useful for the production of modified forms of avermectin and of the
CC intermediates in its biosynthesis, for use as drugs, veterinary drugs
CC and agrochemicals.
XX
SQ Sequence 3972 AA;

Query Match 100.0%; Score 20829; DB 21; Length 3972;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 VQRMDGGEEPRPAAGEVLGVADEADGGVVFVFPGQGPQWPGMGRELLDASDVFRESVRAC 60

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Qy        121 LGEIAAAHVSGGLSLADAARVVTLWSQAQTTLAGTGALVSVAATPDELLPRIAPWTEDNP 180
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Qy        181 ARLAVAAVNGPRSTVVSGAREAVADLVADLTAAQVRTRMIPVDVPAHSPLMYAIEERVVS 240
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Qy        361 VLSARLTALSPTQQQSLLLDLVRAHTMAVLNDDGNERTASDAGPSASFAHLGFDSVMGVE 420
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Qy        481 DPIAIIGMACRFPGGVRSPKDLWELAASGGDAIGPFPTDRGWPTEQRHAQDPTQPGTFYP 540
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Qy        781 LSVADVDVVEGHGTGTTLGDPIEAQALLATYGQRAGDRPLWLGSLKSNIGHTMAAAGVGG 840
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Qy        841 VIKMVMALREGVLPRTLHVDKPSPQVDWSAGAVRLLTEAVPWPGDAAGRLRRAGVSSFGI 900
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Qy        901 GGTNAHVILEEAPAAGGCVAGGGVLEGAPGLAISVAESVAAPVAVSAPVAESVPVPVPVP 960
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Qy       1381 HHTHPHPHTHLDLPTYPFQHQHYWLESSQPGAGSGSGAGAGSGAGSGRAGTAGGTAEVES 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 HHTHPHPHTHLDLPTYPFQHQHYWLESSQPGAGSGSGAGAGSGAGSGRAGTAGGTAEVES 1440

Qy       1441 RFWDAVARQDLETVATTLAVPPSAGLDTVVPALSAWHRHQHDQARINTWTYQETWKPLTL 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 RFWDAVARQDLETVATTLAVPPSAGLDTVVPALSAWHRHQHDQARINTWTYQETWKPLTL 1500

Qy       1501 PTTHQPHQTWLIAIPETQTHHPHITNILTNLHHHGITPIPLTLNHTHTNPQHLHHTLHHT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 PTTHQPHQTWLIAIPETQTHHPHITNILTNLHHHGITPIPLTLNHTHTNPQHLHHTLHHT 1560

Qy       1561 RQQAQNHTTGAITGLLSLLALDETPHPHHPHTPTGTLLNLTLTQTHTQTHPPTPLWYATT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 RQQAQNHTTGAITGLLSLLALDETPHPHHPHTPTGTLLNLTLTQTHTQTHPPTPLWYATT 1620

Qy       1621 NATTTHPNDPLTHPTQAQTWGLARTTLLEHPTHTAGIIDLPTTPTPHTLQHLTQTLTQPH 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 NATTTHPNDPLTHPTQAQTWGLARTTLLEHPTHTAGIIDLPTTPTPHTLQHLTQTLTQPH 1680

Qy       1681 HQTQLAIRTTGTHTRRLTPTTLTPTHQPPTPTPHGTTLITGGTGALATHLTHHLTTHQPT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 HQTQLAIRTTGTHTRRLTPTTLTPTHQPPTPTPHGTTLITGGTGALATHLTHHLTTHQPT 1740

Qy       1741 QHLLLTSRTGPHTPHAQHLTTQLQQKGIHLTITTCDTSNPDQLQQLLNTIPPQHPLTTVI 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 QHLLLTSRTGPHTPHAQHLTTQLQQKGIHLTITTCDTSNPDQLQQLLNTIPPQHPLTTVI 1800

Qy       1801 HTAGILDDATLTNLTPTQLNNVLRAKAHSAHLLHQLTQHTPLTAFVLYSSAAATFGAPGQ 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 HTAGILDDATLTNLTPTQLNNVLRAKAHSAHLLHQLTQHTPLTAFVLYSSAAATFGAPGQ 1860
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